

GenCore version 6.2.1  
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2007, 19:53:50 ; Search time 7245 Seconds  
(without alignments)  
21790.305 Million cell updates/sec

Title: US-09-944-929-82  
Perfect score: 2284  
Sequence: 1 ggggagcatccgctgggtc.....ataaatctttgttactcaa 2284

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :

GenEmbl:\*

1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2284	100.0	2284	2	BD140585	BD140585 Polypepti
2	2284	100.0	2284	2	BD378361	BD378361 SECRETED
3	2284	100.0	2284	2	AR252736	AR252736 Sequence
4	2284	100.0	2284	2	DD028540	DD028540 Secreted
5	2284	100.0	2284	2	DD031661	DD031661 COMPOSITI
6	2284	100.0	2284	2	DD039442	DD039442 Secreted
7	2284	100.0	2284	2	DD249590	DD249590 Secreted
8	2284	100.0	2284	2	AR429104	AR429104 Sequence
9	2284	100.0	2284	2	AR534995	AR534995 Sequence
10	2284	100.0	2284	2	AR691142	AR691142 Sequence
11	2284	100.0	2284	2	AR693626	AR693626 Sequence
12	2284	100.0	2284	2	AR705580	AR705580 Sequence
13	2284	100.0	2284	2	AR706178	AR706178 Sequence
14	2284	100.0	2284	2	AR708652	AR708652 Sequence
15	2284	100.0	2284	2	AR757551	AR757551 Sequence
16	2284	100.0	2284	2	AR759051	AR759051 Sequence
17	2284	100.0	2284	2	AR776365	AR776365 Sequence
18	2284	100.0	2284	2	AR809069	AR809069 Sequence

19	2284	100.0	2284	2	AR809329	AR809329 Sequence
20	2284	100.0	2284	2	AR810275	AR810275 Sequence
21	2284	100.0	2284	2	AR834082	AR834082 Sequence
22	2284	100.0	2284	2	AR860940	AR860940 Sequence
23	2284	100.0	2284	2	AR861403	AR861403 Sequence
24	2284	100.0	2284	2	AR862498	AR862498 Sequence
25	2284	100.0	2284	2	AR869150	AR869150 Sequence
26	2284	100.0	2284	2	AR891893	AR891893 Sequence
27	2284	100.0	2284	2	AR897166	AR897166 Sequence
28	2284	100.0	2284	2	AR902010	AR902010 Sequence
29	2284	100.0	2284	2	AR914822	AR914822 Sequence
30	2284	100.0	2284	2	AX403627	AX403627 Sequence
31	2284	100.0	2284	5	AY358563	AY358563 Homo sapi
32	2245.6	98.3	2297	2	AX883044	AX883044 Sequence
33	2245.6	98.3	2297	2	BD160088	BD160088 Primer fo
34	2245.6	98.3	2297	5	AK023622	AK023622 Homo sapi
35	2218.8	97.1	2333	5	BC032998	BC032998 Homo sapi
36	2045.8	89.6	2221	2	AX876122	AX876122 Sequence
37	2045.8	89.6	2221	2	BD155963	BD155963 Primer fo
38	2045.8	89.6	2221	2	BD447120	BD447120 Method fo
39	2045.8	89.6	2221	2	CQ776818	CQ776818 Sequence
40	2045.8	89.6	2221	5	AK001160	AK001160 Homo sapi
41	1939.4	84.9	2015	2	BD227259	BD227259 Secreted
42	1920.2	84.1	2345	5	AB060888	AB060888 Macaca fa
C 43	1687.2	73.9	188344	12	AC131617	AC131617 Homo sapi
C 44	1684	73.7	144000	5	AC007621	AC007621 Homo sapi
45	751.8	32.9	1907	14	BC120333	BC120333 Bos tauru
46	731.8	32.0	735	2	CQ735543	CQ735543 Sequence
47	690.8	30.2	2288	6	BC039930	BC039930 Mus muscu
48	670.6	29.4	2286	2	BD447563	BD447563 Method fo
49	670.6	29.4	2286	2	CQ777667	CQ777667 Sequence
50	661.8	29.0	805	2	AX869834	AX869834 Sequence
51	661.8	29.0	805	2	BD149896	BD149896 Primer fo
52	583.6	25.6	855	2	AX867136	AX867136 Sequence
53	583.6	25.6	855	2	BD147198	BD147198 Primer fo
54	558.4	24.4	560	2	CS321164	CS321164 Sequence
55	511.8	22.4	517	2	BD458602	BD458602 NOVEL POL
56	499.6	21.9	548	2	BD059530	BD059530 Secreted
57	497.6	21.8	747	7	BV677619	BV677619 MANSCl _7
C 58	470.2	20.6	522	2	AX874802	AX874802 Sequence
C 59	470.2	20.6	522	2	BD154864	BD154864 Primer fo
60	422.6	18.5	196033	12	AC162418	AC162418 Bos tauru
C 61	422.6	18.5	209109	12	AC149660	AC149660 Bos tauru
62	412.6	18.1	188300	6	AC163198	AC163198 Mus muscu
63	412.6	18.1	195236	6	AC126692	AC126692 Mus muscu
64	412.6	18.1	244911	12	AC159128	AC159128 Mus muscu
C 65	395.8	17.3	250782	12	AC128093	AC128093 Rattus no
C 66	391.8	17.2	224870	12	AC129657	AC129657 Rattus no
67	386.8	16.9	422	2	BD071236	BD071236 Secreted
68	326.4	14.3	188344	12	AC131617	AC131617 Homo sapi
C 69	315.6	13.8	424	7	G27546	G27546 human STS S
70	270.2	11.8	295	2	AX894034	AX894034 Sequence
71	270.2	11.8	295	2	BD029567	BD029567 Sequence
72	270.2	11.8	295	2	AR729828	AR729828 Sequence
73	262.2	11.5	1326	6	BC031372	BC031372 Mus muscu
74	245.2	10.7	7617	5	AL391693	AL391693 Human DNA
75	245.2	10.7	178976	12	AL391095	AL391095 Homo sapi
C 76	244.8	10.7	140974	5	AC068533	AC068533 Homo sapi
77	244.6	10.7	198838	12	AC093647	AC093647 Homo sapi
C 78	244.4	10.7	83528	5	AC073254	AC073254 Homo sapi
79	244.4	10.7	150942	5	AC017070	AC017070 Homo sapi
80	244.2	10.7	204588	12	AC183827	AC183827 Pan trogl
C 81	244	10.7	28372	5	DQ667173	DQ667173 Homo sapi
82	244	10.7	237931	5	AC022098	AC022098 Homo sapi
C 83	243.6	10.7	174559	5	AC015720	AC015720 Homo sapi
84	243.6	10.7	175033	5	AL445931	AL445931 Human DNA
85	243.4	10.7	47036	5	AC002104	AC002104 Genomic s
86	243.2	10.6	222222	5	AC188182	AC188182 Pongo pyg
87	243	10.6	150512	5	AC114324	AC114324 Homo sapi
C 88	243	10.6	158989	12	AC068735	AC068735 Homo sapi
C 89	243	10.6	182835	12	AC069569	AC069569 Homo sapi
90	242.8	10.6	63158	12	AC136364	AC136364 Homo sapi
C 91	242.8	10.6	133814	12	AC027550	AC027550 Homo sapi





238	237.6	10.4	189062	12	AP001106	AP001106 Homo sapi
C 239	237.4	10.4	42265	5	AC007136	AC007136 Homo sapi
240	237.4	10.4	42588	5	AC079360	AC079360 Homo sapi
241	237.4	10.4	61546	12	AC127489	AC127489 Homo sapi
242	237.4	10.4	74545	2	AR659565	AR659565 Sequence
C 243	237.4	10.4	113241	5	HUAC002425	AC002425 Homo sapi
244	237.4	10.4	131860	2	AR659689	AR659689 Sequence
C 245	237.4	10.4	137371	5	AC026411	AC026411 Homo sapi
246	237.4	10.4	148290	5	AL359199	AL359199 Human DNA
247	237.4	10.4	150902	12	AC018391	AC018391 Homo sapi
C 248	237.4	10.4	167006	5	AL158159	AL158159 Human chr
249	237.4	10.4	167254	5	CNS05TDS	AL357093 Human DNA
250	237.4	10.4	167390	5	AC007263	AC007263 Homo sapi
C 251	237.4	10.4	170039	12	AC138814	AC138814 Homo sapi
C 252	237.4	10.4	182289	5	AC138894	AC138894 Homo sapi
253	237.4	10.4	184125	12	AC145283	AC145283 Homo sapi
254	237.4	10.4	195588	5	AC020765	AC020765 Homo sapi
255	237.4	10.4	200542	5	CNS01RG3	AL157736 Human chr
256	237.4	10.4	202478	5	AC006560	AC006560 Homo sapi
257	237.4	10.4	208932	12	AC137487	AC137487 Homo sapi
258	237.4	10.4	239008	12	AC022460	AC022460 Homo sapi
C 259	237.2	10.4	45746	5	AC005619	AC005619 Homo sapi
C 260	237.2	10.4	99545	5	AC026115	AC026115 Homo sapi
261	237.2	10.4	120883	12	CT009524	CT009524 Homo sapi
C 262	237.2	10.4	151834	5	AC005399	AC005399 Homo sapi
C 263	237.2	10.4	156507	12	AC036184	AC036184 Homo sapi
264	237.2	10.4	161940	12	AC079289	AC079289 Homo sapi
265	237.2	10.4	207818	5	AC019206	AC019206 Homo sapi
C 266	237.2	10.4	260409	5	AC004019	AC004019 Homo sapi
C 267	237	10.4	601	2	AR660594	AR660594 Sequence
C 268	237	10.4	601	2	AR664602	AR664602 Sequence
269	237	10.4	41087	5	HSJ659F15	AL096791 Human DNA
C 270	237	10.4	45670	5	AL391094	AL391094 Human DNA
C 271	237	10.4	96376	12	AC007626	AC007626 Homo sapi
272	237	10.4	100000	5	AP000065	AP000065 Homo sapi
273	237	10.4	103699	5	AC034305	AC034305 Homo sapi
274	237	10.4	124281	5	AL136101	AL136101 Human DNA
275	237	10.4	143039	5	AC016559	AC016559 Homo sapi
C 276	237	10.4	158527	5	AL356575	AL356575 Human DNA
277	237	10.4	173452	5	AC003013	AC003013 Human PAC
278	237	10.4	179789	5	AC069543	AC069543 Homo sapi
279	236.8	10.4	718	7	BV561102	BV561102 qfy86g08.
C 280	236.8	10.4	152037	2	CS350835	CS350835 Sequence
C 281	236.8	10.4	152037	5	HS167A19	AL031427 Human DNA
C 282	236.8	10.4	152937	12	AC024350	AC024350 Homo sapi
283	236.8	10.4	167099	5	AC110079	AC110079 Homo sapi
284	236.8	10.4	184598	5	AL139406	AL139406 Human DNA
285	236.6	10.4	44890	5	AC005778	AC005778 Homo sapi
286	236.6	10.4	79319	5	AL512274	AL512274 Human DNA
C 287	236.6	10.4	158591	5	AC010188	AC010188 Homo sapi
288	236.6	10.4	170388	12	AC027750	AC027750 Homo sapi
289	236.6	10.4	171193	5	AC183807	AC183807 Pan trogl
290	236.6	10.4	175833	5	AC046135	AC046135 Homo sapi
291	236.6	10.4	177623	12	AC067825	AC067825 Homo sapi
292	236.6	10.4	182632	5	AC007282	AC007282 Homo sapi
C 293	236.6	10.4	182956	12	AC068297	AC068297 Homo sapi
294	236.6	10.4	208237	5	AC182586	AC182586 Pan trogl
295	236.4	10.4	579	2	AX871164	AX871164 Sequence
C 296	236.4	10.4	579	2	BD151226	BD151226 Primer fo
C 297	236.4	10.4	1555	2	AX878552	AX878552 Sequence
C 298	236.4	10.4	1555	2	BD157296	BD157296 Primer fo
C 299	236.4	10.4	1555	5	AK021652	AK021652 Homo sapi
C 300	236.4	10.4	30826	5	AL807743	AL807743 Human DNA
C 301	236.4	10.4	41257	5	AC005330	AC005330 Homo sapi
302	236.4	10.4	56935	5	AL591802	AL591802 Human DNA
303	236.4	10.4	110000	12	AC146444_0	AC146444 Pan trogl
304	236.4	10.4	110000	12	AC146444_1	Continuation (2 of
305	236.4	10.4	118695	5	HSJ672M15	AL049643 Human DNA
306	236.4	10.4	154902	5	AC005799	AC005799 Homo sapi
C 307	236.4	10.4	172476	5	AC007736	AC007736 Homo sapi
C 308	236.4	10.4	191681	5	AC079210	AC079210 Homo sapi
309	236.4	10.4	215960	12	AC144881	AC144881 Gorilla g
310	236.4	10.4	218733	5	AC091809	AC091809 Homo sapi

311	236.4	10.4	218802	12	AC183640	AC183640 Pan trogl
C 312	236.4	10.4	233062	5	AC100787	AC100787 Homo sapi
313	236.2	10.3	701	7	BV588739	BV588739 G591P6361
314	236.2	10.3	78065	5	AC005355	AC005355 Homo sapi
315	236.2	10.3	89421	5	AP001965	AP001965 Homo sapi
C 316	236.2	10.3	130381	5	AC002402	AC002402 Human Chr
317	236.2	10.3	139632	5	AC145334	AC145334 Pan trogl
C 318	236.2	10.3	157393	12	AC036212	AC036212 Homo sapi
C 319	236.2	10.3	162696	12	AC090417	AC090417 Homo sapi
320	236.2	10.3	164229	5	AC092671	AC092671 Homo sapi
321	236.2	10.3	165536	5	AC093600	AC093600 Homo sapi
C 322	236.2	10.3	180179	12	AC018881	AC018881 Homo sapi
C 323	236.2	10.3	180766	5	AC090691	AC090691 Homo sapi
C 324	236.2	10.3	182303	5	AL356750	AL356750 Human DNA
C 325	236.2	10.3	188712	5	AC016582	AC016582 Homo sapi
326	236.2	10.3	189357	12	AC160025	AC160025 Pan trogl
327	236.2	10.3	197770	12	BX322632	BX322632 Homo sapi
328	236.2	10.3	208185	12	AC009105	AC009105 Homo sapi
C 329	236	10.3	57084	5	AL158813	AL158813 Human DNA
C 330	236	10.3	97114	5	AL356389	AL356389 Human DNA
331	236	10.3	103146	5	HS187N21	Z98036 Human DNA s
C 332	236	10.3	121068	5	AC015876	AC015876 Homo sapi
333	236	10.3	129266	5	AL731567	AL731567 Human DNA
C 334	236	10.3	146500	5	AC004453	AC004453 Homo sapi
335	236	10.3	151828	5	AL354740	AL354740 Human DNA
336	236	10.3	167512	12	AC015708	AC015708 Homo sapi
337	236	10.3	168174	2	AR584462	AR584462 Sequence
338	236	10.3	168273	2	AR584403	AR584403 Sequence
339	236	10.3	168898	12	AC026974	AC026974 Homo sapi
C 340	236	10.3	170790	12	AC068238	AC068238 Homo sapi
C 341	236	10.3	173341	12	AC021954	AC021954 Homo sapi
C 342	236	10.3	175382	5	AC112135	AC112135 Homo sapi
C 343	236	10.3	178026	12	AC146438	AC146438 Pan trogl
C 344	236	10.3	187795	12	AC025405	AC025405 Homo sapi
C 345	236	10.3	188296	5	AC022324	AC022324 Homo sapi
C 346	236	10.3	188470	12	AC093005	AC093005 Homo sapi
347	235.8	10.3	1415	5	BC037814	BC037814 Homo sapi
348	235.8	10.3	76170	5	AC108512	AC108512 Homo sapi
C 349	235.8	10.3	120955	5	HUAC002310	AC002310 Human Chr
C 350	235.8	10.3	127334	5	AC109579	AC109579 Homo sapi
351	235.8	10.3	127686	12	AL591683	AL591683 Homo sapi
C 352	235.8	10.3	140773	12	AC023308	AC023308 Homo sapi
C 353	235.8	10.3	152355	5	AC005668	AC005668 Homo sapi
C 354	235.8	10.3	168606	5	AC109133	AC109133 Homo sapi
C 355	235.8	10.3	169934	12	AC135837	AC135837 Papio anu
356	235.8	10.3	174021	5	AL358612	AL358612 Human DNA
357	235.8	10.3	177147	5	AC007539	AC007539 Homo sapi
358	235.8	10.3	191111	5	AC006080	AC006080 Homo sapi
359	235.8	10.3	194730	5	AC136967	AC136967 Papio anu
360	235.6	10.3	42265	5	AC007136	AC007136 Homo sapi
361	235.6	10.3	75224	5	AC134510	AC134510 Homo sapi
C 362	235.6	10.3	88848	5	AC107377	AC107377 Homo sapi
363	235.6	10.3	124949	5	AL358794	AL358794 Human DNA
364	235.6	10.3	128871	5	AL157838	AL157838 Human DNA
C 365	235.6	10.3	142707	5	HSJ279A18	AL049696 Human DNA
366	235.6	10.3	150136	5	AC187992	AC187992 Pan trogl
367	235.6	10.3	159875	5	AC148692	AC148692 Macaca mu
368	235.6	10.3	163417	5	AC183550	AC183550 Pan trogl
C 369	235.6	10.3	164795	5	AP002518	AP002518 Homo sapi
370	235.6	10.3	176267	5	AC148660	AC148660 Macaca mu
C 371	235.6	10.3	179759	12	AC132868	AC132868 Homo sapi
C 372	235.6	10.3	181938	12	AP001149	AP001149 Homo sapi
373	235.6	10.3	183032	12	AC143326	AC143326 Homo sapi
374	235.6	10.3	186687	5	AC134943	AC134943 Homo sapi
375	235.6	10.3	189143	12	AC142077	AC142077 Homo sapi
C 376	235.6	10.3	191280	12	AC087389	AC087389 Homo sapi
C 377	235.6	10.3	206192	5	AL133173	AL133173 Human DNA
378	235.4	10.3	18968	2	CQ413230	CQ413230 Sequence
379	235.4	10.3	83557	5	AL138735	AL138735 Human DNA
C 380	235.4	10.3	100608	2	CQ869961	CQ869961 Sequence
C 381	235.4	10.3	106585	5	AL160392	AL160392 Human DNA
382	235.4	10.3	122903	5	AC005833	AC005833 Homo sapi
C 383	235.4	10.3	135404	5	AC084024	AC084024 Homo sapi

384	235.4	10.3	153640	5	AL445669	AL445669 Human DNA
385	235.4	10.3	187275	5	AL732366	AL732366 Human DNA
C 386	235.4	10.3	187960	5	AP000866	AP000866 Homo sapi
C 387	235.4	10.3	202889	5	AC010552	AC010552 Homo sapi
388	235.4	10.3	205715	12	AC007604	AC007604 Homo sapi
C 389	235.4	10.3	214426	5	DQ431198	DQ431198 Homo sapi
C 390	235.4	10.3	214776	12	AC165191	AC165191 Homo sapi
C 391	235.2	10.3	757	7	BV662024	BV662024 S217P6184
392	235.2	10.3	916	7	BV572142	BV572142 GS91P6326
393	235.2	10.3	37680	12	AL359985	AL359985 Homo sapi
394	235.2	10.3	43452	5	AC007901	AC007901 Homo sapi
395	235.2	10.3	55034	5	AC021072	AC021072 Homo sapi
C 396	235.2	10.3	110000	12	AC092950	AC092950 Homo sapi
397	235.2	10.3	117711	5	AP000662	AP000662 Homo sapi
398	235.2	10.3	144578	5	AC092948	AC092948 Homo sapi
C 399	235.2	10.3	156842	12	AC026284	AC026284 Homo sapi
C 400	235.2	10.3	162996	5	AC006441	AC006441 Homo sapi
401	235.2	10.3	164297	12	AC012138	AC012138 Homo sapi
402	235.2	10.3	176206	5	AC009967	AC009967 Homo sapi
C 403	235.2	10.3	178059	5	AC144411	AC144411 Homo sapi
404	235.2	10.3	179880	12	AC188380	AC188380 Pan trogl
405	235.2	10.3	182341	12	AC073337	AC073337 Homo sapi
C 406	235.2	10.3	184841	12	AC129486	AC129486 Homo sapi
C 407	235.2	10.3	185980	5	AC090610	AC090610 Homo sapi
408	235.2	10.3	195913	12	AC022988	AC022988 Homo sapi
409	235.2	10.3	197782	5	AC012377	AC012377 Homo sapi
C 410	235.2	10.3	199992	12	AC021522	AC021522 Homo sapi
C 411	235.2	10.3	217921	5	AC019163	AC019163 Homo sapi
C 412	235.2	10.3	238417	2	CQ870127	CQ870127 Sequence
C 413	235	10.3	38173	5	AC093235	AC093235 Homo sapi
C 414	235	10.3	39967	5	AL136983	AL136983 Human DNA
415	235	10.3	62825	5	AL136960	AL136960 Human DNA
C 416	235	10.3	66144	12	AC031991	AC031991 Homo sapi
C 417	235	10.3	82806	5	AC007111	AC007111 Homo sapi
418	235	10.3	114631	5	AC084876	AC084876 Homo sapi
C 419	235	10.3	117899	5	AC016590	AC016590 Homo sapi
C 420	235	10.3	135173	5	AC008806	AC008806 Homo sapi
421	235	10.3	152103	12	AC012130	AC012130 Homo sapi
422	235	10.3	158456	5	AC092198	AC092198 Homo sapi
423	235	10.3	163924	12	AL162592	AL162592 Homo sapi
424	235	10.3	168113	5	BX664608	BX664608 Human DNA
425	235	10.3	168117	12	BX664620	BX664620 Homo sapi
426	235	10.3	171267	12	AC040979	AC040979 Homo sapi
C 427	235	10.3	175067	12	AC040898	AC040898 Homo sapi
428	235	10.3	179350	5	AC026351	AC026351 Homo sapi
429	235	10.3	180388	5	HUMRETLAS	LL1910 Human retin
430	235	10.3	180782	5	AF551763	AF551763 Homo sapi
431	235	10.3	186609	5	AC083872	AC083872 Homo sapi
432	235	10.3	191935	5	AL356128	AL356128 Human DNA
C 433	235	10.3	199759	5	AC009065	AC009065 Homo sapi
434	235	10.3	200822	5	AL591806	AL591806 Human DNA
C 435	235	10.3	206361	5	AC159216	AC159216 Pan trogl
C 436	235	10.3	216765	12	AC169000	AC169000 Colobus g
C 437	235	10.3	220353	12	AC168999	AC168999 Colobus g
C 438	235	10.3	239434	12	AC012171	AC012171 Homo sapi
439	234.8	10.3	765	7	BV676217	BV676217 S217P6055
C 440	234.8	10.3	20890	5	HSU29895	U29895 Human 4-hyd
C 441	234.8	10.3	39233	5	AC005626	AC005626 Homo sapi
C 442	234.8	10.3	39801	5	AC005955	AC005955 Homo sapi
C 443	234.8	10.3	82732	5	AL512347	AL512347 Human DNA
444	234.8	10.3	97065	12	AP000768	AP000768 Homo sapi
C 445	234.8	10.3	117297	5	AL672040	AL672040 Human DNA
446	234.8	10.3	131906	12	AC083983	AC083983 Homo sapi
447	234.8	10.3	137411	5	AC092066	AC092066 Homo sapi
448	234.8	10.3	146181	5	AP001269	AP001269 Homo sapi
C 449	234.8	10.3	151828	5	AL354740	AL354740 Human DNA
450	234.8	10.3	162413	5	AC091530	AC091530 Papio anu
451	234.8	10.3	163144	12	AL365399	AL365399 Homo sapi
C 452	234.8	10.3	173126	5	AC005988	AC005988 Homo sapi
C 453	234.8	10.3	179993	12	AC015879	AC015879 Homo sapi
454	234.8	10.3	181102	5	AC090058	AC090058 Homo sapi
C 455	234.8	10.3	220120	5	AC145906	AC145906 Pan trogl
C 456	234.8	10.3	262483	5	CT005239	CT005239 Pan trogl
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AL356747	Human DNA					
AC110011	Homo sapi					
AP000621	Homo sapi					
AP000436	Homo sapi					
AC092326	Homo sapi					
AC025426	Homo sapi					
AC055810	Homo sapi					
AL450311	Human DNA					
AC136431	Homo sapi					
AL136178	Human DNA					
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AC010373	Homo sapi					
AC138962	Homo sapi					
AC141623	Homo sapi					
AC141075	Homo sapi					
AC136441	Homo sapi					
AC140895	Homo sapi					
AC138897	Homo sapi					
AC140896	Homo sapi					
AC146081	Pan trogl					
AC140909	Homo sapi					
AC136434	Homo sapi					
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AC140875	Homo sapi					
AC126760	Homo sapi					
AC021159	Homo sapi					
AC140522	Homo sapi					
AL359184	Human DNA					
AC160860	Homo sapi					
AC154091	Homo sapi					
AC005808	Homo sapi					
AL124292	Homo sapi					
AL391415	Human DNA					
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AP000680	Homo sapi					
AC170757	Macaca mu					
AC108861	Homo sapi					
AL391280	Human DNA					
AC104472	Homo sapi					
AC013403	Homo sapi					
AC024973	Homo sapi					
AC171635	Rhesus Ma					
AC112128	Homo sapi					
AC021695	Homo sapi					
AC126773	Homo sapi					
AL596304	Homo sapi					
AX590980	Sequence					
BV590452	GS91P6414					
CS373942	Sequence					
AC012333	Homo sapi					
AC027746	Homo sapi					
AL033528	Human DNA					
AL109825	Human DNA					
AL353998	Homo sapi					
BX470102	Human DNA					
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AC027319	Homo sapi					
AL162832	Human chr					
AC096632	Homo sapi					
AC068818	Homo sapi					
AC015734	Homo sapi					
AC129624	Homo sapi					
AC002350	Homo sapi					
AC166591	Pan trogl					
AC097640	Homo sapi					
BX855602	Human DNA					
AL355100	Homo sapi					
AC135178	Homo sapi					
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AC022489	Homo sapi					

C 530	234.2	10.3	196380	5	AC188102	AC188102 Pongo pyg
C 531	234.2	10.3	197605	5	AC096770	AC096770 Homo sapi
C 532	234.2	10.3	200452	5	AC015804	AC015804 Homo sapi
C 533	234.2	10.3	227737	5	AC160055	AC160055 Pan trogl
C 534	234	10.2	679	7	BV556693	BV556693 S222P6127
C 535	234	10.2	778	7	BV528567	BV528567 G591P6142
C 536	234	10.2	885	7	BV524987	BV524987 G591P6077
C 537	234	10.2	30098	12	BX294170	BX294170 Homo sapi
C 538	234	10.2	40847	5	AL731696	AL731696 Human DNA
C 539	234	10.2	42107	5	AC004409	AC004409 Homo Sapi
C 540	234	10.2	54146	5	BX248244	BX248244 Human DNA
C 541	234	10.2	91025	5	AL359270	AL359270 Human DNA
C 542	234	10.2	99109	5	AL805934	AL805934 Human DNA
C 543	234	10.2	107226	5	AC010618	AC010618 Homo sapi
C 544	234	10.2	110773	12	BX005259	BX005259 Homo sapi
C 545	234	10.2	110820	5	AC105020	AC105020 Homo sapi
C 546	234	10.2	126347	5	HS58A9	AL031285 Human DNA
C 547	234	10.2	126625	5	AY028079	AY028079 Homo sapi
C 548	234	10.2	135173	5	AC008806	AC008806 Homo sapi
C 549	234	10.2	143389	2	CS200149	CS200149 Sequence
C 550	234	10.2	150314	2	CS200143	CS200143 Sequence
C 551	234	10.2	152714	5	BS000156	BS000156 Pan trogl
C 552	234	10.2	152825	5	BS000164	BS000164 Pan trogl
C 553	234	10.2	158676	12	AC133921	AC133921 Homo sapi
C 554	234	10.2	158755	5	AP004291	AP004291 Homo sapi
C 555	234	10.2	163893	12	AC137497	AC137497 Homo sapi
C 556	234	10.2	176051	12	AC156747	AC156747 Macaca mu
C 557	234	10.2	183689	12	AC146129	AC146129 Pan trogl
C 558	234	10.2	191827	5	AC093904	AC093904 Homo sapi
C 559	234	10.2	194602	5	AC113188	AC113188 Homo sapi
C 560	234	10.2	200899	12	AC141291	AC141291 Homo sapi
C 561	234	10.2	204622	5	AC157524	AC157524 Pan trogl
C 562	234	10.2	220895	2	CQ861455	CQ861455 Sequence
C 563	234	10.2	220895	5	HS250D10	Z99716 Human DNA s
C 564	234	10.2	230038	12	AC187615	AC187615 Pan trogl
C 565	234	10.2	298345	12	AC161616	AC161616 Pan trogl
C 566	233.8	10.2	751	7	BV487437	BV487437 S216P6520
C 567	233.8	10.2	9552	5	AY764184	AY764184 Homo sapi
C 568	233.8	10.2	71903	5	AL607035	AL607035 Human DNA
C 569	233.8	10.2	74054	5	AC064824	AC064824 Homo sapi
C 570	233.8	10.2	77192	12	AL713858_3	Continuation (4 of
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C 572	233.8	10.2	90940	5	AC104052	AC104052 Homo sapi
C 573	233.8	10.2	94651	12	AL389882	AL389882 Homo sapi
C 574	233.8	10.2	107603	5	HS934G17	AL021155 Human DNA
C 575	233.8	10.2	110000	12	AL831785_0	AL831785 Homo sapi
C 576	233.8	10.2	110837	5	AC092455	AC092455 Homo sapi
C 577	233.8	10.2	118616	5	AL157706	AL157706 Human DNA
C 578	233.8	10.2	140915	12	AC022361	AC022361 Homo sapi
C 579	233.8	10.2	143697	12	AL358572	AL358572 Homo sapi
C 580	233.8	10.2	151382	5	AC112221	AC112221 Homo sapi
C 581	233.8	10.2	154080	12	AC024416	AC024416 Homo sapi
C 582	233.8	10.2	156826	12	AC055767	AC055767 Homo sapi
C 583	233.8	10.2	159273	12	AC025001	AC025001 Homo sapi
C 584	233.8	10.2	160410	5	AC092324	AC092324 Homo sapi
C 585	233.8	10.2	161946	5	AC094014	AC094014 Papio anu
C 586	233.8	10.2	163384	5	AC009180	AC009180 Homo sapi
C 587	233.8	10.2	170787	5	AC121247	AC121247 Homo sapi
C 588	233.8	10.2	172238	5	AC090942	AC090942 Homo sapi
C 589	233.8	10.2	179938	5	AC185347	AC185347 Pan trogl
C 590	233.8	10.2	182171	5	AC066589	AC066589 Homo sapi
C 591	233.8	10.2	185146	12	AC104311	AC104311 Homo sapi
C 592	233.8	10.2	185232	12	AL611948	AL611948 Homo sapi
C 593	233.8	10.2	192465	5	AC187989	AC187989 Pan trogl
C 594	233.8	10.2	194844	5	AC160656	AC160656 Pan trogl
C 595	233.8	10.2	205130	12	AC105425	AC105425 Homo sapi
C 596	233.8	10.2	208989	5	AC027124	AC027124 Homo sapi
C 597	233.6	10.2	796	7	BV589028	BV589028 G591P6377
C 598	233.6	10.2	809	7	BV646799	BV646799 S217P6025
C 599	233.6	10.2	39470	5	AC005390	AC005390 Homo sapi
C 600	233.6	10.2	69663	12	AC090747	AC090747 Homo sapi
C 601	233.6	10.2	76326	5	AC105762	AC105762 Homo sapi
C 602	233.6	10.2	87758	5	AC068768	AC068768 Homo sapi

C 603	233.6	10.2	91830	5	AL365436	AL365436 Human DNA
C 604	233.6	10.2	117000	5	AC069222	AC069222 Homo sapi
C 605	233.6	10.2	126491	5	AL589764	AL589764 Human DNA
C 606	233.6	10.2	144041	12	AP001766	AP001766 Homo sapi
C 607	233.6	10.2	157358	5	AC009163	AC009163 Homo sapi
C 608	233.6	10.2	160552	2	AR635088	AR635088 Sequence
C 609	233.6	10.2	160552	2	AR897366	AR897366 Sequence
C 610	233.6	10.2	166992	12	AC022883	AC022883 Homo sapi
C 611	233.6	10.2	172744	5	AC183617	AC183617 Pan trogl
C 612	233.6	10.2	180080	5	CT737307	CT737307 CH251-89L
C 613	233.6	10.2	183263	5	AC092685	AC092685 Homo sapi
C 614	233.6	10.2	186168	12	AL391279	AL391279 Homo sapi
C 615	233.6	10.2	194447	5	AC150208	AC150208 Pan trogl
C 616	233.4	10.2	41461	5	AC010646	AC010646 Homo sapi
C 617	233.4	10.2	66992	12	AC091166	AC091166 Homo sapi
C 618	233.4	10.2	76481	5	AC096511	AC096511 Homo sapi
C 619	233.4	10.2	86973	5	AC079402	AC079402 Homo sapi
C 620	233.4	10.2	110000	12	BX322548_1	Continuation (2 of
C 621	233.4	10.2	110000	12	BX322548_2	Continuation (3 of
C 622	233.4	10.2	128800	5	AB053170	AB053170 Homo sapi
C 623	233.4	10.2	129711	5	AC110768	AC110768 Homo sapi
C 624	233.4	10.2	133568	5	HS16915	Z93015 Human DNA s
C 625	233.4	10.2	135762	12	AC139785	AC139785 Homo sapi
C 626	233.4	10.2	149061	5	AC098805	AC098805 Homo sapi
C 627	233.4	10.2	149578	12	AC139820	AC139820 Homo sapi
C 628	233.4	10.2	152336	12	AC009594	AC009594 Homo sapi
C 629	233.4	10.2	154295	5	AC087833	AC087833 Papio anu
C 630	233.4	10.2	155127	5	AC008532	AC008532 Homo sapi
C 631	233.4	10.2	157981	5	AC005184	AC005184 Homo sapi
C 632	233.4	10.2	158083	5	AL162493	AL162493 Human DNA
C 633	233.4	10.2	159707	5	AC013403	AC013403 Homo sapi
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C 635	233.4	10.2	161608	12	AC140835	AC140835 Homo sapi
C 636	233.4	10.2	162750	5	AL355365	AL355365 Human DNA
C 637	233.4	10.2	165004	12	AC139465	AC139465 Homo sapi
C 638	233.4	10.2	165868	5	AC010651	AC010651 Homo sapi
C 639	233.4	10.2	170861	12	AC025698	AC025698 Homo sapi
C 640	233.4	10.2	172807	12	AC136617	AC136617 Homo sapi
C 641	233.4	10.2	176144	12	AC140872	AC140872 Homo sapi
C 642	233.4	10.2	177908	5	AC091817	AC091817 Homo sapi
C 643	233.4	10.2	177963	12	AC139461	AC139461 Homo sapi
C 644	233.4	10.2	180463	5	AC018978	AC018978 Homo sapi
C 645	233.4	10.2	180482	5	AC183296	AC183296 Pan trogl
C 646	233.4	10.2	180551	5	HUAC004158	AC004158 Homo sapi
C 647	233.4	10.2	181780	5	AC185245	AC185245 Pan trogl
C 648	233.4	10.2	182012	5	AL359846	AL359846 Human DNA
C 649	233.4	10.2	183430	5	AL391827	AL391827 Human DNA
C 650	233.4	10.2	184125	5	AC160650	AC160650 Pan trogl
C 651	233.4	10.2	185047	5	AC025289	AC025289 Homo sapi
C 652	233.4	10.2	185047	5	AC026472	AC026472 Homo sapi
C 653	233.4	10.2	188868	5	AC023232	AC023232 Homo sapi
C 654	233.4	10.2	194779	5	AC138811	AC138811 Homo sapi
C 655	233.4	10.2	196048	12	AC139469	AC139469 Homo sapi
C 656	233.4	10.2	202847	12	AC140713	AC140713 Homo sapi
C 657	233.4	10.2	203759	12	AC141601	AC141601 Homo sapi
C 658	233.4	10.2	206769	5	AC186385	AC186385 Pan trogl
C 659	233.4	10.2	220283	5	AC021443	AC021443 Homo sapi
C 660	233.4	10.2	232369	12	AC139825	AC139825 Homo sapi
C 661	233.4	10.2	288323	12	AC140887	AC140887 Homo sapi
C 662	233.2	10.2	778	7	BV566542	BV566542 rll38b09.
C 663	233.2	10.2	1701	2	AX033917	AX033917 Sequence
C 664	233.2	10.2	3347	5	HSMB04927	AL833614 Homo sapi
C 665	233.2	10.2	56458	5	HS342B11	AL008719 Human DNA
C 666	233.2	10.2	59241	5	AC006388	AC006388 Homo sapi
C 667	233.2	10.2	83039	5	AL137074	AL137074 Human DNA
C 668	233.2	10.2	126238	5	AC138472	AC138472 Homo sapi
C 669	233.2	10.2	126679	5	HSDJ534B8	AL121905 Human DNA
C 670	233.2	10.2	128444	12	AF214634	AF214634 Homo sapi
C 671	233.2	10.2	133021	12	CT476828	CT476828 Homo sapi
C 672	233.2	10.2	141612	5	AC079093	AC079093 Homo sapi
C 673	233.2	10.2	142790	5	AL445685	AL445685 Human DNA
C 674	233.2	10.2	151834	5	AP004195	AP004195 Homo sapi
C 675	233.2	10.2	152757	5	AC018475	AC018475 Homo sapi



c 676	233.2	10.2	157091	12	AC027772	AC027772 Homo sapi
c 677	233.2	10.2	158481	5	AL158063	AL158063 Human DNA
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c 679	233.2	10.2	167294	12	AC013814	AC013814 Homo sapi
c 680	233.2	10.2	170127	12	AC171648	AC171648 Macaca mu
c 681	233.2	10.2	173411	5	AC092754	AC092754 Homo sapi
c 682	233.2	10.2	175263	5	AC023102	AC023102 Homo sapi
c 683	233.2	10.2	180306	12	AC169845	AC169845 Macaca mu
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c 688	233.2	10.2	188788	5	AP002380	AP002380 Homo sapi
c 689	233.2	10.2	197136	5	AC146149	AC146149 Pan trogl
c 690	233.2	10.2	199730	12	AC083940	AC083940 Homo sapi
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c 692	233.2	10.2	218644	5	AC147079	AC147079 Pan trogl
c 693	233.2	10.2	218724	12	AC025889	AC025889 Homo sapi
c 694	233.2	10.2	229379	5	AC010746	AC010746 Homo sapi
c 695	233.2	10.2	280473	12	AC068823	AC068823 Homo sapi
c 696	233.2	10.2	328866	12	AC107203	AC107203 Homo sapi
c 697	233	10.2	662	7	BV584473	BV584473 G591P6286
c 698	233	10.2	90577	5	AL135912	AL135912 Human DNA
c 699	233	10.2	96717	5	AL359182	AL359182 Human DNA
c 700	233	10.2	102822	5	AC104407	AC104407 Homo sapi
c 701	233	10.2	111990	5	AL360294	AL360294 Human DNA
c 702	233	10.2	122552	5	CNS01DRS	AL118555 Human chr
c 703	233	10.2	132720	5	AC093269	AC093269 Homo sapi
c 704	233	10.2	151660	12	AC027450	AC027450 Homo sapi
c 705	233	10.2	154102	12	AC183603	AC183603 Pan trogl
c 706	233	10.2	154827	5	AL592221	AL592221 Human DNA
c 707	233	10.2	156754	5	AC021055	AC021055 Homo sapi
c 708	233	10.2	156777	12	AC114972	AC114972 Homo sapi
c 709	233	10.2	157777	12	AC183683	AC183683 Pan trogl
c 710	233	10.2	159504	5	AC104436	AC104436 Homo sapi
c 711	233	10.2	164721	12	AC013657	AC013657 Homo sapi
c 712	233	10.2	171617	12	AC016053	AC016053 Homo sapi
c 713	233	10.2	172010	5	AC083876	AC083876 Homo sapi
c 714	233	10.2	175064	12	AC012230	AC012230 Homo sapi
c 715	233	10.2	180991	5	AC160056	AC160056 Pan trogl
c 716	233	10.2	181074	12	AC146626	AC146626 Papio anu
c 717	233	10.2	181673	5	AC148825	AC148825 Pan trogl
c 718	233	10.2	184730	12	AC146676	AC146676 Papio anu
c 719	233	10.2	189694	12	AC187742	AC187742 Pan trogl
c 720	233	10.2	229612	12	AL161647	AL161647 Homo sapi
c 721	233	10.2	251039	12	AL592230	AL592230 Homo sapi
c 722	232.8	10.2	9846	5	AL359506	AL359506 Human DNA
c 723	232.8	10.2	55442	5	BX119919	BX119919 Human DNA
c 724	232.8	10.2	61834	5	DQ314871	DQ314871 Homo sapi
c 725	232.8	10.2	79470	12	AL391000	AL391000 Homo sapi
c 726	232.8	10.2	83111	5	HS125I3	AL0333528 Human DNA
c 727	232.8	10.2	140292	5	CNS01DU8	AL133223 Human chr
c 728	232.8	10.2	144260	5	AC006299	AC006299 Homo sapi
c 729	232.8	10.2	145937	12	AL355600	AL355600 Homo sapi
c 730	232.8	10.2	146961	12	AL355525	AL355525 Homo sapi
c 731	232.8	10.2	150290	5	HS509L4	Z99496 Human DNA s
c 732	232.8	10.2	158466	5	AP004292	AP004292 Homo sapi
c 733	232.8	10.2	159423	5	AC008429	AC008429 Homo sapi
c 734	232.8	10.2	160151	5	AC098595	AC098595 Homo sapi
c 735	232.8	10.2	160237	12	AC149093	AC149093 Pan trogl
c 736	232.8	10.2	160815	12	AP001895	AP001895 Homo sapi
c 737	232.8	10.2	163372	12	AC087744	AC087744 Homo sapi
c 738	232.8	10.2	166336	5	AL445467	AL445467 Human DNA
c 739	232.8	10.2	172004	5	AL158032	AL158032 Human DNA
c 740	232.8	10.2	174044	5	AC183799	AC183799 Pan trogl
c 741	232.8	10.2	176278	5	AC024028	AC024028 Homo sapi
c 742	232.8	10.2	176709	5	AC011737	AC011737 Homo sapi
c 743	232.8	10.2	179396	12	AC017056	AC017056 Homo sapi
c 744	232.8	10.2	184129	5	AC083799	AC083799 Homo sapi
c 745	232.8	10.2	186783	5	AC090355	AC090355 Homo sapi
c 746	232.8	10.2	187167	12	AP001563	AP001563 Homo sapi
c 747	232.8	10.2	187215	12	AC013783	AC013783 Homo sapi
c 748	232.8	10.2	188134	5	AL354797	AL354797 Human DNA
c 749	232.8	10.2	188956	5	AL591493	AL591493 Homo sapi
c 750	232.8	10.2	189539	5	AL357493	AL357493 Human DNA
c 751	232.8	10.2	199785	5	AL355512	AL355512 Human DNA
c 752	232.8	10.2	202383	5	AC009973	AC009973 Homo sapi
c 753	232.8	10.2	202392	5	AC079061	AC079061 Homo sapi
c 754	232.8	10.2	216457	5	CNS01RGI	AL157689 Human chr
c 755	232.8	10.2	217081	5	AC182731	AC182731 Pan trogl
c 756	232.8	10.2	254112	12	CR762382	CR762382 Homo sapi
c 757	232.6	10.2	461	2	CQ517361	CQ517361 Sequence
c 758	232.6	10.2	766	7	BV569996	BV569996 G591P6085
c 759	232.6	10.2	15835	5	AY338232	AY338232 Homo sapi
c 760	232.6	10.2	51923	5	AL356983	AL356983 Human DNA
c 761	232.6	10.2	62449	12	AC061985	AC061985 Homo sapi
c 762	232.6	10.2	63332	5	AC024938	AC024938 Homo sapi
c 763	232.6	10.2	67332	5	AP001468	AP001468 Homo sapi
c 764	232.6	10.2	74429	5	AY523969	AY523969 Homo sapi
c 765	232.6	10.2	100301	5	HS317E23	AL020996 Human DNA
c 766	232.6	10.2	102509	5	AL953897	AL953897 Human DNA
c 767	232.6	10.2	103608	5	AL139161	AL139161 Human DNA
c 768	232.6	10.2	114532	12	AC016547	AC016547 Homo sapi
c 769	232.6	10.2	129747	5	HS465N24	AL031432 Human DNA
c 770	232.6	10.2	132066	5	AL953882	AL953882 Human DNA
c 771	232.6	10.2	135668	5	AC139667	AC139667 Homo sapi
c 772	232.6	10.2	137496	5	AC005288	AC005288 Homo sapi
c 773	232.6	10.2	138459	12	AC090795	AC090795 Homo sapi
c 774	232.6	10.2	143747	5	HS370M22	Z82206 Human DNA s
c 775	232.6	10.2	148504	5	AC138732	AC138732 Pongo PY9
c 776	232.6	10.2	156365	12	AC183959	AC183959 Pan trogl
c 777	232.6	10.2	160892	12	AC023910	AC023910 Homo sapi
c 778	232.6	10.2	164330	12	AC016928	AC016928 Homo sapi
c 779	232.6	10.2	168833	12	AC021706	AC021706 Homo sapi
c 780	232.6	10.2	169714	12	AC138876	AC138876 Homo sapi
c 781	232.6	10.2	176975	5	AC008050	AC008050 Homo sapi
c 782	232.6	10.2	179538	12	AC024740	AC024740 Homo sapi
c 783	232.6	10.2	186330	5	AC007376	AC007376 Homo sapi
c 784	232.6	10.2	187723	5	AC016889	AC016889 Homo sapi
c 785	232.6	10.2	189149	12	AC046171	AC046171 Homo sapi
c 786	232.6	10.2	201625	12	AC012144	AC012144 Homo sapi
c 787	232.6	10.2	202233	5	AC003664	AC003664 Homo sapi
c 788	232.6	10.2	202850	5	AC183546	AC183546 Pan trogl
c 789	232.6	10.2	203611	5	AC146448	AC146448 Pan trogl
c 790	232.6	10.2	215960	12	AC144881	AC144881 Gorilla g
c 791	232.6	10.2	224271	5	AC026803	AC026803 Homo sapi
c 792	232.6	10.2	236109	5	CT009602	CT009602 PTB-121B2
c 793	232.6	10.2	319064	12	CT009516	CT009516 Homo sapi
c 794	232.6	10.2	340000	5	AP001759	AP001759 Homo sapi
c 795	232.4	10.2	62038	5	AC108469	AC108469 Homo sapi
c 796	232.4	10.2	69013	5	CR753842	CR753842 Human DNA
c 797	232.4	10.2	90732	5	AL670886	AL670886 Human DNA
c 798	232.4	10.2	94060	12	AF216673	AF216673 Homo sapi
c 799	232.4	10.2	100234	12	CR759702	CR759702 Homo sapi
c 800	232.4	10.2	102215	12	CR933564	CR933564 Homo sapi
c 801	232.4	10.2	105842	5	AC107387	AC107387 Homo sapi
c 802	232.4	10.2	110000	5	BA000025_02	Continuation (3 of
c 803	232.4	10.2	113650	5	CR759787	CR759787 Human DNA
c 804	232.4	10.2	116556	5	AC133435	AC133435 Homo sapi
c 805	232.4	10.2	117338	5	HS173D1	AL031984 Human DNA
c 806	232.4	10.2	127140	5	AL136137	AL136137 Human DNA
c 807	232.4	10.2	132551	5	CR354443	CR354443 Human DNA
c 808	232.4	10.2	135578	5	AF064861	AF064861 Homo sapi
c 809	232.4	10.2	136493	5	AL662899	AL662899 Human DNA
c 810	232.4	10.2	141372	12	AC011779	AC011779 Homo sapi
c 811	232.4	10.2	141843	5	AF129408	AF129408 Homo sapi
c 812	232.4	10.2	155513	5	BS000094	BS000094 Pan trogl
c 813	232.4	10.2	159766	5	AC104942	AC104942 Homo sapi
c 814	232.4	10.2	163682	5	HSDJ711I7	AL132713 Human DNA
c 815	232.4	10.2	166239	12	AC078965	AC078965 Homo sapi
c 816	232.4	10.2	168822	5	AC007511	AC007511 Homo sapi
c 817	232.4	10.2	171427	2	CS200179	CS200179 Sequence
c 818	232.4	10.2	173023	5	AL354898	AL354898 Human DNA
c 819	232.4	10.2	173094	12	AL603629	AL603629 Homo sapi
c 820	232.4	10.2	174551	5	AC010598	AC010598 Homo sapi
c 821	232.4	10.2	175104	5	AC130449	AC130449 Homo sapi

822	232.4	10.2	175567	5	AC079447	AC079447 Homo sapi	895	232	10.2	171272	12	AC084707	AC084707 Homo sapi
823	232.4	10.2	175825	5	HS106H8	Z97195 Human DNA s	c 896	232	10.2	171426	12	AL391664	AL391664 Homo sapi
c 824	232.4	10.2	179485	5	AC005939	AC005939 Homo sapi	897	232	10.2	172969	5	AC090574	AC090574 Homo sapi
825	232.4	10.2	181946	12	AC097330	AC097330 Pan trogl	898	232	10.2	173025	12	AL391596	AL391596 Homo sapi
826	232.4	10.2	182123	12	AC002399	AC002399 Homo sapi	c 899	232	10.2	174074	5	AC018891	AC018891 Homo sapi
c 827	232.4	10.2	182509	5	AC112211	AC112211 Homo sapi	900	232	10.2	174162	5	AC099789	AC099789 Homo sapi
828	232.4	10.2	183097	12	AC027638	AC027638 Homo sapi	c 901	232	10.2	174396	12	AC021645	AC021645 Homo sapi
829	232.4	10.2	183773	5	AC087284	AC087284 Homo sapi	902	232	10.2	176742	5	AC007386	AC007386 Homo sapi
830	232.4	10.2	183827	5	AC005899	AC005899 Homo sapi	903	232	10.2	176806	12	AC090438	AC090438 Homo sapi
c 831	232.4	10.2	184666	5	DJ201G24	AF129756 Homo sapi	904	232	10.2	176924	5	AC069410	AC069410 Homo sapi
832	232.4	10.2	189379	5	AC009030	AC009030 Homo sapi	905	232	10.2	182350	5	BS000243	BS000243 Pan trogl
833	232.4	10.2	190017	5	AC090589	AC090589 Homo sapi	c 906	232	10.2	187303	5	AC069226	AC069226 Homo sapi
c 834	232.4	10.2	190149	5	AC146127	AC146127 Pan trogl	c 907	232	10.2	189672	5	AL133480	AL133480 Human DNA
835	232.4	10.2	196319	5	CNS01DT4	AL132639 Human chr	908	232	10.2	190215	12	AC016975	AC016975 Homo sapi
c 836	232.4	10.2	208066	5	AC146483	AC146483 Pan trogl	909	232	10.2	192104	5	AC006994	AC006994 Homo sapi
837	232.4	10.2	211780	5	AC146006	AC146006 Pan trogl	c 910	232	10.2	193039	12	AC090690	AC090690 Homo sapi
c 838	232.4	10.2	340000	5	HS21C079	AL163279 Homo sapi	c 911	232	10.2	193369	12	AC114889	AC114889 Pan trogl
839	232.4	10.2	349980	2	CS039420	CS039420 Sequence	912	232	10.2	193421	5	AC107294	AC107294 Homo sapi
840	232.2	10.2	679	7	BV482411	BV482411 rmq13a12.	913	232	10.2	195600	12	AC079094	AC079094 Homo sapi
c 841	232.2	10.2	55870	5	AL645585	AL645585 Human DNA	c 914	232	10.2	207620	5	AP001331	AP001331 Homo sapi
842	232.2	10.2	55932	12	AC025791	AC025791 Homo sapi	c 915	232	10.2	212337	5	AC013746	AC013746 Homo sapi
c 843	232.2	10.2	83521	5	AC129510	AC129510 Homo sapi	c 916	232	10.2	226699	5	AC022146	AC022146 Homo sapi
844	232.2	10.2	84562	12	AC140700	AC140700 Homo sapi	917	232	10.2	260209	2	DD139819	DD139819 Sulfatase
c 845	232.2	10.2	84928	12	AC141231	AC141231 Homo sapi	918	232	10.2	260209	2	AX573201	AX573201 Sequence
c 846	232.2	10.2	98404	12	AL355676	AL355676 Homo sapi	c 919	232	10.2	309662	12	AC004469	AC004469 Homo sapi
c 847	232.2	10.2	108768	5	AC105053	AC105053 Homo sapi	920	232	10.2	340000	5	AP001759	AP001759 Homo sapi
c 848	232.2	10.2	110000	12	AL137126_0	AL137126 Homo sapi	921	231.8	10.1	601	2	AR665920	AR665920 Sequence
849	232.2	10.2	112168	5	BX572623	BX572623 Human DNA	922	231.8	10.1	702	7	BV474401	BV474401 G591P6293
c 850	232.2	10.2	122591	5	AL157786	AL157786 Human DNA	923	231.8	10.1	733	7	BV630049	BV630049 S217P6229
851	232.2	10.2	123530	12	AL356369	AL356369 Homo sapi	924	231.8	10.1	769	7	BV500774	BV500774 S222P6228
852	232.2	10.2	123775	12	AC046156	AC046156 Homo sapi	925	231.8	10.1	18396	2	AR659722	AR659722 Sequence
c 853	232.2	10.2	137924	12	AC026684	AC026684 Homo sapi	c 926	231.8	10.1	59731	5	AC068442	AC068442 Homo sapi
854	232.2	10.2	143291	5	AL137792	AL137792 Human DNA	927	231.8	10.1	105499	5	AC093335	AC093335 Homo sapi
855	232.2	10.2	148348	12	AC104074	AC104074 Homo sapi	928	231.8	10.1	106331	12	AC138226	AC138226 Homo sapi
856	232.2	10.2	151735	12	AC015611	AC015611 Homo sapi	c 929	231.8	10.1	115968	5	AL365277	AL365277 Human DNA
857	232.2	10.2	155867	5	AC109455	AC109455 Homo sapi	c 930	231.8	10.1	117751	5	AC020913	AC020913 Homo sapi
858	232.2	10.2	158905	5	AC005666	AC005666 Homo sapi	931	231.8	10.1	124524	5	BX255972	BX255972 Human DNA
c 859	232.2	10.2	161355	5	HSDJ60O19	AL080314 Human DNA	c 932	231.8	10.1	127661	12	AP001261	AP001261 Homo sapi
c 860	232.2	10.2	165942	5	AC104943	AL104943 Homo sapi	933	231.8	10.1	133728	5	AL139220	AL139220 Human DNA
c 861	232.2	10.2	166256	5	AC173999	AC173999 Pan trogl	c 934	231.8	10.1	149163	12	AC073835	AC073835 Homo sapi
862	232.2	10.2	166985	5	AC009927	AC009927 Homo sapi	935	231.8	10.1	150660	5	AL157372	AL157372 Human DNA
c 863	232.2	10.2	170848	12	AC093630	AC093630 Homo sapi	c 936	231.8	10.1	155454	5	AC183281	AC183281 Pan trogl
864	232.2	10.2	174562	12	AC005848	AC005848 Homo sapi	937	231.8	10.1	160535	5	AP000729	AP000729 Homo sapi
865	232.2	10.2	178056	5	AC008536	AC008536 Homo sapi	c 938	231.8	10.1	160826	12	AC010354	AC010354 Homo sapi
866	232.2	10.2	178691	5	AC009704	AC009704 Homo sapi	c 939	231.8	10.1	162133	12	AC068569	AC068569 Homo sapi
c 867	232.2	10.2	181020	5	AC009119	AC009119 Homo sapi	c 940	231.8	10.1	164394	5	AC116904	AC116904 Homo sapi
c 868	232.2	10.2	189840	5	AC012320	AC012320 Homo sapi	c 941	231.8	10.1	167336	12	AC021350	AC021350 Homo sapi
c 869	232.2	10.2	192324	5	AC096920	AC096920 Homo sapi	942	231.8	10.1	167523	5	AC145983	AC145983 Pan trogl
870	232.2	10.2	196954	5	AC022148	AC022148 Homo sapi	943	231.8	10.1	168501	5	AC068594	AC068594 Homo sapi
c 871	232.2	10.2	197225	5	AC093835	AC093835 Homo sapi	944	231.8	10.1	169089	5	AC055725	AC055725 Homo sapi
c 872	232.2	10.2	212103	5	CNS01DV4	AL133453 Human chr	c 945	231.8	10.1	170686	12	AC137059	AC137059 Papio anu
c 873	232.2	10.2	215786	5	AC022916	AC022916 Homo sapi	946	231.8	10.1	171898	5	AC111182	AC111182 Homo sapi
c 874	232	10.2	34234	5	HSJUCA4	Z74019 Human DNA s	947	231.8	10.1	175023	5	AC011037	AC011037 Homo sapi
c 875	232	10.2	37194	5	HSV210E9	Z70280 Human DNA s	948	231.8	10.1	175827	5	AL358472	AL358472 Human DNA
876	232	10.2	39374	5	AC005256	AC005256 Homo sapi	949	231.8	10.1	181508	12	AC183643	AC183643 Pan trogl
877	232	10.2	40307	5	AC025155	AC025155 Homo sapi	c 950	231.8	10.1	184886	5	AC005358	AC005358 Homo sapi
878	232	10.2	40662	5	AL645758	AL645758 Human DNA	c 951	231.8	10.1	185820	5	HS1009E24	AL109804 Human DNA
879	232	10.2	58072	12	AC136758	AC136758 Homo sapi	c 952	231.8	10.1	189821	5	AL354735	AL354735 Human DNA
880	232	10.2	64359	5	AC005233	AC005233 Homo sapi	c 953	231.8	10.1	190155	12	AC105184	AC105184 Homo sapi
881	232	10.2	75008	5	AP000471	AP000471 Homo sapi	c 954	231.8	10.1	190558	12	AP001403	AP001403 Homo sapi
c 882	232	10.2	105583	12	AC084258	AC084258 Homo sapi	c 955	231.8	10.1	190744	5	AC005038	AC005038 Homo sapi
883	232	10.2	144834	5	AC073345	AC073345 Homo sapi	956	231.8	10.1	192296	5	AC009654	AC009654 Homo sapi
884	232	10.2	152339	12	AC083931	AC083931 Homo sapi	957	231.8	10.1	198410	12	AP000831	AP000831 Homo sapi
c 885	232	10.2	154034	5	AC087620	AC087620 Homo sapi	958	231.8	10.1	206329	12	AC017113	AC017113 Homo sapi
c 886	232	10.2	154599	12	AC016997	AC016997 Homo sapi	c 959	231.8	10.1	206647	5	AP002898	AP002898 Homo sapi
c 887	232	10.2	157021	12	AC020991	AC020991 Homo sapi	c 960	231.8	10.1	207433	2	AX326809	AX326809 Sequence
c 888	232	10.2	159863	5	AP002349	AC002349 Homo sapi	961	231.8	10.1	224761	5	AC026894	AC026894 Homo sapi
889	232	10.2	161406	5	AP002376	AP002376 Homo sapi	962	231.8	10.1	241278	5	AC097268	AC097268 Pan trogl
890	232	10.2	162554	5	AC079354	AC079354 Homo sapi	963	231.8	10.1	256164	5	HSA400877	AJ400877 Homo sapi
c 891	232	10.2	162996	12	AC051655	AC051655 Homo sapi	c 964	231.6	10.1	461	2	CQ487560	CQ487560 Sequence
c 892	232	10.2	167762	5	AC183682	AC183682 Pan trogl	965	231.6	10.1	31852	5	HSDJ689C5	AL118503 Human DNA
c 893	232	10.2	168963	12	AC009705	AC009705 Homo sapi	966	231.6	10.1	33417	5	AC104537	AC104537 Homo sapi
c 894	232	10.2	170245	5	HS109F14	AL022721 Human DNA	967	231.6	10.1	37001	5	AC005513	AC005513 Homo sapi

968	231.6	10.1	44219	5	AC005512	AC005512 Homo sapi	1041	231.6	10.1	200493	5	AP005270	AP005270 Homo sapi
C 969	231.6	10.1	44717	5	AY207046	AY207046 Homo sapi	C1042	231.6	10.1	206860	12	AC025689	AC025689 Homo sapi
970	231.6	10.1	48852	5	CR936875	CR936875 Human DNA	1043	231.6	10.1	209545	12	AC087848	AC087848 Homo sapi
971	231.6	10.1	57896	12	AC090775	AC090775 Homo sapi	1044	231.6	10.1	211627	5	AL161651	AL161651 Human DNA
972	231.6	10.1	61698	5	AL662870	AL662870 Human DNA	1045	231.6	10.1	212999	5	DQ436495	DQ436495 Homo sapi
C 973	231.6	10.1	62449	12	AC061985	AC061985 Homo sapi	1046	231.6	10.1	215273	5	AC126121	AC126121 Homo sapi
974	231.6	10.1	65544	12	AC120025	AC120025 Homo sapi	C1047	231.6	10.1	230696	5	AC007221	AC007221 Homo sapi
975	231.6	10.1	65612	12	AC087452	AC087452 Homo sapi	C1048	231.6	10.1	232574	12	AL158037	AL158037 Homo sapi
C 976	231.6	10.1	68984	5	AC135592	AC135592 Homo sapi	C1049	231.6	10.1	280140	12	AC055751	AC055751 Homo sapi
977	231.6	10.1	85787	5	AC073069	AC073069 Homo sapi	1050	231.6	10.1	305000	5	HSXDPA	AL590762 Homo sapi
C 978	231.6	10.1	91830	5	AL365436	AL365436 Human DNA	1051	231.6	10.1	349980	2	CS039418	CS039418 Sequence
979	231.6	10.1	103780	5	AL773541	AL773541 Human DNA	1052	231.4	10.1	601	2	AR665921	AR665921 Sequence
980	231.6	10.1	104070	5	AC008955	AC008955 Homo sapi	1053	231.4	10.1	752	7	BV589457	BV589457 G591P6335
981	231.6	10.1	105045	2	AR659622	AR659622 Sequence	C1054	231.4	10.1	29848	5	U73023	U73023 Homo sapien
982	231.6	10.1	107045	2	AR659731	AR659731 Sequence	C1055	231.4	10.1	102101	5	AL359816	AL359816 Human DNA
C 983	231.6	10.1	109891	5	HS112K5	Z85987 Human DNA s	1057	231.4	10.1	111566	5	AC069417	AC069417 Homo sapi
C 984	231.6	10.1	110000	5	BA000025_10	Continuation (11 o	1058	231.4	10.1	119147	5	AC098873	AL357314 Human DNA
985	231.6	10.1	110208	5	EX927194	BX927194 Human DNA	C1059	231.4	10.1	131716	12	AC025833	AC025833 Homo sapi
C 986	231.6	10.1	112018	5	AB023050	AB023050 Homo sapi	C1060	231.4	10.1	134793	5	AC020922	AC020922 Homo sapi
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c1311	230.6	10.1	177531	2	DD156330	DD156330 Means and	1384	230.4	10.1	202544	5	AC104447	AC104447 Homo sapi
c1312	230.6	10.1	177531	2	DD156882	DD156882 Means and	c1385	230.4	10.1	203418	12	AC063958	AC063958 Homo sapi
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c1314	230.6	10.1	177531	2	AX707892	AX707892 Sequence	c1387	230.4	10.1	216161	5	AC024558	AC024558 Homo sapi
c1315	230.6	10.1	177531	5	AC005020	AC005020 Homo sapi	1388	230.4	10.1	216264	5	AC099518	AC099518 Homo sapi
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ALIGNMENTS

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LOCUS	B D140585	2284 bp	DNA	linear	PAT 18-SEP-2002	
DEFINITION	Polypeptides and nucleic acids encoding the same.					
ACCESSION	B D140585					
VERSION	B D140585.1	GI:23235530				
KEYWORDS	JP 2002505850-A/68.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;					
	Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 2284)					
AUTHORS	Wood,W.I., Goddard,A., Gurney,A.L., Yuan,J., Baker,K.P. and Zheng,J.					
TITLE	Polypeptides and nucleic acids encoding the same					
JOURNAL	Patent: JP 2002505850-A 68 26-FEB-2002;					
	GENENTECH INC					
COMMENT	OS Homo sapiens (human)					
	PN JP 2002505850-A/68					
	PD 26-FEB-2002					
	PF 01-DEC-1998 JP 2000523338					
	PR 03-DEC-1997 US 60/067411,11-DEC-1997 US 60/069334 PR					
	11-DEC-1997 US 60/069335,11-DEC-1997 US 60/069278 PR					
	12-DEC-1997 US 60/069425,16-DEC-1997 US 60/069696 PR					
	16-DEC-1997 US 60/069694,16-DEC-1997 US 60/069702 PR					
	17-DEC-1997 US 60/069870,17-DEC-1997 US 60/069873 PR					
	18-DEC-1997 US 60/068017,05-JAN-1998 US 60/070440 PR					
	09-FEB-1998 US 60/074086,09-FEB-1998 US 60/074092 PR					
	25-FEB-1998 US 60/075945					
	PI WILLIAM I WOOD,AUDREY GODDARD,AUSTIN L GURNEY,JEAN YUAN,KEVIN					
	PI P BAKER,					
	PI JIAN ZHENG					
	PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC					
	C12P21/02,					
	PC C12P21/08,C12Q1/68,C12N15/00,C12N5/00					
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	/db_xref="taxon:9606"					
ORIGIN						



Query Match		100.0%;	Score 2284;	DB 2;	Length 2284;
Best Local Similarity		100.0%;	Pred. No. 0;		
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				0;	Gaps
				0;	
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DB	1	GGGAGCATCGGTGCGTCTCGCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGC	60		
QY	61	GGGCGACAGAGCTGTCTCGCACCTGGATGGCAGAGGGGCGCGGGTCTCTCGAC	120		
DB	61	GGGCGACAGAGCTGTCTCGCACCTGGATGGCAGAGGGGCGCGGGTCTCTCGAC	120		
QY	121	GCACAGAGAAATCTCATCTGTGACGCTTCTTAAAGCAAATAAGACAGAGGAG	180		
DB	121	GCACAGAGAAATCTCATCTGTGACGCTTCTTAAAGCAAATAAGACAGAGGAG	180		
QY	181	GATTATCCTTGACCTTTGAAGACCAAAATAAACTGAAATTTAAATGTTCTTCGGGGA	240		
DB	181	GATTATCCTTGACCTTTGAAGACCAAAATAAACTGAAATTTAAATGTTCTTCGGGGA	240		
QY	241	GAAGGAGCTTGACTTACACTTTGGTAATAATTGCTTCTTGACACTAAGGCTGTCTGCT	300		
DB	241	GAAGGAGCTTGACTTACACTTTGGTAATAATTGCTTCTTGACACTAAGGCTGTCTGCT	300		
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DB	361	TCATAAGGAATCAGAGGCAATGAGCCGATATATACTTCAACTCAAGAAGACTGCATTAAT	420		
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ACCESSION BD378361  
VERSION BD378361.1 GI:92277455  
KEYWORDS JP 2003524387-A/68.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE unclassified sequences.  
1 (bases 1 to 2284)  
AUTHORS Roy,M.A., Napier,M.A., Tumas,D., Kljavin,I.J., Hillan,K.J.,  
Gurney,A.L., Grimaldi,C.J., Godowski,P.J., Goddard,A.,  
Gerritsen,M.E., Filvaroff,E., Dan, Eaton,L., Botstein,D.,  
Baker,K.P., Ferrara,N. and Wood,W.I.

TITLE SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING  
THE SAME

JOURNAL Patent: JP 2003524387-A 68 19-AUG-2003;  
Genentech Inc,Kevin P Baker,David Botstein,Dan L Eaton, Napoleone  
Ferrara, Ellen Filvaroff,Mary E Gerritsen,Audrey Goddard,Paul J  
Godowski, Christopher J Grimaldi,Austin L Gurney,Kenneth J Hillan,  
Ivar J Kljavin, Mary A Napier,Margaret Ann Roy,Daniel Tumas,William  
I Wood

COMMENT OS Homo Sapien  
PN JP 2003524387-A/68  
PD 19-AUG-2003  
PF 01-DEC-1999 JP 2000585407  
PR 01-DEC-1998 US US9825108,16-DEC-1998 US 60/112850, PR  
22-DEC-1998 US 60/113296  
PI margaret ann roy,mary a napier,daniel tumas,ivar j kljavin, PI  
kenneth j hillan,austin l gurney,christopher  
PI j grimaldi,paul j  
PI godowski,  
PI audrey goddard,mary e gerritsen,ellen filvaroff,dan PI 1  
eaton,david botstein,  
PI kevin p baker,napoleone ferrara,william i wood CC  
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Db 2281 TCAA 2284  
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DEFINITION Sequence 514 from patent US 6478825.  
ACCESSION AR252736  
VERSION AR252736.1 GI:27300644  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2284)  
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.  
TITLE Implant, method of making same and use of the implant for the treatment of bone defects  
JOURNAL Patent: US 6478825-A 514 12-NOV-2002;  
Osteotech, Inc.; Eatontown, NJ  
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COMMENT

DD028540 2284 bp DNA linear PAT 04-NOV-2005  
Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same.  
DD028540  
DD028540.1 GI:92561177  
JP 2004203742-A/369.  
unidentified  
unidentified  
unclassified sequences.  
1 (bases 1 to 2284)  
Grimaldi,C.J., Ashkenazi,A.J., Desnoyers,L., Baker,K.P.,  
Godowski,P.J., Goddard,A., Gerritsen,M.E., Gerber,H., Fong,S.,  
Ferrara,N., Eaton,D.L., Botstein,D., Gurney,A.L., Kljavin,I.J.,  
Napier,M.A., Zhang,Z., Wood,W.I., Williams,M.P., Tumas,D.,  
Watanabe,C.K., Stewart,T.A., Roy,M.A., Paoni,N.F. and Pan,J.  
Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
Patent: JP 2004203742-A 369 22-JUL-2004;  
Genentech Inc,Kevin Baker,Jian Chen,Audrey Goddard,Austin Gurney,  
Victoria Smith,Colin K Watanabe,William I Wood,Jean Yuan  
OS Homo Sapien  
PN JP 2004203742-A/369  
PD 22-JUL-2004  
PF 25-SEP-2002 JP 2002341509  
PR 02-JUN-1999 US US9912252,23-JUN-1999 US 60/141037, PR  
26-JUL-1999 US 60/145698,20-JUL-1999 US 60/144758, PR  
06-JAN-2000 US US0000376,11-FEB-2000 US US0003565, PR  
18-FEB-2000 US US0004341,22-FEB-2000 US US0004414, PR  
24-FEB-2000 US US0004914,24-FEB-2000 US US0005004, PR  
02-MAR-2000 US US0005841,15-MAR-2000 US US0006884, PR  
05-JAN-2000 US US0000219,20-DEC-1999 US US9930911, PR

16-DEC-1999	US	US9930095,28-JUL-1999	US	60/146222, PR
17-AUG-1999	US	60/149396,15-SEP-1999	US	US9921090, PR
15-SEP-1999	US	US9921547,08-OCT-1999	US	60/158663, PR
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20-MAR-2000	US	US0007377,07-JUL-1999	US	60/143048 PI
christopher j grimaldi,avi j ashkenazi,luc desnoyers,kevin p PI				
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PI	paul j	godowski,audrey goddard,mary e gerritsen,hanspeter PI		
gerber,				
PI	sherman fong,napoleone ferrara,dan l eaton,david botstein, PI			
austin l gurney,				
PI	ivar j	kljavin,mary a napier,zemin zhang,william PI i		
wood,mickey				
PI	p williams,			
PI	daniel tumas,colin k watanabe,timothy a stewart,margaret ann			
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Db 1861 GTCTCAAACTCCTGACCTAGTGATCCACCCCTCCTCGGCTCCCAAAGTCTGGGATTACA 1920  
  
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DD031661  
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DEFINITION COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED  
DISEASES.  
ACCESSION DD031661  
VERSION DD031661.1 GI:92605001  
KEYWORDS JP 2004516227-A/57.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2284)  
AUTHORS Watanabe,C.K., Yan,M., Shelton,D.L., Smith,V., Stewart,T.A.,  
Wood,W.I., Tumas,D., Gurney,A.L., Pennica,D., Ashkenazi,A.J.,  
Baker,K.P., Lu,Y., Pan,J., Kabakoff,R.C., Henzel,W., Hebert,C. and  
Goddard,A.  
TITLE COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED  
JOURNAL Patent: JP 2004516227-A 57 03-JUN-2004;  
Genentech Inc et al  
COMMENT OS Homo sapiens  
PN JP 2004516227-A/57  
PD 03-JUN-2004  
PF 02-MAR-2000 JP 2000603379  
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18-FEB-2000 US US0004341,22-FEB-2000 US US0004414, PR  
30-NOV-1999 US US9928409,01-DEC-1999 US US9928301, PR  
01-DEC-1999 US US9928634,02-DEC-1999 US US9928551, PR  
18-FEB-2000 US US0004342,02-DEC-1999 US US9928565, PR  
16-DEC-1999 US US9930095,20-DEC-1999 US US9930999, PR  
30-DEC-1999 US US9931274,05-JAN-2000 US US0000219, PR

06-JAN-2000 US US0000277,06-JAN-2000 US US0000376, PR  
11-FEB-2000 US US0003565,29-NOV-1999 US US9928214, PR  
15-SEP-1999 US US9921090,05-OCT-1999 US US9923089, PR  
04-MAY-1999 US 60/132371,14-MAY-1999 US 60/134287, PR  
02-JUN-1999 US US9912252,23-JUN-1999 US 60/141037, PR  
20-JUL-1999 US 60/144758,26-JUL-1999 US 60/145698, PR  
28-JUL-1999 US 60/146222,20-APR-1999 US US9908615, PR  
23-MAR-1999 US 60/125775,12-MAR-1999 US 60/123957, PR  
10-MAR-1999 US 60/123618,08-MAR-1999 US US9905028, PR  
28-APR-1999 US 60/131445,12-APR-1999 US 60/128849, PR  
01-SEP-1999 US US9920111,08-SEP-1999 US US9920594, PR  
13-SEP-1999 US US9920944,15-SEP-1999 US US9921547, PR  
29-OCT-1999 US 60/162506  
PI colin k watanabe,minhong yan,david l shelton,victoria smith,  
PI timothy a stewart,william i wood,daniel tumas,austin l gurney,  
PI diane pennica,avi j ashkenazi,kevin p baker,yanmei lu,james  
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CC  
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Db 1441 AGAATCCTTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAATATTGATCAAT 1500

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RESULT 6

DD039442

LOCUS

DEFINITION

DD039442

Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same.

DD039442

VERSION

DD039442.1 GI:92629391

KEYWORDS

JP 2004522402-A/369.

SOURCE

unidentified

ORGANISM

unclassified

unclassified sequences.

REFERENCE

1 (bases 1 to 2284)

AUTHORS

Zhang,Z., Wood,W.I., Ashkenazi,A.J., Botstein,D., Napier,M.A., Kljavin,I.J., Gurney,A.L., Grimaldi,C.J., Godowski,P.J., Goddard,A., Paoni,N.F., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,M.P., Baker,K.P., Pan,J., Roy,M.A., Gerritsen,M.E., Gerber,H., Fong,S., Ferrara,N., Eaton,D.L. and Desnoyers,L.

TITLE

Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

JOURNAL

Patent: JP 2004522402-A 369 29-JUL-2004;

Genentech Inc,Kevin Baker,Jian Chen,Audrey Goddard,Austin Gurney, Victoria Smith,Colin K Watanabe,William I Wood,Jean Yuan

COMMENT

OS Homo Sapien

PN JP 2004522402-A/369

PD 29-JUL-2004

PF 30-MAR-2000 JP 2001500766

PR 06-JAN-2000 US US0000376,11-FEB-2000 US US0003565, PR 18-FEB-2000 US US0004341,22-FEB-2000 US US0004414, PR 24-FEB-2000 US US0004914,24-FEB-2000 US US0005004, PR 05-JAN-2000 US US000219,17-AUG-1999 US 60/149396, PR 15-SEP-1999 US US9921547,15-MAR-2000 US US0006884, PR

23-JUN-1999	US	60/141037,07-JUL-1999	US	60/143048, PR
20-JUL-1999	US	60/144758,26-JUL-1999	US	60/145698, PR
28-JUL-1999	US	60/146222,15-SEP-1999	US	US9921090, PR
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PI a napier,				botstein,mary
PI ivar j kljavin,austin l gurney,christopher j grimaldi,paul j				
PI godowski,				
PI audrey goddard,nicholas f paoni,timothy				
PI a steward,daniel tumas,				
PI colin k watanabe,mickey p williams,kevin p baker,james pan,				
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RESULT 7  
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LOCUS  
DEFINITION Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same.  
ACCESSION DD249590  
VERSION DD249590.1 GI:99025485  
KEYWORDS JP 2005304500-A/369.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 2284)  
AUTHORS Napier,M.A., Kljavin,I.J., Gurney,A.L., Grimaldi,C.J., Watanabe,C.K., Stewart,T.A., Zhang,Z., Wood,W.I., Williams,P.M., Tumas,D., Godowski,P.J., Goddard,A., Gerritsen,M.E., Gerber,H., Fong,S., Paoni,N.F., Pan,J., Roy,M.A., Ferrara,N., Eaton,D.L., Desnoyers,L., Botstein,D., Baker,K.P. and Ashkenazi,A.J.  
TITLE Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
JOURNAL Patent: JP 2005304500-A 369 04-NOV-2005;  
Genentech Inc,Kevin Baker,Jian Chen,Audrey Goddard,Austin Gurney,Victoria Smith,Colin K Watanabe,William I Wood,Jean Yuan  
OS Homo Sapien  
PN JP 2005304500-A/369  
PD 04-NOV-2005  
PF 14-MAR-2005 JP 2005117472  
PR 11-FEB-2000 US T/US00/03565,06-JAN-2000 US T/US00/00376, PR 05-JAN-2000 US T/US00/00219,20-DEC-1999 US T/US99/30911, PR 16-DEC-1999 US T/US99/30095,22-FEB-2000 US T/US00/04414, PR 17-AUG-1999 US 60/149396,20-MAR-2000 US T/US00/07377, PR 15-MAR-2000 US T/US00/05884,02-MAR-2000 US T/US00/05841, PR 24-FEB-2000 US T/US00/05004,28-JUL-1999 US 60/146222, PR

01-DEC-1999 US T/US99/28301,30-NOV-1999 US T/US99/28313, PR  
08-OCT-1999 US 60/158663,15-SEP-1999 US T/US99/21547, PR  
15-SEP-1999 US T/US99/21090,18-FEB-2000 US T/US00/04341, PR  
24-FEB-2000 US T/US00/04914,26-JUL-1999 US 60/145698, PR  
23-JUN-1999 US 60/141037,07-JUL-1999 US 60/143048, PR  
02-JUN-1999 US T/US99/12252,20-JUL-1999 US 60/144758 PI  
PI napier,ivar j kljavin,austin l gurney,christopher j pi grimaldi,  
PI colin k watanabe,timothy a stewart,zemin zhang,william i wood,  
PI p mickey williams,daniel tumas,paul j godowski,audrey goddard,  
PI mary e gerritsen,hanspeter gerber,sherman fong,nicholas f pi  
PI paoni,james pan,  
PI margaret ann roy,napoleone ferrara,dan l eaton,luc desnoyers,  
PI david botstein,kevin p baker,avi j ashkenazi  
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LOCUS AR534995 2284 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 82 from patent US 6734288.  
ACCESSION AR534995  
VERSION AR534995.1 GI:53925785  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 2284)  
AUTHORS Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L. and Wood,W.I.  
TITLE Antibodies against a secreted polypeptide that stimulates release of proteoglycans from cartilage  
JOURNAL Patent: US 6734288-A 82 11-MAY-2004;  
Genentech, Inc.; San Francisco, CA  
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Db	1981	AGTGGGAACCAAAATTAGGTAAATTTGGGTAAATCTGTCTCTAAAATATTAGCTAAAAACAA	2040
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Db	2041	AGCTCTATGTAAAGTAATAAAGTATAATTGCCATATAAAATTTCAAATTCAACTGGCTTT	2100
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QY	2161	TAAATCAAACTGTTTATATATCAATTTCTAATGGATTTGCTTTTCTTTTATATGGATTCTT	2220
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QY	2281	TCAA	2284
Db	2281	TCAA	2284

RESULT	10
AR691142	
LOCUS	AR691142 linear PAT 13-SEP-2005
DEFINITION	Sequence 82 from patent US 6908993.
ACCESSION	AR691142
VERSION	AR691142.1 GI:74478541
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified. 1 (bases 1 to 2284)
AUTHORS	Botstein,D., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Roy,M.A. and Wood,W.I.
TITLE	secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: US 6908993-A 82 21-JUN-2005; Genentech, Inc.; South San Francisco, CA
FEATURES	Location/Qualifiers 1..2284 /organism="unknown" /mol type="genomic DNA"
source	

	Query Match	100.0%;	Score 2284;	DB 2;	Length 2284;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2284;	Conservative	0;	Mismatches	0; Indels
					0; Gaps
					0;
Qy	1	GCGGAGCATCCGTCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCGC	60		
Db	1	GCGGAGCATCCGTCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCGC	60		
Qy	61	GGGCGGACAGAGCTGTCTCGCACCTGGATGGCAGAGGGGCGCGGGGTCTCTCGAC	120		

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QY 1861 GTCTCAAACTCCTGACCTAGTGATCCACCCTCCTCGGCTCCCAAAGTGTGGGATTACA 1920  
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QY 1921 GGCAATGAGCCACACAGCTGGCCCCCTTCTGTGTTTATGTTGGTTTGTGAGAAGGAATGA 1980  
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QY 2281 TCAA 2284  
Db 2281 TCAA 2284

RESULT 11  
AR693626  
LOCUS AR693626 2284 bp DNA linear PAT 14-SEP-2005  
DEFINITION Sequence 514 from patent US 6913919.  
ACCESSION AR693626  
VERSION AR693626.1 GI:75184121  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2284)  
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Gurney,A.L., Roy,M.A. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: US 6913919-A 514 05-JUL-2005;  
Genetech, Inc.; South San Francisco, CA  
FEATURES  
source Location/Qualifiers  
1..2284  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 100.0%; Score 2284; DB 2; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ACTCGAAAAACAGCTAGACAAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCC 540  
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Qy 2281 TCAA 2284

Db 2281 TCAA 2284

RESULT 12

AR705580

LOCUS AR705580 2284 bp DNA linear PAT 20-SEP-2005

DEFINITION Sequence 82 from patent US 6929947.

ACCESSION AR705580

VERSION AR705580.1 GI:75924126

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2284)

AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Roy,M.A. and Wood,W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: US 6929947-A 82 16-AUG-2005; Genentech, Inc.; South San Francisco, CA

FEATURES

source Location/Qualifiers

1..2284

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 2284; DB 2; Length 2284;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGATTTCGCCGTCCTTCCCGC 60

Db 1 GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGATTTCGCCGTCCTTCCCGC 60



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Db	2281		

RESULT 14  
AR708652  
LOCUS AR708652 2284 bp DNA linear PAT 21-SEP-2005  
DEFINITION Sequence 82 from patent US 6936254.  
ACCESSION AR708652  
VERSION AR708652.1 GI:75998546  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2284)  
AUTHORS Baker,K.P., Botstein,D., Eaton,D.L., Ferrara,N., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Hillan,K.J., Kljavin,I.J., Napier,M.A., Roy,M.A., Tumas,D. and Wood,W.I.  
TITLE Method of inducing fetal hemoglobin synthesis  
JOURNAL Patent: US 6936254-A 82 30-AUG-2005;  
Genentech, Inc.; South San Francisco, CA  
FEATURES  
source location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 2284; DB 2; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AR757551  
VERSION AR757551.1 GI:83322728  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2284)  
AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.  
TITLE PRO844 polypeptides  
JOURNAL Patent: US 6953836-A 514 11-OCT-2005;  
Genentech, Inc.; South San Francisco, CA  
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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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DE	Human PRO361	nucleotide	sequence.			
PN	WO9928462-A2.					
PD	10-JUN-1999.					
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PN	WO200032776-A2.					
PD	08-JUN-2000.					
PA	(GETH ) GENENTECH INC.					
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ID	AAF44268	standard;	cdNA;	2284	BP.	
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PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
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PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
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PN	US2002173463-A1.					

PD 21-NOV-2002.  
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Best Local Similarity 100.0%; Pred. No. 0;  
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PN US2002150976-A1.  
PD 17-OCT-2002.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 0;  
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PN US2002142958-A1.  
PD 03-OCT-2002.  
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RESULT 8  
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PN US2003027162-A1.  
PD 06-FEB-2003.  
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PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 0;  
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PN US2002132981-A1.  
PD 19-SEP-2002.  
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PD 14-NOV-2002.  
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PN US2003022187-A1.  
PD 30-JAN-2003.  
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PN US2003027985-A1.  
PD 06-FEB-2003.  
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Best Local Similarity 100.0%; Pred. No. 0;



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PN US2003017476-A1.  
PD 23-JAN-2003.  
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Best Local Similarity 100.0%; Pred. No. 0;  
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ID ABX17261 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 8; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 17  
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DE cDNA encoding human pro361 protein.  
PN US2002127643-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 8; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 18  
ID ACA04368 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #15.  
PN US2002165143-A1.  
PD 07-NOV-2002.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 0;  
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ID ACA68116 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 0;  
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DE Human secreted and transmembrane polypeptide PRO361 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
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PN US2003017981-A1.  
PD 23-JAN-2003.  
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ID ADA38025 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 0;  
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DE Human cDNA encoding secreted/transmembrane protein, PRO361.  
PN US2003059831-A1.

PD 27-MAR-2003.  
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Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 26  
ID ADA28150 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 27  
ID ADA94730 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 28  
ID ADA38955 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 29  
ID ADA93076 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 30  
ID ACH65633 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 31  
ID ADA22637 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO361.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 32  
ID ACD39623 standard; cDNA; 2284 BP.  
DE Human cDNA encoding PRO846.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 33  
ID ADA06803 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #146.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 34  
ID ADA39496 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 35  
ID ADB96522 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 2284; DB 9; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 36  
ID ADC57994 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 37  
ID ADC25838 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2002142419-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 38  
ID ADC25596 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2002156004-A1.  
PD 24-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 39  
ID ADC55358 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 40  
ID ADC12225 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 41  
ID ADC56647 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 42  
ID ADC11692 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 43  
ID ADC25717 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003077698-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 44  
ID ADC14814 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 45  
ID ADD08346 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 46  
ID ADC82171 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 47  
ID ADD07813 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 48  
ID ADC82704 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 49  
ID ADD08884 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 50  
ID ADD07133 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 51  
ID ADC83380 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 52  
ID ADD55487 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 53  
ID ADD56445 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 54  
ID ADD54883 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 55  
ID ADE31902 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 56  
ID ADE27037 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 57  
ID ADE26504 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 58  
ID ADF67441 standard; cDNA; 2284 BP.  
DE Human PRO361 nucleotide sequence SEQ ID NO:514.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 59  
ID ADH27502 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003083479-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 60  
ID ADI35695 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 61  
ID ADI00188 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 62  
ID ABX75504 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane protein PRO361 cDNA.  
PN US2002142959-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 63  
ID ABX78062 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 64  
ID ABX80474 standard; DNA; 2284 BP.  
DE Novel human secreted or transmembrane protein PRO846 DNA.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 65  
ID ACA69380 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 66  
ID ABX90451 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane protein cDNA, #182.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 67  
ID ABX64297 standard; cDNA; 2284 BP.  
DE cDNA encoding human PRO361 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 68  
ID ABX89495 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #15.  
PN US2002132768-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 10; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 69  
ID ADE71551 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003096742-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 70  
ID ADF35640 standard; cDNA; 2284 BP.  
DE cDNA encoding human PRO361 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 71  
ID ADG11890 standard; cDNA; 2284 BP.  
DE cDNA encoding human PRO361 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 72  
ID ADG63494 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003211570-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 73  
ID ADH19760 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 74  
ID ADH21253 standard; cDNA; 2284 BP.



DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 75  
ID ADH20293 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003219856-A1..  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 76  
ID ADH43223 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003207401-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 77  
ID ADN00461 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2004091972-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 12; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 78  
ID ADU25385 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2004220385-A1.  
PD 04-NOV-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 13; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 79  
ID ADY39548 standard; cDNA; 2284 BP.  
DE Human mucin/chitinase homolog PRO361 precursor cDNA.  
PN US2005048613-A1.  
PD 03-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 14; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 80  
ID ADY73829 standard; cDNA; 2284 BP.  
DE Human PRO361 cDNA, SEQ ID NO: 82.  
PN US2005059115-A1.  
PD 17-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 14; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 81  
ID AEA38662 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane protein cDNA, #215.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 14; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 82  
ID AEH50178 standard; cDNA; 2284 BP.  
DE Human cDNA clone DNA45410-1250 SEQ ID NO: 82.  
PN US2006105427-A1.  
PD 18-MAY-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 15; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 83  
ID AEI36386 standard; cDNA; 2284 BP.  
DE Human PRO protein coding sequence - SEQ ID 82.  
PN US2006127983-A1.

PD 15-JUN-2006.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 15; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 84  
ID AAC58593 standard; cDNA; 2418 BP.  
DE Human PRO361 protein UNQ316 encoding cDNA SEQ ID NO:71.  
PN WO200053758-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 2284; DB 3; Length 2418;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 85  
ID AAC59840 standard; DNA; 2342 BP.  
DE Human secreted protein encoding DNA clone vo27 1.  
PN WO200055375-A1.  
PD 21-SEP-2000.  
PA (ALPH-) ALPHAGENE INC.  
Query Match 99.4%; Score 2271.4; DB 3; Length 2342;  
Best Local Similarity 99.9%; Pred. No. 0;  
RESULT 86  
ID AAH18096 standard; cDNA; 2297 BP.  
DE Human cDNA sequence SEQ ID NO:17949.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 98.3%; Score 2245.6; DB 4; Length 2297;  
Best Local Similarity 99.8%; Pred. No. 0;  
RESULT 87  
ID AAH13971 standard; cDNA; 2221 BP.  
DE Human cDNA sequence SEQ ID NO:11027.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 89.6%; Score 2045.8; DB 4; Length 2221;  
Best Local Similarity 95.2%; Pred. No. 0;  
RESULT 88  
ID ADJ75252 standard; DNA; 2221 BP.  
DE Marker gene SEQ ID NO:504.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 89.6%; Score 2045.8; DB 12; Length 2221;  
Best Local Similarity 95.2%; Pred. No. 0;  
RESULT 89  
ID ADN05895 standard; cDNA; 2221 BP.  
DE Antipsoriatic cDNA sequence #1179.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 89.6%; Score 2045.8; DB 12; Length 2221;  
Best Local Similarity 95.2%; Pred. No. 0;  
RESULT 90  
ID AAA16637 standard; cDNA; 2015 BP.  
DE Human secreted protein clone cf85\_1 nucleotide sequence SEQ ID NO:39.  
PN WO200009552-A1.  
PD 24-FEB-2000.  
PA (GEMY ) GENETICS INST INC.  
Query Match 84.9%; Score 1939.4; DB 3; Length 2015;  
Best Local Similarity 99.5%; Pred. No. 0;  
RESULT 91  
ID AAH99840 standard; cDNA; 1423 BP.  
DE Human protein encoding cDNA sequence SEQ ID NO:675.  
PN WO200153455-A2.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 58.4%; Score 1333.2; DB 4; Length 1423;  
Best Local Similarity 97.3%; Pred. No. 0;  
RESULT 92  
ID AAS78315 standard; cDNA; 2487 BP.  
DE DNA encoding novel human diagnostic protein #14119.  
PN WO200175067-A2.  
PD 11-OCT-2001.

PA (HYSE-) HYSEQ INC. 46.9%; Score 1071.2; DB 5; Length 2487;  
Query Match  
Best Local Similarity 99.7%; Pred. No. 1.9e-263;  
RESULT 93  
ID ABL89648 standard; cDNA; 842 BP.  
DE Human polynucleotide SEQ ID NO 210.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 98.0%; Pred. No. 5e-193;  
Length 842;  
RESULT 94  
ID ADJ76101 standard; DNA; 2286 BP.  
DE Marker gene SEQ ID NO:1353.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match  
Best Local Similarity 62.7%; Pred. No. 7.1e-161;  
Length 2286;  
RESULT 95  
ID AAH07904 standard; cDNA; 805 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:4739.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 29.0%; Score 661.8; DB 4; Length 805;  
Length 805;  
RESULT 96  
ID AAH05206 standard; cDNA; 855 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:2041.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 25.6%; Score 583.6; DB 4; Length 855;  
Length 855;  
RESULT 97  
ID AEF89594 standard; cDNA; 560 BP.  
DE Human cDNA down-regulated in melanoma samples, SEQ ID NO:946.  
PN WO2006002433-A2.  
PD 05-JAN-2006.  
PA (VERI-) VERIDEX LLC.  
Query Match  
Best Local Similarity 24.4%; Score 558.4; DB 15; Length 560;  
Length 560;  
RESULT 98  
ID ACL57227 standard; cDNA; 532 BP.  
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:3362.  
PN WO2005000087-A2.  
PD 06-JAN-2005.  
PA (CHIR) CHIRON CORP.  
Query Match  
Best Local Similarity 23.2%; Score 530.4; DB 14; Length 532;  
Length 532;  
RESULT 99  
ID AAC76591 standard; cDNA; 517 BP.  
DE Human ORFX ORF2146 polynucleotide sequence SEQ ID NO:4291.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 22.4%; Score 511.8; DB 3; Length 517;  
Length 517;  
RESULT 100  
ID ABV88065 standard; cDNA; 513 BP.  
DE Human colon cancer related cDNA SEQ ID NO 1376.  
PN WO200258534-A2.  
PD 01-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 22.4%; Score 511.4; DB 6; Length 513;  
Length 513;  
RESULT 101  
ID ABV87510 standard; cDNA; 513 BP.  
DE Human colon cancer related cDNA SEQ ID NO 821.  
PN WO200258534-A2.  
PD 01-AUG-2002.  
PA (CORI-) CORIXA CORP.

Query Match  
Best Local Similarity 22.4%; Score 511; DB 6; Length 513;  
Length 513;  
RESULT 102  
ID AAV87407 standard; cDNA; 548 BP.  
DE EST clone CP85.  
PN WO9845435-A2.  
PD 15-OCT-1998.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 21.9%; Score 499.6; DB 2; Length 548;  
Length 548;  
RESULT 103  
ID AAH12872 standard; cDNA; 522 BP.  
DE Human cDNA clone (3'-primer) SEQ ID NO:9707.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match  
Best Local Similarity 20.6%; Score 470.2; DB 4; Length 522;  
Length 522;  
RESULT 104  
ID AAV89087 standard; cDNA; 422 BP.  
DE EST clone CC335.  
PN WO9845436-A2.  
PD 15-OCT-1998.  
PA (GEMY) GENETICS INST INC.  
Query Match  
Best Local Similarity 16.9%; Score 386.8; DB 2; Length 422;  
Length 422;  
RESULT 105  
ID AAC05822 standard; cDNA; 295 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 9897.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST) GENSET.  
Query Match  
Best Local Similarity 11.8%; Score 270.2; DB 3; Length 295;  
Length 295;  
RESULT 106  
ID ABX53012 standard; cDNA; 402 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #2941.  
PN US2002137160-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match  
Best Local Similarity 11.7%; Score 266.2; DB 8; Length 402;  
Length 402;  
RESULT 107  
ID AAT24664 standard; cDNA to mRNA; 324 BP.  
DE Human gene signature HUMGS06728.  
PN WO9514772-A1.  
PD 01-JUN-1995.  
PA (MATS/) MATSUBARA K.  
PA (OKUB/) OKUBO K.  
Query Match  
Best Local Similarity 10.8%; Score 245.6; DB 2; Length 324;  
Length 324;  
RESULT 108  
ID ACH44978 standard; cDNA; 478 BP.  
DE Human foetal brain CDNA #5703.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Query Match  
Best Local Similarity 10.7%; Score 243.4; DB 9; Length 478;  
Length 478;  
RESULT 109  
ID ABQ76673 standard; DNA; 160820 BP.  
DE Androgen receptor signalling pathway-associated DNA AB043547.  
PN WO200282081-A2.  
PD 17-OCT-2002.  
PA (UYRP) UNIV ROCHESTER.  
Query Match  
Best Local Similarity 10.6%; Score 241.6; DB 8; Length 160820;  
Length 160820;

Best Local Similarity 78.8%; Pred. No. 3.6e-50;  
RESULT 110  
ID AAK81252 standard; DNA; 7601 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36064.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.5%; Score 239.8; DB 4; Length 7601;  
Best Local Similarity 85.1%; Pred. No. 2.6e-50;  
RESULT 111  
ID AAK81254 standard; DNA; 31203 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36066.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.5%; Score 239.8; DB 4; Length 31203;  
Best Local Similarity 85.1%; Pred. No. 4.9e-50;  
RESULT 112  
ID AAK87418 standard; DNA; 4026 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42230.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.5%; Score 239.2; DB 4; Length 4026;  
Best Local Similarity 83.7%; Pred. No. 2.8e-50;  
RESULT 113  
ID ADQ97804 standard; DNA; 50807 BP.  
DE Human cancer associated sequence HD10-048, SEQ ID 781.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.4%; Score 238.6; DB 12; Length 50807;  
Best Local Similarity 82.4%; Pred. No. 1.3e-49;  
RESULT 114  
ID AAK81253 standard; DNA; 19174 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36065.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.4%; Score 238.2; DB 4; Length 19174;  
Best Local Similarity 84.8%; Pred. No. 1e-49;  
RESULT 115  
ID ADZ42280 standard; DNA; 73100 BP.  
DE Human endothelin converting-enzyme 1 gene with C776A/ T66564C SNPs Seq 7.  
PN JP2005110606-A.  
PD 28-APR-2005.  
PA (KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN IYAKUHIN IRYO KIK.  
Query Match 10.4%; Score 238.2; DB 14; Length 73100;  
Best Local Similarity 83.7%; Pred. No. 1.9e-49;  
RESULT 116  
ID ABK94411 standard; DNA; 109906 BP.  
DE DNA encoding endothelin converting enzyme 1 (BCE-1) #1.  
PN WO200224747-A2.  
PD 28-MAR-2002.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 10.4%; Score 238.2; DB 6; Length 109906;  
Best Local Similarity 83.7%; Pred. No. 2.2e-49;  
RESULT 117  
ID ADL08112 standard; DNA; 109906 BP.  
DE Human gene associated with low HDL-C ECE1.  
PN US2004043389-A1.  
PD 04-MAR-2004.  
PA (VITI-) VITIVITY INC.  
Query Match 10.4%; Score 238.2; DB 12; Length 109906;  
Best Local Similarity 83.7%; Pred. No. 2.2e-49;  
RESULT 118  
ID AAL07322 standard; DNA; 7566 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 10010.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.4%; Score 237.6; DB 4; Length 7566;

Best Local Similarity 83.4%; Pred. No. 9.6e-50;  
RESULT 119  
ID AEF74705 standard; DNA; 152037 BP.  
DE Human polynucleotide #219.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 10.4%; Score 236.8; DB 15; Length 152037;  
Best Local Similarity 77.2%; Pred. No. 5.9e-49;  
RESULT 120  
ID ADZ12943 standard; DNA; 126488 BP.  
DE Human cancer-associated genomic DNA #40.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 10.4%; Score 236.6; DB 14; Length 126488;  
Best Local Similarity 76.1%; Pred. No. 6.1e-49;  
RESULT 121  
ID AAH09234 standard; CDNA; 579 BP.  
DE Human CDNA clone (3'-primer) SEQ ID NO:6069.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 10.4%; Score 236.4; DB 4; Length 579;  
Best Local Similarity 89.0%; Pred. No. 6.1e-50;  
RESULT 122  
ID AAH15304 standard; CDNA; 1555 BP.  
DE Human CDNA sequence SEQ ID NO:13457.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 10.4%; Score 236.4; DB 4; Length 1555;  
Best Local Similarity 89.0%; Pred. No. 9.6e-50;  
RESULT 123  
ID ABQ88198 standard; CDNA; 154902 BP.  
DE Human osteoblast differentiation related CDNA SEQ ID NO 105.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC) PROCTER & GAMBLE CO.  
Query Match 10.4%; Score 236.4; DB 6; Length 154902;  
Best Local Similarity 89.0%; Pred. No. 7.5e-49;  
RESULT 124  
ID ABZ73998 standard; DNA; 13186 BP.  
DE Secreted protein gene 136 genomic fragment HFTAS49, SEQ ID NO:1145.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.3%; Score 236; DB 8; Length 13186;  
Best Local Similarity 84.2%; Pred. No. 3.2e-49;  
RESULT 125  
ID ADC20710 standard; DNA; 13187 BP.  
DE Human secreted protein-related DNA sequence #128.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.3%; Score 236; DB 10; Length 13187;  
Best Local Similarity 84.2%; Pred. No. 3.2e-49;  
RESULT 126  
ID ABZ73997 standard; DNA; 13862 BP.  
DE Secreted protein gene 136 genomic fragment HFTAS49, SEQ ID NO:1144.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.3%; Score 236; DB 8; Length 13862;  
Best Local Similarity 84.2%; Pred. No. 3.2e-49;  
RESULT 127  
ID ADC20709 standard; DNA; 13862 BP.  
DE Human secreted protein-related DNA sequence #127.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.



Query Match 10.3%; Score 236; DB 10; Length 13862;  
Best Local Similarity 84.2%; Pred. No. 3.2e-49;  
RESULT 128  
ID ABT11173 standard; DNA; 168174 BP.  
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 63.  
PN WO200262825-A2.  
PD 15-AUG-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.3%; Score 236; DB 6; Length 168174;  
Best Local Similarity 80.1%; Pred. No. 9.9e-49;  
RESULT 129  
ID ABT11114 standard; DNA; 168273 BP.  
DE Human 5-lipoxygenase gene related DNA sequence SEQ ID No 2.  
PN WO200262825-A2.  
PD 15-AUG-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.3%; Score 236; DB 6; Length 168273;  
Best Local Similarity 80.1%; Pred. No. 9.9e-49;  
RESULT 130  
ID AAK81392 standard; DNA; 773 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36204.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.3%; Score 235.8; DB 4; Length 773;  
Best Local Similarity 76.3%; Pred. No. 9.9e-50;  
RESULT 131  
ID AAK78813 standard; DNA; 51469 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33625.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.3%; Score 235.8; DB 4; Length 51469;  
Best Local Similarity 83.8%; Pred. No. 6.6e-49;  
RESULT 132  
ID AAK70270 standard; DNA; 51469 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25082.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.3%; Score 235.8; DB 4; Length 51469;  
Best Local Similarity 83.8%; Pred. No. 6.6e-49;  
RESULT 133  
ID AAK69322 standard; DNA; 51469 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24134.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.3%; Score 235.8; DB 4; Length 51469;  
Best Local Similarity 83.8%; Pred. No. 6.6e-49;  
RESULT 134  
ID ADQ97733 standard; DNA; 121167 BP.  
DE Human cancer associated sequence HD10-035, SEQ ID 710.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.3%; Score 235.8; DB 12; Length 121167;  
Best Local Similarity 63.7%; Pred. No. 9.6e-49;  
RESULT 135  
ID ADL62089 standard; DNA; 18968 BP.  
DE Human ovarian cancer DNA marker #20301.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.3%; Score 235.4; DB 5; Length 18968;  
Best Local Similarity 84.0%; Pred. No. 5.3e-49;  
RESULT 136  
ID ABD32769 standard; DNA; 100608 BP.  
DE Human cancer-associated genomic DNA HD16-031.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.3%; Score 235.4; DB 13; Length 100608;

Best Local Similarity 85.1%; Pred. No. 1.1e-48;  
RESULT 137  
ID ABD32868 standard; DNA; 238417 BP.  
DE Human cancer-associated genomic DNA HD17-053.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.3%; Score 235.2; DB 13; Length 238417;  
Best Local Similarity 79.5%; Pred. No. 1.9e-48;  
RESULT 138  
ID ABZ70982 standard; DNA; 11173 BP.  
DE Human HKR1 related DNA sequence SEQ ID NO:10.  
PN WO2003004513-A1.  
PD 16-JAN-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.3%; Score 235; DB 9; Length 11173;  
Best Local Similarity 76.6%; Pred. No. 5.3e-49;  
RESULT 139  
ID ADE43582 standard; DNA; 128034 BP.  
DE Polymorphic human IDE genomic sequence, SEQ ID 187.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
Query Match 10.3%; Score 235; DB 10; Length 128034;  
Best Local Similarity 85.4%; Pred. No. 1.6e-48;  
RESULT 140  
ID ADE43581 standard; DNA; 128034 BP.  
DE Human IDE genomic sequence, SEQ ID 186.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
Query Match 10.3%; Score 235; DB 10; Length 128034;  
Best Local Similarity 85.4%; Pred. No. 1.6e-48;  
RESULT 141  
ID ADH54059 standard; DNA; 128034 BP.  
DE Human IDE gene DNA sequence SeqID186.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 10.3%; Score 235; DB 12; Length 128034;  
Best Local Similarity 85.4%; Pred. No. 1.6e-48;  
RESULT 142  
ID ADH54060 standard; DNA; 128034 BP.  
DE Human IDE gene variant DNA sequence SeqID187.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 10.3%; Score 235; DB 12; Length 128034;  
Best Local Similarity 85.4%; Pred. No. 1.6e-48;  
RESULT 143  
ID ADE43315 standard; DNA; 202100 BP.  
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
Query Match 10.3%; Score 235; DB 10; Length 202100;  
Best Local Similarity 85.4%; Pred. No. 1.9e-48;  
RESULT 144  
ID ADH54357 standard; DNA; 202100 BP.  
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
Query Match 10.3%; Score 235; DB 12; Length 202100;  
Best Local Similarity 85.4%; Pred. No. 1.9e-48;  
RESULT 145  
ID ACN44854 standard; DNA; 31277 BP.  
DE Human genomic sequence hCG22132.  
PN WO2003073826-A2.  
PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.3%; Score 234.8; DB 11; Length 31277;  
Best Local Similarity 86.1%; Pred. No. 9.5e-49;  
RESULT 146  
ID ABK83462 standard; cDNA; 39801 BP.  
DE Human cDNA differentially expressed in granulocytic cells #33.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.3%; Score 234.8; DB 6; Length 39801;  
Best Local Similarity 87.3%; Pred. No. 1.1e-48;  
RESULT 147  
Query Match 10.3%; Score 234.4; DB 10; Length 110000;  
Best Local Similarity 70.4%; Pred. No. 2.1e-48;  
RESULT 148  
ID ACN44006 standard; DNA; 127369 BP.  
DE Human genomic sequence hCG1810774.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.3%; Score 234.2; DB 11; Length 127369;  
Best Local Similarity 84.6%; Pred. No. 2.5e-48;  
RESULT 149  
ID ABK83459 standard; cDNA; 128978 BP.  
DE Human cDNA differentially expressed in granulocytic cells #30.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.3%; Score 234.2; DB 6; Length 128978;  
Best Local Similarity 85.8%; Pred. No. 2.5e-48;  
RESULT 150  
ID AAD54587 standard; DNA; 128978 BP.  
DE Human LIM kinase (LIMK) DNA #6.  
PN WO200299048-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 10.3%; Score 234.2; DB 8; Length 128978;  
Best Local Similarity 85.8%; Pred. No. 2.5e-48;  
RESULT 151  
ID ADR52994 standard; DNA; 128978 BP.  
DE Drug therapy altered expressed gene #345.  
PN WO2004072265-A2.  
PD 26-AUG-2004.  
PA (AMHP ) WYETH.  
PA (BURC/) BURCZYNSKI M.  
PA (TWIN/) TWINE N.  
PA (DORN/) DORNER A J.  
PA (TREP/) TREPICCHIO W L.  
Query Match 10.3%; Score 234.2; DB 13; Length 128978;  
Best Local Similarity 85.8%; Pred. No. 2.5e-48;  
RESULT 152  
ID ADX07226 standard; DNA; 128978 BP.  
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1791.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 10.3%; Score 234.2; DB 14; Length 128978;  
Best Local Similarity 85.8%; Pred. No. 2.5e-48;  
RESULT 153  
ID ABK42516 standard; DNA; 31871 BP.  
DE Genomic sequence #415 encoding novel human connective tissue polypeptide.  
PN WO200155343-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 234; DB 4; Length 31871;  
Best Local Similarity 80.8%; Pred. No. 1.5e-48;  
RESULT 154  
ID ADB60672 standard; DNA; 31871 BP.  
DE Connective tissue related genomic DNA #415.  
PN US2003054375-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 234; DB 9; Length 31871;

Best Local Similarity 80.8%; Pred. No. 1.5e-48;  
RESULT 155  
ID AAK68089 standard; DNA; 40742 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22901.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 234; DB 4; Length 40742;  
Best Local Similarity 80.8%; Pred. No. 1.7e-48;  
RESULT 156  
ID AAK79886 standard; DNA; 40742 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34698.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 234; DB 4; Length 40742;  
Best Local Similarity 80.8%; Pred. No. 1.7e-48;  
RESULT 157  
ID AED89390 standard; DNA; 143389 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 30.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 10.2%; Score 234; DB 14; Length 143389;  
Best Local Similarity 89.2%; Pred. No. 3e-48;  
RESULT 158  
ID AED89384 standard; DNA; 150314 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 24.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 10.2%; Score 234; DB 14; Length 150314;  
Best Local Similarity 89.2%; Pred. No. 3.1e-48;  
RESULT 159  
ID ABK84798 standard; cDNA; 220895 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1369.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.2%; Score 234; DB 6; Length 220895;  
Best Local Similarity 80.8%; Pred. No. 3.6e-48;  
RESULT 160  
ID ADR52737 standard; DNA; 220895 BP.  
DE Drug therapy altered expressed gene #88.  
PN WO2004072265-A2.  
PD 26-AUG-2004.  
PA (AMHP ) WYETH.  
PA (BURC/) BURCZYNSKI M.  
PA (TWIN/) TWINE N.  
PA (DORN/) DORNER A J.  
PA (TREP/) TREPICCHIO W L.  
Query Match 10.2%; Score 234; DB 13; Length 220895;  
Best Local Similarity 80.8%; Pred. No. 3.6e-48;  
RESULT 161  
ID ADN30029 standard; DNA; 7001 BP.  
DE Human cytokine-inducible kinase associated DNA #5.  
PN US2004101857-A1.  
PD 27-MAY-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.2%; Score 233.8; DB 12; Length 7001;  
Best Local Similarity 87.3%; Pred. No. 8.7e-49;  
RESULT 162  
ID ADQ97703 standard; DNA; 103665 BP.  
DE Human cancer associated sequence HD10-031, SEQ ID 680.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 233.8; DB 12; Length 103665;  
Best Local Similarity 83.6%; Pred. No. 2.9e-48;  
RESULT 163  
ID AED18064 standard; DNA; 107603 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 315.  
PN WO2005098041-A2.

PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 10.2%; Score 233.8; DB 14; Length 107603;  
Best Local Similarity 83.7%; Pred. No. 3e-48;  
RESULT 164  
ID AAD02697 standard; DNA; 160552 BP.  
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.  
PN WO200106015-A1.  
PD 25-JAN-2001.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 10.2%; Score 233.6; DB 4; Length 160552;  
Best Local Similarity 86.8%; Pred. No. 4e-48;  
RESULT 165  
ID AAV83945 standard; DNA; 1701 BP.  
DE Bacterial artificial chromosome (BAC)-F2 contig 5.  
PN WO9851790-A1.  
PD 19-NOV-1998.  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
Query Match 10.2%; Score 233.2; DB 2; Length 1701;  
Best Local Similarity 82.4%; Pred. No. 6.6e-49;  
RESULT 166  
ID ABQ80846 standard; cDNA; 2195 BP.  
DE Tyrosine specific protein phosphatase 23.87 coding sequence.  
PN CN1352275-A.  
PD 05-JUN-2002.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match 10.2%; Score 233.2; DB 6; Length 2195;  
Best Local Similarity 88.3%; Pred. No. 7.4e-49;  
RESULT 167  
ID ADK43203 standard; DNA; 176001 BP.  
DE Human protein tyrosine phosphatase, receptor type alpha (PTPRA) gDNA 2.  
PN WO2004011623-A2.  
PD 05-FEB-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.2%; Score 233.2; DB 12; Length 176001;  
Best Local Similarity 82.4%; Pred. No. 5.3e-48;  
RESULT 168  
ID ABT10147 standard; cDNA; 185035 BP.  
DE Human breast cancer associated coding sequence SEQ ID NO: 281.  
PN WO200259271-A2.  
PD 01-AUG-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.2%; Score 233.2; DB 6; Length 185035;  
Best Local Similarity 88.3%; Pred. No. 5.4e-48;  
RESULT 169  
ID ACA64951 standard; DNA; 185035 BP.  
DE Human FEN1 DNA corresponding to AC004770.  
PN DE10127572-A1.  
PD 05-DEC-2002.  
PA (PATH-) PATHOARRAY GMBH.  
Query Match 10.2%; Score 233.2; DB 8; Length 185035;  
Best Local Similarity 88.3%; Pred. No. 5.4e-48;  
RESULT 170  
ID ADQ20284 standard; DNA; 185035 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3104.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.2%; Score 233.2; DB 12; Length 185035;  
Best Local Similarity 88.3%; Pred. No. 5.4e-48;  
RESULT 171  
ID ADK43195 standard; DNA; 186739 BP.  
DE Human protein tyrosine phosphatase, receptor type alpha (PTPRA) gDNA.  
PN WO2004011623-A2.  
PD 05-FEB-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.2%; Score 233.2; DB 12; Length 186739;  
Best Local Similarity 82.4%; Pred. No. 5.4e-48;  
RESULT 172  
ID ACN44514 standard; DNA; 256493 BP.  
DE Human genomic sequence hCG17361.  
PN WO2003073826-A2.  
PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.2%; Score 233; DB 11; Length 256493;  
Best Local Similarity 76.8%; Pred. No. 7e-48;  
RESULT 173  
ID ADQ97870 standard; DNA; 121160 BP.  
DE Human cancer associated sequence HD11-015, SEQ ID 847.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 232.8; DB 12; Length 121160;  
Best Local Similarity 88.6%; Pred. No. 5.6e-48;  
RESULT 174  
ID ADQ97183 standard; DNA; 138627 BP.  
DE Human cancer associated sequence HD08-011, SEQ ID 159.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.2%; Score 232.8; DB 12; Length 138627;  
Best Local Similarity 87.3%; Pred. No. 6e-48;  
RESULT 175  
ID ABV49209 standard; cDNA; 461 BP.  
DE Human prostate expression marker cDNA 49200.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.2%; Score 232.6; DB 5; Length 461;  
Best Local Similarity 83.2%; Pred. No. 5.2e-49;  
RESULT 176  
ID ABQ88176 standard; cDNA; 100301 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 83.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.2%; Score 232.6; DB 6; Length 100301;  
Best Local Similarity 85.5%; Pred. No. 5.8e-48;  
RESULT 177  
ID ADQ20754 standard; DNA; 100301 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3574.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.2%; Score 232.6; DB 12; Length 100301;  
Best Local Similarity 85.5%; Pred. No. 5.8e-48;  
RESULT 178  
ID ADL13684 standard; DNA; 247509 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #216.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.2%; Score 232.6; DB 10; Length 247509;  
Best Local Similarity 84.3%; Pred. No. 8.8e-48;  
RESULT 179  
Query Match 10.2%; Score 232.4; DB 9; Length 102457;  
Best Local Similarity 85.0%; Pred. No. 6.6e-48;  
RESULT 180  
Query Match 10.2%; Score 232.4; DB 9; Length 110000;  
Best Local Similarity 82.7%; Pred. No. 6.8e-48;  
RESULT 181  
Query Match 10.2%; Score 232.4; DB 12; Length 110000;  
Best Local Similarity 82.7%; Pred. No. 6.8e-48;  
RESULT 182  
Query Match 10.2%; Score 232.4; DB 14; Length 110000;  
Best Local Similarity 82.7%; Pred. No. 6.8e-48;  
RESULT 183  
ID AED34666 standard; DNA; 458207 BP.  
DE ABL1 genomic DNA SEQ ID NO 2.  
PN WO2005094291-A2.  
PD 13-OCT-2005.  
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.  
Query Match 10.2%; Score 232.4; DB 14; Length 110000;  
Best Local Similarity 88.9%; Pred. No. 6.8e-48;  
RESULT 184



ID AED89420 standard; DNA; 171427 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 60.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 10.2%; Score 232.4; DB 14; Length 171427;  
Best Local Similarity 83.8%; Pred. No. 8.4e-48;  
RESULT 185  
ID AED18538 standard; DNA; 184666 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 789.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 10.2%; Score 232.4; DB 14; Length 184666;  
Best Local Similarity 88.9%; Pred. No. 8.6e-48;  
RESULT 186  
ID AAK85311 standard; DNA; 19497 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40123.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 232.2; DB 4; Length 19497;  
Best Local Similarity 84.5%; Pred. No. 3.5e-48;  
RESULT 187  
ID AAK82215 standard; DNA; 31934 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37027.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 232.2; DB 4; Length 31934;  
Best Local Similarity 80.3%; Pred. No. 4.4e-48;  
RESULT 188  
ID ABA19342 standard; DNA; 13102 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 11673.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 232; DB 5; Length 13102;  
Best Local Similarity 79.0%; Pred. No. 3.3e-48;  
RESULT 189  
ID AAS28623 standard; DNA; 15366 BP.  
DE Genomic sequence #463 encoding for novel human respiratory antigen.  
PN WO200155448-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 232; DB 4; Length 15366;  
Best Local Similarity 84.0%; Pred. No. 3.6e-48;  
RESULT 190  
ID ADG41819 standard; DNA; 15366 BP.  
DE Human respiratory system associated genomic DNA seq id 1057.  
PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 232; DB 10; Length 15366;  
Best Local Similarity 84.0%; Pred. No. 3.6e-48;  
RESULT 191  
ID ADI97593 standard; DNA; 15366 BP.  
DE Human respiratory system associated polypeptide-related DNA SeqID1057.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.2%; Score 232; DB 11; Length 15366;  
Best Local Similarity 84.0%; Pred. No. 3.6e-48;  
RESULT 192  
ID ADP13586 standard; DNA; 170245 BP.  
DE Renal cell carcinoma differentially expressed gene #322.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.

PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
Query Match 10.2%; Score 232; DB 12; Length 170245;  
Best Local Similarity 79.0%; Pred. No. 1.1e-47;  
RESULT 193  
ID ABS56564 standard; DNA; 260209 BP.  
DE Human SULF2 genomic DNA sequence.  
PN WO200259327-A2.  
PD 01-AUG-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 10.2%; Score 232; DB 6; Length 260209;  
Best Local Similarity 85.2%; Pred. No. 1.3e-47;  
RESULT 194  
ID ADN16204 standard; DNA; 260209 BP.  
DE Human sulfatase SULF1 gene.  
PN WO2004031365-A2.  
PD 15-APR-2004.  
PA (REGC ) UNIV CALIFORNIA.  
PA (THIO-) THIOS PHARM INC.  
Query Match 10.2%; Score 232; DB 12; Length 260209;  
Best Local Similarity 85.2%; Pred. No. 1.3e-47;  
RESULT 195  
ID ADD72080 standard; CDNA; 1434 BP.  
DE Human urinary specific nucleic acid sequence SEQ ID NO:364.  
PN WO2003060146-A2.  
PD 24-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match 10.1%; Score 231.8; DB 10; Length 1434;  
Best Local Similarity 78.6%; Pred. No. 1.4e-48;  
RESULT 196  
ID ABA07182 standard; DNA; 4748 BP.  
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 501.  
PN WO200155206-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 231.8; DB 4; Length 4748;  
Best Local Similarity 81.4%; Pred. No. 2.4e-48;  
RESULT 197  
ID AAK89814 standard; DNA; 4748 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3390.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 231.8; DB 4; Length 4748;  
Best Local Similarity 81.4%; Pred. No. 2.4e-48;  
RESULT 198  
ID AAK80364 standard; DNA; 18544 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35176.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 231.8; DB 4; Length 18544;  
Best Local Similarity 83.6%; Pred. No. 4.4e-48;  
RESULT 199  
ID ADP65343 standard; DNA; 57038 BP.  
DE Human sequence from clone RP5-1009E24 on chromosome 20 Contains DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 10.1%; Score 231.8; DB 11; Length 57038;  
Best Local Similarity 63.2%; Pred. No. 7.3e-48;  
RESULT 200  
ID ADP65471 standard; DNA; 92794 BP.  
DE Human sequence from clone RP5-1009E24 on chromosome 20 DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 10.1%; Score 231.8; DB 11; Length 92794;  
Best Local Similarity 63.2%; Pred. No. 9e-48;  
RESULT 201  
Query Match 10.1%; Score 231.8; DB 10; Length 110000;  
Best Local Similarity 87.2%; Pred. No. 9.8e-48;  
RESULT 202

ID ABZ72040 standard; DNA; 207433 BP.  
DE Gene 216 H194BAC1098L22 nucleotide sequence SEQ ID NO 5.  
PN WO200178894-A2.  
PD 25-OCT-2001.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 10.1%; Score 231.8; DB 5; Length 207433;  
RESULT 203  
ID ABX74891 standard; DNA; 207433 BP.  
DE BAC1098L22 DNA sequence.  
PN WO200283077-A2.  
PD 24-OCT-2002.  
PA (SCHE ) SCHERING CORP.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 10.1%; Score 231.8; DB 8; Length 207433;  
RESULT 204  
ID ADJ36614 standard; DNA; 207433 BP.  
DE Bacterial artificial chromosome RPCI-11.  
PN US2004002470-A1.  
PD 01-JAN-2004.  
PA (KEIT/) KEITH T.  
PA (LITT/) LITTLE R D.  
PA (VEER/) VAN EERDEWEGH P.  
PA (DUPU/) DUPUIS J.  
PA (DMAS/) DEL MASTRO R G.  
PA (SIMO/) SIMON J.  
PA (ALLE/) ALLEN K.  
PA (PAND/) PANDIT S.  
Query Match  
Best Local Similarity 10.1%; Score 231.8; DB 12; Length 207433;  
RESULT 205  
ID ADL81193 standard; DNA; 207433 BP.  
DE BAC1098L22 DNA sequence.  
PN US2004023215-A1.  
PD 05-FEB-2004.  
PA (KEIT/) KEITH T.  
PA (LITT/) LITTLE R D.  
PA (EERD/) EERDEWEGH P V.  
PA (DUPU/) DUPUIS J.  
PA (DMAS/) DEL MASTRO R G.  
PA (SIMO/) SIMON J.  
PA (ALLE/) ALLEN K.  
PA (PAND/) PANDIT S.  
Query Match  
Best Local Similarity 10.1%; Score 231.8; DB 12; Length 207433;  
RESULT 206  
ID ABV19436 standard; cDNA; 461 BP.  
DE Human prostate expression marker cDNA 19427.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 5; Length 461;  
RESULT 207  
ID AAL05229 standard; DNA; 23748 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7917.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 4; Length 23748;  
RESULT 208  
ID ABL98112 standard; DNA; 23748 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2764.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 4; Length 23748;  
RESULT 209  
ID ACF62730 standard; DNA; 164702 BP.  
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:658.

PN WO2003013534-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 8; Length 164702;  
RESULT 210  
ID ADB20845 standard; DNA; 164702 BP.  
DE MRP1 based cancer related nucleic acid SEQ ID NO:658.  
PN WO2003013533-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 8; Length 164702;  
RESULT 211  
ID ADB87934 standard; DNA; 164702 BP.  
DE Human UGT1A1 gene sequence SEQ ID NO:658.  
PN WO2003013536-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 10; Length 164702;  
RESULT 212  
ID ADB96917 standard; DNA; 164702 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:658.  
PN WO2003013537-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 10; Length 164702;  
RESULT 213  
ID ADB92108 standard; DNA; 164702 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:658.  
PN WO2003013535-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 10; Length 164702;  
RESULT 214  
ID ADL13638 standard; DNA; 186528 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #170.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 10.1%; Score 231.6; DB 10; Length 186528;  
RESULT 215  
ID ABA14926 standard; DNA; 840 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7257.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.1%; Score 231.4; DB 5; Length 840;  
RESULT 216  
ID ABA14923 standard; DNA; 3765 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7254.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.1%; Score 231.4; DB 5; Length 3765;  
RESULT 217  
ID ABA14921 standard; DNA; 6867 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7252.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.1%; Score 231.4; DB 5; Length 6867;  
RESULT 218  
ID ABA14924 standard; DNA; 7270 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7255.  
PN WO200159063-A2.

PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 231.4; DB 5; Length 7270;  
Best Local Similarity 85.0%; Pred. No. 3.6e-48;  
RESULT 219  
ID AAK67891 standard; DNA; 8515 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22703.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 231.4; DB 4; Length 8515;  
Best Local Similarity 74.7%; Pred. No. 3.9e-48;  
RESULT 220  
ID ABD33424 standard; DNA; 39451 BP.  
DE Human cancer-associated (CA) gene HD07-079.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.1%; Score 231.4; DB 13; Length 39451;  
Best Local Similarity 85.0%; Pred. No. 7.8e-48;  
RESULT 221  
ID AEJ13546 standard; DNA; 39451 BP.  
DE Cancer-associated gene sequence - SEQ ID 554.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 10.1%; Score 231.4; DB 15; Length 39451;  
Best Local Similarity 85.0%; Pred. No. 7.8e-48;  
RESULT 222  
ID ADG86768 standard; DNA; 104245 BP.  
DE Human clone RP1-109F14 from chromosome 6p21.2-21.3.  
PN US2003224514-A1.  
PD 04-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.1%; Score 231.4; DB 12; Length 104245;  
Best Local Similarity 85.0%; Pred. No. 1.2e-47;  
RESULT 223  
ID ADL34706 standard; DNA; 104245 BP.  
DE Human PPAR-delta DNA fragment SEQ ID 4.  
PN US2004063129-A1.  
PD 01-APR-2004.  
PA (GAAR/) GAARDE W.  
PA (FREI/) FREIER S M.  
PA (WATT/) WATT A T.  
Query Match 10.1%; Score 231.4; DB 12; Length 104245;  
Best Local Similarity 85.0%; Pred. No. 1.2e-47;  
RESULT 224  
Query Match 10.1%; Score 231.4; DB 12; Length 110000;  
Best Local Similarity 82.7%; Pred. No. 1.2e-47;  
RESULT 225  
ID AAD48308 standard; DNA; 114693 BP.  
DE Human transporter protein encoding gene.  
Query Match 10.1%; Score 231.4; DB 8; Length 114693;  
Best Local Similarity 80.6%; Pred. No. 1.3e-47;  
RESULT 226  
ID AEF75216 standard; DNA; 135928 BP.  
DE Human polynucleotide #730.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 10.1%; Score 231.4; DB 15; Length 135928;  
Best Local Similarity 86.2%; Pred. No. 1.4e-47;  
RESULT 227  
ID ADP45593 standard; DNA; 147300 BP.  
DE Human Rho family guanine-nucleotide exchange factor KIAA0861 gDNA.  
PN WO2004047623-A2.  
PD 10-JUN-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.1%; Score 231.4; DB 12; Length 147300;  
Best Local Similarity 86.2%; Pred. No. 1.4e-47;  
RESULT 228

ID ADX98570 standard; DNA; 147700 BP.  
DE Human guanine-nucleotide exchange factor KIAA0861 genomic DNA.  
Query Match 10.1%; Score 231.4; DB 14; Length 147700;  
Best Local Similarity 86.2%; Pred. No. 1.4e-47;  
RESULT 229  
ID AEE96613 standard; DNA; 147700 BP.  
DE KIAA0861 genomic DNA sequence, SEQ ID NO:1.  
PN WO2005118856-A1.  
PD 15-DEC-2005.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.1%; Score 231.4; DB 15; Length 147700;  
Best Local Similarity 86.2%; Pred. No. 1.4e-47;  
RESULT 230  
ID ADP13586 standard; DNA; 170245 BP.  
DE Renal cell carcinoma differentially expressed gene #322.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
Query Match 10.1%; Score 231.4; DB 12; Length 170245;  
Best Local Similarity 85.0%; Pred. No. 1.5e-47;  
RESULT 231  
ID AED89398 standard; DNA; 171162 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 38.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 10.1%; Score 231.4; DB 14; Length 171162;  
Best Local Similarity 87.5%; Pred. No. 1.5e-47;  
RESULT 232  
ID AEE06394 standard; DNA; 267966 BP.  
DE Glycogen synthase kinase-3beta (GSK-3beta) gene.  
PN WO2005108582-A1.  
PD 17-NOV-2005.  
PA (GARV-) GARVAN INST MEDICAL RES.  
Query Match 10.1%; Score 231.4; DB 14; Length 267966;  
Best Local Similarity 80.6%; Pred. No. 1.8e-47;  
RESULT 233  
ID ACN44570 standard; DNA; 19640 BP.  
DE Human genomic sequence hCG38237.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.1%; Score 231.2; DB 11; Length 19640;  
Best Local Similarity 85.7%; Pred. No. 6.4e-48;  
RESULT 234  
ID AEE04781 standard; DNA; 112679 BP.  
DE Cancer-associated gene SEQ ID NO:99.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 10.1%; Score 231.2; DB 14; Length 112679;  
Best Local Similarity 84.5%; Pred. No. 1.4e-47;  
RESULT 235  
ID ABD33075 standard; DNA; 152759 BP.  
DE Human cancer-associated (CA) gene HD07-002.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.1%; Score 231.2; DB 13; Length 152759;  
Best Local Similarity 83.3%; Pred. No. 1.6e-47;  
RESULT 236  
ID AEJ13002 standard; DNA; 152759 BP.  
DE Cancer-associated gene sequence - SEQ ID 10.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.



Query Match 10.1%; Score 231.2; DB 15; Length 152759;  
Best Local Similarity 83.3%; Pred. No. 1.6e-47;  
RESULT 237  
ID AAL03321 standard; DNA; 292 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 6009.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 231; DB 4; Length 292;  
Best Local Similarity 89.1%; Pred. No. 1.1e-48;  
RESULT 238  
ID ACN44490 standard; DNA; 32865 BP.  
DE Human genomic sequence hCG25375.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.1%; Score 231; DB 11; Length 32865;  
Best Local Similarity 85.2%; Pred. No. 9.1e-48;  
RESULT 239  
ID ABD33436 standard; DNA; 52710 BP.  
DE Human cancer-associated (CA) gene HD07-082.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.1%; Score 231; DB 13; Length 52710;  
Best Local Similarity 85.2%; Pred. No. 1.1e-47;  
RESULT 240  
ID AEJ13564 standard; DNA; 52710 BP.  
DE Cancer-associated gene sequence - SEQ ID 572.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 10.1%; Score 231; DB 15; Length 52710;  
Best Local Similarity 85.2%; Pred. No. 1.1e-47;  
RESULT 241  
ID ADH77123 standard; DNA; 126001 BP.  
DE Human PAZ/PIWI domain-containing protein polynucleotide #3.  
PN US2003232442-A1.  
PD 18-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.1%; Score 231; DB 12; Length 126001;  
Best Local Similarity 85.2%; Pred. No. 1.7e-47;  
RESULT 242  
ID ADD71332 standard; DNA; 720 BP.  
DE Glutamine:fructose-6-phosphate amide transferase 1 gene intron 13.  
PN WO2003023063-A1.  
PD 20-MAR-2003.  
PA (SANY ) SANKYO CO LTD.  
Query Match 10.1%; Score 230.8; DB 10; Length 720;  
Best Local Similarity 81.4%; Pred. No. 1.8e-48;  
RESULT 243  
ID ADA02576 standard; DNA; 87878 BP.  
DE Human FKBP5 carcinoma associated gene, SEQ ID NO:1094.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.1%; Score 230.8; DB 9; Length 87878;  
Best Local Similarity 79.4%; Pred. No. 1.6e-47;  
RESULT 244  
ID ADB72314 standard; DNA; 87878 BP.  
DE Human FKBP5 Gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.1%; Score 230.8; DB 10; Length 87878;  
Best Local Similarity 79.4%; Pred. No. 1.6e-47;  
RESULT 245  
ID ADE95824 standard; DNA; 87878 BP.  
DE Human FKBP5 gene genomic DNA sequence.  
PN WO2003039484-A2.  
PD 15-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.

Query Match 10.1%; Score 230.8; DB 10; Length 87878;  
Best Local Similarity 79.4%; Pred. No. 1.6e-47;  
RESULT 246  
ID AEK60095 standard; DNA; 87878 BP.  
DE Human FKBP5 genomic sequence, SEQ ID NO: 82.  
PN US2006204982-A1.  
PD 14-SEP-2006.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 10.1%; Score 230.8; DB 15; Length 87878;  
Best Local Similarity 79.4%; Pred. No. 1.6e-47;  
RESULT 247  
ID ADD71350 standard; DNA; 93390 BP.  
DE Glutamine:fructose-6-phosphate amide transferase 1 genomic sequence.  
PN WO2003023063-A1.  
PD 20-MAR-2003.  
PA (SANY ) SANKYO CO LTD.  
Query Match 10.1%; Score 230.8; DB 10; Length 93390;  
Best Local Similarity 81.4%; Pred. No. 1.6e-47;  
RESULT 248  
ID AAK67371 standard; DNA; 13496 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22183.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230.6; DB 4; Length 13496;  
Best Local Similarity 85.4%; Pred. No. 7.7e-48;  
RESULT 249  
ID AAS28364 standard; DNA; 17498 BP.  
DE Genomic sequence #204 encoding for novel human respiratory antigen.  
PN WO200155448-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230.6; DB 4; Length 17498;  
Best Local Similarity 81.8%; Pred. No. 8.7e-48;  
RESULT 250  
ID ADG41560 standard; DNA; 17498 BP.  
DE Human respiratory system associated genomic DNA seq id 798.  
PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230.6; DB 10; Length 17498;  
Best Local Similarity 81.8%; Pred. No. 8.7e-48;  
RESULT 251  
ID ADI97334 standard; DNA; 17498 BP.  
DE Human respiratory system associated polypeptide-related DNA SeqID798.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230.6; DB 11; Length 17498;  
Best Local Similarity 81.8%; Pred. No. 8.7e-48;  
RESULT 252  
ID AEC74895 standard; DNA; 69914 BP.  
DE Human tyrosine phosphatase PTPN22 genomic DNA.  
Query Match 10.1%; Score 230.6; DB 14; Length 69914;  
Best Local Similarity 72.7%; Pred. No. 1.6e-47;  
RESULT 253  
ID ABD33104 standard; DNA; 130877 BP.  
DE Human cancer-associated (CA) gene HD07-009.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.1%; Score 230.6; DB 13; Length 130877;  
Best Local Similarity 80.0%; Pred. No. 2.1e-47;  
RESULT 254  
ID AEJ13046 standard; DNA; 130877 BP.  
DE Cancer-associated gene sequence - SEQ ID 54.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 10.1%; Score 230.6; DB 15; Length 130877;  
Best Local Similarity 80.0%; Pred. No. 2.1e-47;

RESULT 255  
ID ADL13962 standard; DNA; 160198 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #494.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.1%; Score 230.6; DB 10; Length 160198;  
Best Local Similarity 82.0%; Pred. No. 2.3e-47;  
RESULT 256  
ID ACF62732 standard; DNA; 177531 BP.  
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:660.  
PN WO2003013534-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 10.1%; Score 230.6; DB 8; Length 177531;  
Best Local Similarity 82.0%; Pred. No. 2.5e-47;  
RESULT 257  
ID ADB20847 standard; DNA; 177531 BP.  
DE MRP1 based cancer related nucleic acid SEQ ID NO:660.  
PN WO2003013533-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 10.1%; Score 230.6; DB 8; Length 177531;  
Best Local Similarity 82.0%; Pred. No. 2.5e-47;  
RESULT 258  
ID ADB87936 standard; DNA; 177531 BP.  
DE Human UGT1A1 gene sequence SEQ ID NO:660.  
PN WO2003013536-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 10.1%; Score 230.6; DB 10; Length 177531;  
Best Local Similarity 82.0%; Pred. No. 2.5e-47;  
RESULT 259  
ID ADB96919 standard; DNA; 177531 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:660.  
PN WO2003013537-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 10.1%; Score 230.6; DB 10; Length 177531;  
Best Local Similarity 82.0%; Pred. No. 2.5e-47;  
RESULT 260  
ID ADB92110 standard; DNA; 177531 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:660.  
PN WO2003013535-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 10.1%; Score 230.6; DB 10; Length 177531;  
Best Local Similarity 82.0%; Pred. No. 2.5e-47;  
RESULT 261  
ID ADH74617 standard; DNA; 177531 BP.  
DE Human BAC clone GS1-259H13 CYP3A5 genomic DNA.  
PN US2003143537-A1.  
PD 31-JUL-2003.  
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
Query Match 10.1%; Score 230.6; DB 10; Length 177531;  
Best Local Similarity 82.0%; Pred. No. 2.5e-47;  
RESULT 262  
ID AAK67462 standard; DNA; 24268 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22274.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230.4; DB 4; Length 24268;  
Best Local Similarity 86.1%; Pred. No. 1.1e-47;  
RESULT 263  
ID ABT44359 standard; DNA; 6777 BP.  
DE Concatenated exons of the human oestrogen receptor beta DNA.  
PN WO2003050133-A1.  
PD 19-JUN-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.1%; Score 230.2; DB 9; Length 6777;  
Best Local Similarity 86.9%; Pred. No. 7.2e-48;  
RESULT 264

ID ADS89097 standard; DNA; 13286 BP.  
DE Human ESR2 gene SEQ ID NO:113.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 10.1%; Score 230.2; DB 13; Length 13286;  
Best Local Similarity 86.9%; Pred. No. 9.7e-48;  
RESULT 265  
ID AAK69104 standard; DNA; 26059 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23916.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230.2; DB 4; Length 26059;  
Best Local Similarity 75.1%; Pred. No. 1.3e-47;  
RESULT 266  
ID ABT44365 standard; DNA; 113000 BP.  
DE Partial genomic sequence of human oestrogen receptor beta DNA.  
PN WO2003050133-A1.  
PD 19-JUN-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.1%; Score 230.2; DB 9; Length 113000;  
Best Local Similarity 86.9%; Pred. No. 2.5e-47;  
RESULT 267  
ID AEF19127 standard; DNA; 188056 BP.  
DE Human NIPBL genomic sequence.  
PN US2006003354-A1.  
PD 05-JAN-2006.  
PA (KRAN/) KRANTZ I D.  
PA (JACK/) JACKSON L G.  
Query Match 10.1%; Score 230.2; DB 15; Length 188056;  
Best Local Similarity 85.6%; Pred. No. 3.2e-47;  
RESULT 268  
ID ADV16961 standard; DNA; 290040 BP.  
DE Human protein associated with myc (PAM) genomic DNA.  
PN EP1481685-A1.  
PD 01-DEC-2004.  
PA (AVET) AVENTIS PHARMA DEUT GMBH.  
Query Match 10.1%; Score 230.2; DB 14; Length 290040;  
Best Local Similarity 75.1%; Pred. No. 3.9e-47;  
RESULT 269  
ID ADU92049 standard; DNA; 290040 BP.  
DE Human PAM (protein associated with myc) genomic DNA.  
PN EP1481680-A1.  
PD 01-DEC-2004.  
PA (AVET) AVENTIS PHARMA DEUT GMBH.  
Query Match 10.1%; Score 230.2; DB 14; Length 290040;  
Best Local Similarity 75.1%; Pred. No. 3.9e-47;  
RESULT 270  
ID AAS43104 standard; DNA; 325791 BP.  
DE Human Oestrogen receptor beta gene.  
PN WO200162793-A2.  
PD 30-AUG-2001.  
PA (PEKE) PE CORP NY.  
Query Match 10.1%; Score 230.2; DB 4; Length 325791;  
Best Local Similarity 86.9%; Pred. No. 4.1e-47;  
RESULT 271  
ID AAI58350 standard; cDNA; 955 BP.  
DE Human polynucleotide SEQ ID NO 553.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.1%; Score 230; DB 4; Length 955;  
Best Local Similarity 87.7%; Pred. No. 3.3e-48;  
RESULT 272  
ID ADQ98558 standard; cDNA; 955 BP.  
DE DNA encoding human GPCR-like protein seqid 228.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 10.1%; Score 230; DB 5; Length 955;  
Best Local Similarity 87.7%; Pred. No. 3.3e-48;  
RESULT 273

ID ADB48318 standard; cDNA; 955 BP.  
DE Novel human CDNA SEQ ID NO 228.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 10.1%; Score 230; DB 9; Length 955;  
Best Local Similarity 87.7%; Pred. No. 3.3e-48;  
RESULT 274  
ID AAL37485 standard; DNA; 17146 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3850.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230; DB 4; Length 17146;  
Best Local Similarity 87.7%; Pred. No. 1.2e-47;  
RESULT 275  
ID ABX60473 standard; cDNA; 17146 BP.  
DE CDNA encoding novel human musculoskeletal system antigen #2817.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 10.1%; Score 230; DB 8; Length 17146;  
Best Local Similarity 87.7%; Pred. No. 1.2e-47;  
RESULT 276  
ID ADJ31223 standard; DNA; 17146 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3850.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230; DB 12; Length 17146;  
Best Local Similarity 87.7%; Pred. No. 1.2e-47;  
RESULT 277  
ID AAL37486 standard; DNA; 30568 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3851.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230; DB 4; Length 30568;  
Best Local Similarity 87.7%; Pred. No. 1.6e-47;  
RESULT 278  
ID ABX60474 standard; cDNA; 30568 BP.  
DE CDNA encoding novel human musculoskeletal system antigen #2818.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 10.1%; Score 230; DB 8; Length 30568;  
Best Local Similarity 87.7%; Pred. No. 1.6e-47;  
RESULT 279  
ID ADJ31224 standard; DNA; 30568 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3851.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 230; DB 12; Length 30568;  
Best Local Similarity 87.7%; Pred. No. 1.6e-47;  
RESULT 280  
ID ABA14925 standard; DNA; 7872 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7256.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 229.8; DB 5; Length 7872;  
Best Local Similarity 84.6%; Pred. No. 9.7e-48;  
RESULT 281  
ID AAK67892 standard; DNA; 24884 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22704.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 229.8; DB 4; Length 24884;  
Best Local Similarity 74.4%; Pred. No. 1.6e-47;  
RESULT 282  
ID ACN44218 standard; DNA; 66972 BP.  
DE Human genomic sequence HCG15409.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.1%; Score 229.8; DB 11; Length 66972;  
Best Local Similarity 79.2%; Pred. No. 2.5e-47;  
RESULT 283  
ID AAD53223 standard; DNA; 487980 BP.  
DE Human chromosome 3 p-arm breakpoint region.  
PN WO200290541-A1.  
PD 14-NOV-2002.  
PA (MURD-) MURDOCH CHILDRENS RES INST.  
PA (DELA/) DELATYCKI M.  
Query Match 10.1%; Score 229.8; DB 8; Length 110000;  
Best Local Similarity 83.5%; Pred. No. 3.2e-47;  
RESULT 284  
ID AED18452 standard; DNA; 180283 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 703.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL) UNIV FLORIDA RES FOUND INC.  
Query Match 10.1%; Score 229.8; DB 14; Length 180283;  
Best Local Similarity 78.5%; Pred. No. 4e-47;  
RESULT 285  
ID AAH15562 standard; cDNA; 1645 BP.  
DE Human CDNA sequence SEQ ID NO:13851.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 10.1%; Score 229.6; DB 4; Length 1645;  
Best Local Similarity 83.0%; Pred. No. 5.4e-48;  
RESULT 286  
ID ABK72689 standard; DNA; 17800 BP.  
DE Human potassium channel interacting protein (PCIP) genomic DNA #3.  
PN WO200226984-A2.  
PD 04-APR-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 10.1%; Score 229.6; DB 6; Length 17800;  
Best Local Similarity 85.4%; Pred. No. 1.6e-47;  
RESULT 287  
ID ADQ97497 standard; DNA; 21850 BP.  
DE Human cancer associated sequence HD09-005, SEQ ID 474.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.1%; Score 229.6; DB 12; Length 21850;  
Best Local Similarity 86.6%; Pred. No. 1.7e-47;  
RESULT 288  
ID AAK76168 standard; DNA; 25541 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30980.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 229.6; DB 4; Length 25541;  
Best Local Similarity 82.9%; Pred. No. 1.9e-47;  
RESULT 289  
ID AAS28368 standard; DNA; 32248 BP.  
DE Genomic sequence #208 encoding for novel human respiratory antigen.  
PN WO200155448-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 229.6; DB 4; Length 32248;  
Best Local Similarity 82.9%; Pred. No. 2.1e-47;  
RESULT 290  
ID ADG41564 standard; DNA; 32248 BP.



DE Human respiratory system associated genomic DNA seq id 802.  
PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 229.6; DB 10; Length 32248;  
Best Local Similarity 82.9%; Pred. No. 2.1e-47;  
RESULT 291  
ID ADI97338 standard; DNA; 32248 BP.  
DE Human respiratory system associated polypeptide-related DNA SeqID802.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 229.6; DB 11; Length 32248;  
Best Local Similarity 82.9%; Pred. No. 2.1e-47;  
RESULT 292  
ID AAK76172 standard; DNA; 34435 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30984.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.1%; Score 229.6; DB 4; Length 34435;  
Best Local Similarity 82.9%; Pred. No. 2.1e-47;  
RESULT 293  
Query Match 10.1%; Score 229.6; DB 8; Length 67571;  
Best Local Similarity 77.2%; Pred. No. 2.9e-47;  
RESULT 294  
ID AEA61148 standard; DNA; 79977 BP.  
DE Human SCNN1B gene genomic sequence SEQ ID NO:58.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB ) BAYER CORP.  
Query Match 10.1%; Score 229.6; DB 14; Length 79977;  
Best Local Similarity 77.6%; Pred. No. 3.1e-47;  
RESULT 295  
ID ADL13556 standard; DNA; 95240 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #88.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.1%; Score 229.6; DB 10; Length 95240;  
Best Local Similarity 84.2%; Pred. No. 3.3e-47;  
RESULT 296  
ID AEI93839 standard; DNA; 97650 BP.  
DE Human glutamate receptor, ionotropic, delta 2 (GRID2) genomic sequence.  
PN WO2006074061-A2.  
PD 13-JUL-2006.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.1%; Score 229.6; DB 15; Length 97650;  
Best Local Similarity 71.5%; Pred. No. 3.4e-47;  
RESULT 297  
ID AED18395 standard; DNA; 128117 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 646.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 10.1%; Score 229.6; DB 14; Length 128117;  
Best Local Similarity 87.9%; Pred. No. 3.8e-47;  
RESULT 298  
ID ACN45054 standard; DNA; 133632 BP.  
DE Human genomic sequence hCG28560.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.1%; Score 229.6; DB 11; Length 133632;  
Best Local Similarity 87.9%; Pred. No. 3.9e-47;  
RESULT 299  
ID ADZ13285 standard; DNA; 133642 BP.  
DE Human cancer-associated genomic DNA #66.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 10.1%; Score 229.6; DB 14; Length 133642;  
Best Local Similarity 87.9%; Pred. No. 3.9e-47;

RESULT 300  
ID AED18452 standard; DNA; 180283 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 703.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 10.1%; Score 229.6; DB 14; Length 180283;  
Best Local Similarity 83.0%; Pred. No. 4.5e-47;  
RESULT 301  
ID ACN44010 standard; DNA; 198522 BP.  
DE Human genomic sequence hCG1643869.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.1%; Score 229.6; DB 11; Length 198522;  
Best Local Similarity 83.0%; Pred. No. 4.7e-47;  
RESULT 302  
ID ADP75180 standard; DNA; 304905 BP.  
DE Human Endophilin 2 gene.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 10.1%; Score 229.6; DB 11; Length 304905;  
Best Local Similarity 87.9%; Pred. No. 5.6e-47;  
RESULT 303  
ID ABD32620 standard; DNA; 27499 BP.  
DE Human cancer-associated genomic DNA HD13-010.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.0%; Score 229.4; DB 13; Length 27499;  
Best Local Similarity 83.7%; Pred. No. 2.2e-47;  
RESULT 304  
ID ACN45006 standard; DNA; 67810 BP.  
DE Human genomic sequence hCG32956.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 229.4; DB 11; Length 67810;  
Best Local Similarity 82.6%; Pred. No. 3.2e-47;  
RESULT 305  
ID AED55989 standard; DNA; 95900 BP.  
DE Human WASPIP DNA.  
PN WO2005100604-A2.  
Query Match 10.0%; Score 229.4; DB 14; Length 95900;  
Best Local Similarity 86.1%; Pred. No. 3.8e-47;  
RESULT 306  
ID ADY70791 standard; DNA; 104424 BP.  
DE Human soluble adenylyl cyclase (SAC) gene SEQ ID NO:21.  
PN CN1548557-A.  
PD 24-NOV-2004.  
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.  
Query Match 10.0%; Score 229.4; DB 14; Length 104424;  
Best Local Similarity 84.9%; Pred. No. 3.9e-47;  
RESULT 307  
ID ADZ46659 standard; DNA; 104424 BP.  
DE Type-II diabetes susceptibility gene SAC, SEQ ID 27.  
PN CN1548553-A.  
PD 24-NOV-2004.  
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.  
Query Match 10.0%; Score 229.4; DB 14; Length 104424;  
Best Local Similarity 84.9%; Pred. No. 3.9e-47;  
RESULT 308  
Query Match 10.0%; Score 229.4; DB 14; Length 110000;  
Best Local Similarity 86.1%; Pred. No. 4e-47;  
RESULT 309  
ID ACN44074 standard; DNA; 128668 BP.  
DE Human genomic sequence hCG40471.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 229.4; DB 11; Length 128668;  
Best Local Similarity 82.7%; Pred. No. 4.3e-47;

RESULT 310  
ID ACN44674 standard; DNA; 129042 BP.  
DE Human genomic sequence hCG27276.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 229.4; DB 11; Length 129042;  
Best Local Similarity 83.7%; Pred. No. 4.3e-47;  
RESULT 311  
ID AAD28763 standard; DNA; 154465 BP.  
DE Human AKAP allelic variant (AKAP10-1) gene.  
PN WO200204489-A2.  
PD 17-JAN-2002.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 6; Length 154465;  
Best Local Similarity 74.9%; Pred. No. 4.7e-47;  
RESULT 312  
ID AAD28762 standard; DNA; 158245 BP.  
DE Human AKAP allelic variant (AKAP10) gene.  
PN WO200204489-A2.  
PD 17-JAN-2002.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 6; Length 158245;  
Best Local Similarity 74.9%; Pred. No. 4.7e-47;  
RESULT 313  
ID AAH02340 standard; DNA; 161425 BP.  
DE Human AKAP10 gene SEQ ID NO: 36.  
PN WO200127857-A2.  
PD 19-APR-2001.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 4; Length 161425;  
Best Local Similarity 74.9%; Pred. No. 4.8e-47;  
RESULT 314  
ID AAH02339 standard; DNA; 162025 BP.  
DE Human AKAP10 gene SEQ ID NO: 35.  
PN WO200127857-A2.  
PD 19-APR-2001.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 4; Length 162025;  
Best Local Similarity 74.9%; Pred. No. 4.8e-47;  
RESULT 315  
ID AAD28758 standard; DNA; 162025 BP.  
DE Human AKAP allelic variant (AKAP10-6) gene.  
PN WO200204489-A2.  
PD 17-JAN-2002.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 6; Length 162025;  
Best Local Similarity 74.9%; Pred. No. 4.8e-47;  
RESULT 316  
ID AAD28759 standard; DNA; 162025 BP.  
DE Human AKAP allelic variant (AKAP10-7) gene.  
PN WO200204489-A2.  
PD 17-JAN-2002.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 6; Length 162025;  
Best Local Similarity 74.9%; Pred. No. 4.8e-47;  
RESULT 317  
ID ADS75958 standard; DNA; 162025 BP.  
DE Human A-kinase anchoring protein 10 allele AKAP10-6 genomic sequence.  
PN WO2004081576-A2.  
PD 23-SEP-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 13; Length 162025;  
Best Local Similarity 74.9%; Pred. No. 4.8e-47;  
RESULT 318  
ID ADS75959 standard; DNA; 162025 BP.  
DE Human A-kinase anchoring protein 10 allele AKAP10-7 genomic sequence.  
PN WO2004081576-A2.  
PD 23-SEP-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 13; Length 162025;  
Best Local Similarity 74.9%; Pred. No. 4.8e-47;  
RESULT 319

ID ADS75963 standard; DNA; 162025 BP.  
DE Human A-kinase anchoring protein 10 allele AKAP10-1 genomic sequence.  
PN WO2004081576-A2.  
PD 23-SEP-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 13; Length 162025;  
Best Local Similarity 74.9%; Pred. No. 4.8e-47;  
RESULT 320  
ID ADS75962 standard; DNA; 162025 BP.  
DE Human A-kinase anchoring protein 10 wild type genomic sequence.  
PN WO2004081576-A2.  
PD 23-SEP-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 10.0%; Score 229.4; DB 13; Length 162025;  
Best Local Similarity 74.9%; Pred. No. 4.8e-47;  
RESULT 321  
ID ACN43938 standard; DNA; 186391 BP.  
DE Human genomic sequence hCG40117.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 229.4; DB 11; Length 186391;  
Best Local Similarity 85.4%; Pred. No. 5.1e-47;  
RESULT 322  
ID ABE04958 standard; DNA; 212235 BP.  
DE Cancer-associated gene SEQ ID NO:276.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 10.0%; Score 229.4; DB 14; Length 212235;  
Best Local Similarity 84.9%; Pred. No. 5.4e-47;  
RESULT 323  
ID ADQ97397 standard; DNA; 225587 BP.  
DE Human cancer associated sequence HD08-043, SEQ ID 374.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.0%; Score 229.4; DB 12; Length 225587;  
Best Local Similarity 82.6%; Pred. No. 5.5e-47;  
RESULT 324  
ID ADL13693 standard; DNA; 231222 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #225.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 10.0%; Score 229.4; DB 10; Length 231222;  
Best Local Similarity 82.9%; Pred. No. 5.6e-47;  
RESULT 325  
ID ABV50077 standard; cDNA; 454 BP.  
DE Human prostate expression marker cDNA 50068.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 10.0%; Score 229.2; DB 8; Length 31670;  
Best Local Similarity 86.8%; Pred. No. 3.8e-48;  
RESULT 326  
ID AAD56093 standard; DNA; 31670 BP.  
DE Human CCR7 carcinoma associated (CA) gene.  
PN WO2003035837-A2.  
PD 01-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 229.2; DB 8; Length 31670;  
Best Local Similarity 83.3%; Pred. No. 2.6e-47;  
RESULT 327  
ID ADA02455 standard; DNA; 31670 BP.  
DE Human CCR7 carcinoma associated gene, SEQ ID NO:974.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 229.2; DB 9; Length 31670;  
Best Local Similarity 83.3%; Pred. No. 2.6e-47;  
RESULT 328  
ID ADB72194 standard; DNA; 31670 BP.

DE Human CCR7 gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match  
Best Local Similarity 10.0%; Score 229.2; DB 10; Length 31670;  
RESULT 329  
ID ADR66958 standard; DNA; 31670 BP.  
DE Human cancer associated gene genomic sequence SEQ ID NO:4.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match  
Best Local Similarity 10.0%; Score 229.2; DB 13; Length 31670;  
RESULT 330  
ID ADZ12484 standard; DNA; 31704 BP.  
DE Human cancer-associated genomic DNA #1.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match  
Best Local Similarity 10.0%; Score 229.2; DB 14; Length 31704;  
RESULT 331  
ID ADQ85988 standard; cDNA; 2373 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2860.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 13; Length 2373;  
RESULT 332  
ID ABT06537 standard; DNA; 2495 BP.  
DE Human oestrogen receptor beta gene fragment.  
PN WO200259347-A2.  
PD 01-AUG-2002.  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 6; Length 2495;  
RESULT 333  
ID ADM83714 standard; DNA; 2495 BP.  
DE Human oestrogen receptor beta gene promoter and partial CDS.  
PN US2003138783-A1.  
PD 24-JUL-2003.  
PA (SUKU/) SUKUMAR S.  
PA (EVRO/) EVRON E.  
PA (DOOL/) DOOLEY W C.  
PA (SACC/) SACCCHI N.  
PA (DAVI/) DAVIDSON N.  
PA (FACK/) FACKLER M J.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 11; Length 2495;  
RESULT 334  
ID AEC22598 standard; DNA; 2495 BP.  
DE Human estrogen receptor beta gene promoter and partial CDS SEQ ID NO:104.  
PN US2005191640-A1.  
PD 01-SEP-2005.  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 14; Length 2495;  
RESULT 335  
ID AAL03517 standard; DNA; 3961 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 6205.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 4; Length 3961;  
RESULT 336  
ID AAL03518 standard; DNA; 3961 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 6206.  
PN WO200155320-A2.

PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 4; Length 3961;  
RESULT 337  
ID AAS36147 standard; DNA; 10758 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1647.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 4; Length 10758;  
RESULT 338  
ID AAS36150 standard; DNA; 10758 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1650.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 4; Length 10758;  
RESULT 339  
ID ADE46841 standard; DNA; 10758 BP.  
DE Human cardiovascular system related genomic DNA #407.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 10; Length 10758;  
RESULT 340  
ID ADE46844 standard; DNA; 10758 BP.  
DE Human cardiovascular system related genomic DNA #410.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 10; Length 10758;  
RESULT 341  
ID ADJ08259 standard; DNA; 10758 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID1647.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 13; Length 10758;  
RESULT 342  
ID ADJ08262 standard; DNA; 10758 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID1650.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 13; Length 10758;  
RESULT 343  
ID AAS36149 standard; DNA; 10759 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1649.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 4; Length 10759;  
RESULT 344  
ID ADE46843 standard; DNA; 10759 BP.  
DE Human cardiovascular system related genomic DNA #409.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 10.0%; Score 229; DB 10; Length 10759;  
RESULT 345  
ID ADJ08261 standard; DNA; 10759 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID1649.  
PN US2004005575-A1.  
PD 08-JAN-2004.



PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 229; DB 13; Length 10759;  
Best Local Similarity 86.3%; Pred. No. 1.8e-47;  
RESULT 346  
ID AD242279 standard; DNA; 14501 BP.  
DE Human urotensin II gene with G7032A SNP Seq 6.  
PN JP2005110606-A.  
PD 28-APR-2005.  
PA (KOKU-) KOKURITSU JUNKANKI BYO CENT SOCHO.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN IYAKUJIN IRYO KIK.  
Query Match 10.0%; Score 229; DB 14; Length 14501;  
Best Local Similarity 85.1%; Pred. No. 2e-47;  
RESULT 347  
ID ADQ59374 standard; DNA; 25899 BP.  
DE Human cancer-associated (CA) gene sequence SEQ ID NO:10.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.0%; Score 229; DB 12; Length 25899;  
Best Local Similarity 85.1%; Pred. No. 2.7e-47;  
RESULT 348  
ID ADT92806 standard; DNA; 50977 BP.  
DE Human DGC8 gene sequence - SEQ ID 1.  
PN JP2004290022-A.  
PD 21-OCT-2004.  
PA (KEIO-) GH KEIO GIJUKU.  
Query Match 10.0%; Score 229; DB 13; Length 50977;  
Best Local Similarity 86.3%; Pred. No. 3.6e-47;  
RESULT 349  
ID ADZ13418 standard; DNA; 85920 BP.  
DE Human cancer-associated genomic DNA #80.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 10.0%; Score 229; DB 14; Length 85920;  
Best Local Similarity 85.1%; Pred. No. 4.6e-47;  
RESULT 350  
ID ABK83568 standard; DNA; 201143 BP.  
DE Human DNA differentially expressed in granulocytic cells #139.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.0%; Score 229; DB 6; Length 201143;  
Best Local Similarity 82.8%; Pred. No. 6.7e-47;  
RESULT 351  
ID ADC87068 standard; DNA; 11995 BP.  
DE Human GPCR gene SEQ ID NO:1521.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 10.0%; Score 228.8; DB 10; Length 11995;  
Best Local Similarity 88.4%; Pred. No. 2.1e-47;  
RESULT 352  
ID AAS27823 standard; DNA; 16489 BP.  
DE DNA encoding novel signal transduction pathway protein, Seq ID 1483.  
PN WO200154733-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228.8; DB 4; Length 16489;  
Best Local Similarity 81.3%; Pred. No. 2.4e-47;  
RESULT 353  
ID ADB94626 standard; DNA; 16489 BP.  
DE Novel human protein DNA #235.  
PN US2002168711-A1.  
PD 14-NOV-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 10.0%; Score 228.8; DB 10; Length 16489;  
Best Local Similarity 81.3%; Pred. No. 2.4e-47;  
RESULT 354  
ID ADH56913 standard; DNA; 68571 BP.

DE Human CARD4 genomic DNA sequence SeqID 1.  
PN US2003219810-A1.  
PD 27-NOV-2003.  
PA (BARN/) BARNES G.  
PA (BERT/) BERTIN J.  
Query Match 10.0%; Score 228.8; DB 12; Length 68571;  
Best Local Similarity 65.5%; Pred. No. 4.6e-47;  
RESULT 355  
ID ADQ59506 standard; DNA; 81968 BP.  
DE Human cancer-associated (CA) gene sequence SEQ ID NO:142.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.0%; Score 228.8; DB 12; Length 81968;  
Best Local Similarity 82.3%; Pred. No. 5e-47;  
RESULT 356  
ID ADZ13883 standard; DNA; 84105 BP.  
DE Human cancer-associated genomic DNA #120.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 10.0%; Score 228.8; DB 14; Length 84105;  
Best Local Similarity 82.3%; Pred. No. 5.1e-47;  
RESULT 357  
Query Match 10.0%; Score 228.8; DB 12; Length 98800;  
Best Local Similarity 87.3%; Pred. No. 5.5e-47;  
RESULT 358  
Query Match 10.0%; Score 228.8; DB 13; Length 98800;  
Best Local Similarity 87.3%; Pred. No. 5.5e-47;  
RESULT 359  
ID ACN44626 standard; DNA; 175077 BP.  
DE Human genomic sequence hCG19724.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 228.8; DB 11; Length 175077;  
Best Local Similarity 72.3%; Pred. No. 7.1e-47;  
RESULT 360  
ID ABA18609 standard; DNA; 538 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 10940.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228.6; DB 5; Length 538;  
Best Local Similarity 86.6%; Pred. No. 5.9e-48;  
RESULT 361  
ID AAS35890 standard; DNA; 10093 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 1390.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228.6; DB 4; Length 10093;  
Best Local Similarity 79.9%; Pred. No. 2.2e-47;  
RESULT 362  
ID ABA07184 standard; DNA; 10093 BP.  
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 503.  
PN WO200155206-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228.6; DB 4; Length 10093;  
Best Local Similarity 79.9%; Pred. No. 2.2e-47;  
RESULT 363  
ID AAK89816 standard; DNA; 10093 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3392.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228.6; DB 4; Length 10093;  
Best Local Similarity 79.9%; Pred. No. 2.2e-47;  
RESULT 364  
ID ADE46584 standard; DNA; 10093 BP.  
DE Human cardiovascular system related genomic DNA #150.  
PN US2003059908-A1.

PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228.6; DB 10; Length 10093;  
Best Local Similarity 79.9%; Pred. No. 2.2e-47;  
RESULT 365  
ID ADJ08002 standard; DNA; 10093 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID1390.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228.6; DB 13; Length 10093;  
Best Local Similarity 79.9%; Pred. No. 2.2e-47;  
RESULT 366  
ID AED89407 standard; DNA; 166111 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 47.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 10.0%; Score 228.6; DB 14; Length 166111;  
Best Local Similarity 83.0%; Pred. No. 7.7e-47;  
RESULT 367  
ID ACN44846 standard; DNA; 330973 BP.  
DE Human genomic sequence hCG22679.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 228.6; DB 11; Length 330973;  
Best Local Similarity 72.7%; Pred. No. 1.1e-46;  
RESULT 368  
ID ADH19017 standard; DNA; 15657 BP.  
DE Human heparin cofactor II (HCF2) gDNA.  
PN WO2003091453-A1.  
PD 06-NOV-2003.  
PA (GENA-) GENAISSANCE PHARM INC.  
Query Match 10.0%; Score 228.4; DB 10; Length 15657;  
Best Local Similarity 81.5%; Pred. No. 3e-47;  
RESULT 369  
ID AAZ32190 standard; DNA; 15848 BP.  
DE Human heparin cofactor II exon 1 to 5 nucleotide sequence.  
PN WO9950454-A2.  
PD 07-OCT-1999.  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 10.0%; Score 228.4; DB 2; Length 15848;  
Best Local Similarity 81.5%; Pred. No. 3e-47;  
RESULT 370  
ID ABN95864 standard; DNA; 15849 BP.  
DE Gene #2362 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.0%; Score 228.4; DB 6; Length 15849;  
Best Local Similarity 81.5%; Pred. No. 3e-47;  
RESULT 371  
ID ACN44482 standard; DNA; 34096 BP.  
DE Human genomic sequence hCG26017.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 228.4; DB 11; Length 34096;  
Best Local Similarity 83.6%; Pred. No. 4.3e-47;  
RESULT 372  
ID ACN45006 standard; DNA; 67810 BP.  
DE Human genomic sequence hCG32956.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 228.4; DB 11; Length 67810;  
Best Local Similarity 87.3%; Pred. No. 5.8e-47;  
RESULT 373  
Query Match 10.0%; Score 228.4; DB 9; Length 110000;  
Best Local Similarity 84.8%; Pred. No. 7.2e-47;  
RESULT 374  
ID ADH76849 standard; DNA; 122557 BP.

DE Melanin-concentrating hormone receptor 1 locus clone.  
PN WO2003104489-A2.  
PD 18-DEC-2003.  
PA (UYPH-) UNIV PHILIPPS MARBURG.  
Query Match 10.0%; Score 228.4; DB 12; Length 122557;  
Best Local Similarity 83.7%; Pred. No. 7.6e-47;  
RESULT 375  
ID AEA61155 standard; DNA; 127602 BP.  
DE Human GLUC gene genomic sequence SEQ ID NO:65.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB ) BAYER CORP.  
Query Match 10.0%; Score 228.4; DB 14; Length 127602;  
Best Local Similarity 83.6%; Pred. No. 7.7e-47;  
RESULT 376  
ID AAS38473 standard; CDNA; 407 BP.  
DE Novel human diagnostic and therapeutic gene #1531.  
PN WO200166753-A2.  
PD 13-SEP-2001.  
PA (CHIR ) CHIRON CORP.  
Query Match 10.0%; Score 228.2; DB 4; Length 407;  
Best Local Similarity 77.9%; Pred. No. 6.6e-48;  
RESULT 377  
ID AED14353 standard; DNA; 3208 BP.  
DE Human cumulus cell differentially expressed gene.  
PN WO2005094306-A2.  
PD 13-OCT-2005.  
PA (UNMS ) UNIV MICHIGAN STATE.  
Query Match 10.0%; Score 228.2; DB 14; Length 3208;  
Best Local Similarity 84.1%; Pred. No. 1.7e-47;  
RESULT 378  
ID AAK68430 standard; DNA; 6007 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23242.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228.2; DB 4; Length 6007;  
Best Local Similarity 78.2%; Pred. No. 2.2e-47;  
RESULT 379  
ID AED17756 standard; DNA; 34200 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 7.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 10.0%; Score 228.2; DB 14; Length 34200;  
Best Local Similarity 82.1%; Pred. No. 4.8e-47;  
RESULT 380  
ID ABS57150 standard; DNA; 63588 BP.  
DE Human gene encoding a serine/threonine kinase.  
Query Match 10.0%; Score 228.2; DB 8; Length 63588;  
Best Local Similarity 82.1%; Pred. No. 6.4e-47;  
RESULT 381  
ID ADQ59187 standard; DNA; 73583 BP.  
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:24.  
PN KR2004008012-A.  
PD 28-JAN-2004.  
PA (KIMH/) KIM H G.  
PA (KIMN/) KIM N G.  
PA (LEEJ/) LEE J S.  
PA (RHEE/) RHEE H S.  
Query Match 10.0%; Score 228.2; DB 12; Length 73583;  
Best Local Similarity 83.3%; Pred. No. 6.8e-47;  
RESULT 382  
ID AEC82893 standard; CDNA; 156321 BP.  
DE Breast cancer associated cDNA SEQ ID NO 461.  
PN WO2005083429-A2.  
PD 09-SEP-2005.  
PA (VERI-) VERIDEX LLC.  
Query Match 10.0%; Score 228.2; DB 14; Length 156321;  
Best Local Similarity 79.5%; Pred. No. 9.5e-47;  
RESULT 383  
ID AEG92892 standard; CDNA; 156321 BP.

DE Human tumor cell cDNA SEQ ID NO:388.  
PN WO2006036025-A1.  
PD 06-APR-2006.  
PA (EISA ) EISAI CO LTD.  
Query Match 10.0%; Score 228.2; DB 15; Length 156321;  
Best Local Similarity 79.5%; Pred. No. 9.5e-47;  
RESULT 384  
ID AEG71009 standard; cDNA; 156321 BP.  
DE Human p53 mutational status predicting gene SEQ ID NO:483.  
PN US2006074565-A1.  
PD 06-APR-2006.  
PA (MILL/) MILLER L D.  
PA (GEOR/) GEORGE J.  
PA (VEGA/) VEGA V B.  
Query Match 10.0%; Score 228.2; DB 15; Length 156321;  
Best Local Similarity 79.5%; Pred. No. 9.5e-47;  
RESULT 385  
ID ACN44958 standard; DNA; 285020 BP.  
DE Human genomic sequence hCG37193.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 228.2; DB 11; Length 285020;  
Best Local Similarity 86.8%; Pred. No. 1.3e-46;  
RESULT 386  
ID ADR07732 standard; cDNA; 2941 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1238.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 10.0%; Score 228; DB 13; Length 2941;  
Best Local Similarity 76.2%; Pred. No. 1.8e-47;  
RESULT 387  
ID AAK84548 standard; DNA; 8387 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39360.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 4; Length 8387;  
Best Local Similarity 87.6%; Pred. No. 2.9e-47;  
RESULT 388  
ID ABA14892 standard; DNA; 8387 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7223.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 5; Length 8387;  
Best Local Similarity 87.6%; Pred. No. 2.9e-47;  
RESULT 389  
ID AAK91515 standard; DNA; 13526 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 5091.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 4; Length 13526;  
Best Local Similarity 83.9%; Pred. No. 3.6e-47;  
RESULT 390  
ID AAS32169 standard; DNA; 13526 BP.  
DE Human liver associated genomic DNA #343.  
PN WO200155355-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 5; Length 13526;  
Best Local Similarity 83.9%; Pred. No. 3.6e-47;  
RESULT 391  
ID ABN90524 standard; DNA; 13526 BP.  
DE Human liver antigen HALSD51 genomic sequence, SEQ ID NO:645.  
PN US2002042096-A1.  
PD 11-APR-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 10.0%; Score 228; DB 6; Length 13526;

Best Local Similarity 83.9%; Pred. No. 3.6e-47;  
RESULT 392  
ID ADJ15437 standard; DNA; 13526 BP.  
DE Human liver-related genomic DNA - SEQ ID 645.  
PN US2003077602-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 11; Length 13526;  
Best Local Similarity 83.9%; Pred. No. 3.6e-47;  
RESULT 393  
ID AAK91514 standard; DNA; 14337 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 5090.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 4; Length 14337;  
Best Local Similarity 83.9%; Pred. No. 3.7e-47;  
RESULT 394  
ID AAS32168 standard; DNA; 14337 BP.  
DE Human liver associated genomic DNA #342.  
PN WO200155355-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 5; Length 14337;  
Best Local Similarity 83.9%; Pred. No. 3.7e-47;  
RESULT 395  
ID ABN90523 standard; DNA; 14337 BP.  
DE Human liver antigen HALSD51 genomic sequence, SEQ ID NO:644.  
PN US2002042096-A1.  
PD 11-APR-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 10.0%; Score 228; DB 6; Length 14337;  
Best Local Similarity 83.9%; Pred. No. 3.7e-47;  
RESULT 396  
ID ADJ15436 standard; DNA; 14337 BP.  
DE Human liver-related genomic DNA - SEQ ID 644.  
PN US2003077602-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 11; Length 14337;  
Best Local Similarity 83.9%; Pred. No. 3.7e-47;  
RESULT 397  
ID AAL04340 standard; DNA; 32194 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7028.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 228; DB 4; Length 32194;  
Best Local Similarity 85.0%; Pred. No. 5.3e-47;  
RESULT 398  
ID ACN43918 standard; DNA; 32607 BP.  
DE Human genomic sequence hCG1644496.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 228; DB 11; Length 32607;  
Best Local Similarity 85.0%; Pred. No. 5.3e-47;  
RESULT 399  
ID ADZ59528 standard; DNA; 37442 BP.  
DE Secondary hyperparathyroidism detection polymorphic gene IL12RB1, SEQ 22.  
PN JP2005102601-A.  
PD 21-APR-2005.  
PA (HYUB-) HYUBITTO GENOMICS KK.  
PA (JIKE-) UNIV JIKEI.  
Query Match 10.0%; Score 228; DB 14; Length 37442;  
Best Local Similarity 85.0%; Pred. No. 5.7e-47;  
RESULT 400  
ID ADZ59517 standard; DNA; 37442 BP.  
DE Secondary hyperparathyroidism detection polymorphic gene IL12RB1, SEQ 11.  
PN JP2005102601-A.  
PD 21-APR-2005.



PA (HYUB-) HYUBITTO GENOMICS KK.  
PA (JIKE-) UNIV JIKEI.  
Query Match 10.0%; Score 228; DB 14; Length 37442;  
Best Local Similarity 85.0%; Pred. No. 5.7e-47;  
RESULT 401  
ID AEB96540 standard; DNA; 37442 BP.  
DE Human IL12RB1 gene, SEQ ID 24.  
Query Match 10.0%; Score 228; DB 14; Length 37442;  
Best Local Similarity 85.0%; Pred. No. 5.7e-47;  
RESULT 402  
ID ABD32754 standard; DNA; 62124 BP.  
DE Human cancer-associated genomic DNA HD16-028.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.0%; Score 228; DB 13; Length 62124;  
Best Local Similarity 85.0%; Pred. No. 7.1e-47;  
RESULT 403  
ID ADQ59518 standard; DNA; 100762 BP.  
DE Human cancer-associated (CA) gene sequence SEQ ID NO:154.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.0%; Score 228; DB 12; Length 100762;  
Best Local Similarity 79.1%; Pred. No. 8.8e-47;  
RESULT 404  
ID ADZ13899 standard; DNA; 100822 BP.  
DE Human cancer-associated genomic DNA #122.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 10.0%; Score 228; DB 14; Length 100822;  
Best Local Similarity 79.1%; Pred. No. 8.8e-47;  
RESULT 405  
ID ADF13116 standard; DNA; 128779 BP.  
DE Hypermethylation site in human breast cancer CpG island locus HBC-45.  
PN US2003129602-A1.  
PD 10-JUL-2003.  
PA (HUAN/) HUANG T H.  
Query Match 10.0%; Score 228; DB 12; Length 128779;  
Best Local Similarity 83.9%; Pred. No. 9.8e-47;  
RESULT 406  
ID ADI37262 standard; DNA; 128779 BP.  
DE Hypermethylation in cancer (HBC) locus-45.  
PN US6605432-B1.  
PD 12-AUG-2003.  
PA (UMOR ) UNIV MISSOURI.  
Query Match 10.0%; Score 228; DB 12; Length 128779;  
Best Local Similarity 83.9%; Pred. No. 9.8e-47;  
RESULT 407  
ID AAK75933 standard; DNA; 9039 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30745.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 227.8; DB 4; Length 9039;  
Best Local Similarity 85.8%; Pred. No. 3.4e-47;  
RESULT 408  
ID AAK85246 standard; DNA; 9039 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40058.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 227.8; DB 4; Length 9039;  
Best Local Similarity 85.8%; Pred. No. 3.4e-47;  
RESULT 409  
ID AAK84138 standard; DNA; 17758 BP..  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38950.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 227.8; DB 4; Length 17758;  
Best Local Similarity 83.4%; Pred. No. 4.5e-47;

RESULT 410  
ID AAD00147 standard; DNA; 35414 BP.  
DE TR12 related DNA-11.  
PN WO200023572-A1.  
PD 27-APR-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 227.8; DB 3; Length 35414;  
Best Local Similarity 85.8%; Pred. No. 6.2e-47;  
RESULT 411  
ID ABL91800 standard; DNA; 39328 BP.  
DE Human lipase endothelial (LIPG) isogene genomic DNA sequence.  
PN WO200216397-A2.  
PD 28-FEB-2002.  
PA (GENA-) GENAISSANCE PHARM INC.  
Query Match 10.0%; Score 227.8; DB 6; Length 39328;  
Best Local Similarity 81.2%; Pred. No. 6.5e-47;  
RESULT 412  
ID AAZ23902 standard; DNA; 49999 BP.  
DE Human LOBO homologue genomic DNA fragment 4.  
PN WO9950284-A2.  
PD 07-OCT-1999.  
PA (ROSE/) ROSENTHAL A.  
Query Match 10.0%; Score 227.8; DB 2; Length 49999;  
Best Local Similarity 83.4%; Pred. No. 7.2e-47;  
RESULT 413  
ID AAX23517 standard; DNA; 50000 BP.  
DE Human kidney aminopeptidase P genomic DNA fragment 1.  
PN WO9911799-A2.  
PD 11-MAR-1999.  
PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.  
Query Match 10.0%; Score 227.8; DB 2; Length 50000;  
Best Local Similarity 80.2%; Pred. No. 7.2e-47;  
RESULT 414  
ID ACN43882 standard; DNA; 60815 BP.  
DE Human genomic sequence hCG1777139.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.8; DB 11; Length 60815;  
Best Local Similarity 84.6%; Pred. No. 7.9e-47;  
RESULT 415  
ID ADP66763 standard; DNA; 75033 BP.  
DE Human endothelial lipase polynucleotide seqid 18.  
PN US2004115653-A1.  
PD 17-JUN-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.0%; Score 227.8; DB 12; Length 75033;  
Best Local Similarity 81.2%; Pred. No. 8.7e-47;  
RESULT 416  
ID ADL27146 standard; DNA; 96593 BP.  
DE Human genomic sequence for PPP3CC.  
PN US2003216558-A1.  
PD 20-NOV-2003.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 10.0%; Score 227.8; DB 11; Length 96593;  
Best Local Similarity 76.6%; Pred. No. 9.7e-47;  
RESULT 417  
ID ADA03068 standard; DNA; 96595 BP.  
DE Human PPP3CC carcinoma associated gene, SEQ ID NO:1586.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.8; DB 9; Length 96595;  
Best Local Similarity 76.6%; Pred. No. 9.7e-47;  
RESULT 418  
ID ADB72806 standard; DNA; 96595 BP.  
DE Human PPP3CC gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.8; DB 10; Length 96595;  
Best Local Similarity 76.6%; Pred. No. 9.7e-47;

RESULT 419  
ID ADA66352 standard; DNA; 96596 BP.  
DE Human PPP3CC gene genomic DNA sequence.  
PN WO2003053224-A2.  
PD 03-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.8; DB 9; Length 96596;  
Best Local Similarity 76.6%; Pred. No. 9.7e-47;  
RESULT 420  
ID ADR52892 standard; DNA; 151152 BP.  
DE Drug therapy altered expressed gene #243.  
PN WO2004072265-A2.  
PD 26-AUG-2004.  
PA (AMHP) WYETH.  
PA (BURC/) BURCZYNSKI M.  
PA (TWIN/) TWINE N.  
PA (DORN/) DORNER A J.  
PA (TREP/) TREPICCHIO W L.  
Query Match 10.0%; Score 227.8; DB 13; Length 151152;  
Best Local Similarity 80.2%; Pred. No. 1.2e-46;  
RESULT 421  
ID ACN44046 standard; DNA; 260027 BP.  
DE Human genomic sequence hCG1735292.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.8; DB 11; Length 260027;  
Best Local Similarity 83.4%; Pred. No. 1.5e-46;  
RESULT 422  
ID ABD33509 standard; cDNA; 5115 BP.  
DE Human cancer-associated (CA) cDNA HR07-099.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.0%; Score 227.6; DB 13; Length 5115;  
Best Local Similarity 84.1%; Pred. No. 2.9e-47;  
RESULT 423  
ID AEJ13675 standard; DNA; 5115 BP.  
DE Cancer-associated protein coding sequence - SEQ ID 683.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 10.0%; Score 227.6; DB 15; Length 5115;  
Best Local Similarity 84.1%; Pred. No. 2.9e-47;  
RESULT 424  
ID ABD33508 standard; DNA; 36871 BP.  
DE Human cancer-associated (CA) gene HD07-099.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 10.0%; Score 227.6; DB 13; Length 36871;  
Best Local Similarity 84.1%; Pred. No. 7.1e-47;  
RESULT 425  
ID AEJ13674 standard; DNA; 36871 BP.  
DE Cancer-associated gene sequence - SEQ ID 682.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 10.0%; Score 227.6; DB 15; Length 36871;  
Best Local Similarity 84.1%; Pred. No. 7.1e-47;  
RESULT 426  
ID AAZ35351 standard; DNA; 41599 BP.  
DE Cosmid including sequence spanning human chromosome 9p21.  
PN WO9967634-A1.  
PD 29-DEC-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 10.0%; Score 227.6; DB 3; Length 41599;  
Best Local Similarity 78.0%; Pred. No. 7.5e-47;  
RESULT 427  
ID ACN44766 standard; DNA; 77478 BP.  
DE Human genomic sequence hCG32368.

PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.6; DB 11; Length 77478;  
Best Local Similarity 82.9%; Pred. No. 9.9e-47;  
RESULT 428  
ID ABN96931 standard; DNA; 99014 BP.  
DE Gene #3429 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.0%; Score 227.6; DB 6; Length 99014;  
Best Local Similarity 85.3%; Pred. No. 1.1e-46;  
RESULT 429  
ID ACN44602 standard; DNA; 126266 BP.  
DE Human genomic sequence hCG1781402.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.6; DB 11; Length 126266;  
Best Local Similarity 81.8%; Pred. No. 1.2e-46;  
RESULT 430  
ID ADH63063 standard; DNA; 132762 BP.  
DE Human fibroblast growth factor receptor 2 related sequence, SEQ ID 17.  
PN WO2003024987-A1.  
PD 27-MAR-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 10.0%; Score 227.6; DB 10; Length 132762;  
Best Local Similarity 81.8%; Pred. No. 1.3e-46;  
RESULT 431  
ID ADZ12560 standard; DNA; 136489 BP.  
DE Human cancer-associated genomic DNA #9.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 10.0%; Score 227.6; DB 14; Length 136489;  
Best Local Similarity 86.5%; Pred. No. 1.3e-46;  
RESULT 432  
ID AED89420 standard; DNA; 171427 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 60.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 10.0%; Score 227.6; DB 14; Length 171427;  
Best Local Similarity 89.2%; Pred. No. 1.4e-46;  
RESULT 433  
ID AED89401 standard; DNA; 177623 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 41.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 10.0%; Score 227.6; DB 14; Length 177623;  
Best Local Similarity 82.9%; Pred. No. 1.4e-46;  
RESULT 434  
ID AAF92831 standard; DNA; 183999 BP.  
DE Human ABC1 genomic DNA.  
PN WO200115676-A2.  
PD 08-MAR-2001.  
PA (UYBR-) UNIV BRITISH COLUMBIA.  
PA (XENO-) XENON GENETICS INC.  
Query Match 10.0%; Score 227.6; DB 4; Length 183999;  
Best Local Similarity 81.6%; Pred. No. 1.5e-46;  
RESULT 435  
ID ADU76470 standard; DNA; 183999 BP.  
DE Human ABC1 genomic sequence.  
PN US2004229275-A1.  
PD 18-NOV-2004.  
PA (HAYD/) HAYDEN M R.  
PA (BROO/) BROOKS-WILSON A R.  
PA (PIMS/) PIMSTONE S N.  
PA (CLEE/) CLEE S M.  
Query Match 10.0%; Score 227.6; DB 13; Length 183999;  
Best Local Similarity 81.6%; Pred. No. 1.5e-46;

RESULT 436  
ID ADZ13735 standard; DNA; 187851 BP.  
DE Human cancer-associated genomic DNA #108.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 10.0%; Score 227.6; DB 14; Length 187851;  
Best Local Similarity 82.9%; Pred. No. 1.5e-46;  
RESULT 437  
ID ADB62937 standard; cDNA; 1988 BP.  
DE Human cDNA encoding clone PLACE60120280.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 10.0%; Score 227.4; DB 10; Length 1988;  
Best Local Similarity 86.0%; Pred. No. 2.2e-47;  
RESULT 438  
ID ABA14762 standard; DNA; 3283 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7093.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 227.4; DB 5; Length 3283;  
Best Local Similarity 83.6%; Pred. No. 2.7e-47;  
RESULT 439  
ID ABA14761 standard; DNA; 3283 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7092.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 10.0%; Score 227.4; DB 5; Length 3283;  
Best Local Similarity 83.6%; Pred. No. 2.7e-47;  
RESULT 440  
ID ACN43926 standard; DNA; 53242 BP.  
DE Human genomic sequence hCG1782215.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.4; DB 11; Length 53242;  
Best Local Similarity 83.6%; Pred. No. 9.4e-47;  
RESULT 441  
ID ABL62910 standard; DNA; 65608 BP.  
DE Breast cancer related gene sequence SEQ ID NO:1247.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 10.0%; Score 227.4; DB 6; Length 65608;  
Best Local Similarity 81.4%; Pred. No. 1e-46;  
RESULT 442  
ID ABL64414 standard; DNA; 65608 BP.  
DE Stomach cancer related gene sequence SEQ ID NO:2751.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 10.0%; Score 227.4; DB 6; Length 65608;  
Best Local Similarity 81.4%; Pred. No. 1e-46;  
RESULT 443  
ID ABL67668 standard; DNA; 65608 BP.  
DE Oesophagus cancer related gene sequence SEQ ID NO:6005.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 10.0%; Score 227.4; DB 6; Length 65608;  
Best Local Similarity 81.4%; Pred. No. 1e-46;  
RESULT 444  
ID ACN44066 standard; DNA; 99886 BP.  
DE Human genomic sequence hCG15674.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 10.0%; Score 227.4; DB 11; Length 99886;  
Best Local Similarity 86.0%; Pred. No. 1.3e-46;

RESULT 445  
ID ADQ17329 standard; DNA; 101685 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 146.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 10.0%; Score 227.4; DB 12; Length 101685;  
Best Local Similarity 86.0%; Pred. No. 1.3e-46;  
RESULT 446  
ID ABQ88207 standard; cDNA; 172570 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 114.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC ) PROCTER & GAMBLE CO.  
Query Match 10.0%; Score 227.4; DB 6; Length 172570;  
Best Local Similarity 83.6%; Pred. No. 1.6e-46;  
RESULT 447  
ID AAK76049 standard; DNA; 2610 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30861.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 227.2; DB 4; Length 2610;  
Best Local Similarity 85.5%; Pred. No. 2.7e-47;  
RESULT 448  
ID AEE05157 standard; DNA; 49617 BP.  
DE Cancer-associated cDNA SEQ ID NO:475.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.9%; Score 227.2; DB 14; Length 49617;  
Best Local Similarity 85.5%; Pred. No. 1e-46;  
RESULT 449  
ID ADZ12791 standard; DNA; 64700 BP.  
DE Human cancer-associated genomic DNA #27.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.9%; Score 227.2; DB 14; Length 64700;  
Best Local Similarity 77.3%; Pred. No. 1.2e-46;  
RESULT 450  
ID ABK90695 standard; DNA; 73467 BP.  
DE DNA encoding human transporter protein.  
Query Match 9.9%; Score 227.2; DB 6; Length 73467;  
Best Local Similarity 81.0%; Pred. No. 1.2e-46;  
RESULT 451  
ID ABX95843 standard; DNA; 73467 BP.  
DE Genomic DNA encoding novel human transporter protein.  
Query Match 9.9%; Score 227.2; DB 8; Length 73467;  
Best Local Similarity 81.0%; Pred. No. 1.2e-46;  
RESULT 452  
ID AEC00670 standard; DNA; 73467 BP.  
DE Human sodium/glucose cotransporter related genomic DNA, SEQ ID NO: 3.  
Query Match 9.9%; Score 227.2; DB 14; Length 73467;  
Best Local Similarity 81.0%; Pred. No. 1.2e-46;  
RESULT 453  
ID ADD71350 standard; DNA; 93390 BP.  
DE Glutamine:fructose-6-phosphate amide transferase 1 genomic sequence.  
PN WO2003023063-A1.  
PD 20-MAR-2003.  
PA (SANY ) SANKYO CO LTD.  
Query Match 9.9%; Score 227.2; DB 10; Length 93390;  
Best Local Similarity 77.3%; Pred. No. 1.4e-46;  
RESULT 454  
ID AED55991 standard; DNA; 98100 BP.  
DE Human BVES DNA.  
Query Match 9.9%; Score 227.2; DB 14; Length 98100;  
Best Local Similarity 82.6%; Pred. No. 1.4e-46;  
RESULT 455  
ID ADP03055 standard; cDNA; 124987 BP.  
DE Human housekeeping gene cDNA #96.  
PN JP2004135552-A.



PD 13-MAY-2004.  
PA (NIGA ) NGK INSULATORS LTD.  
Query Match 9.9%; Score 227.2; DB 12; Length 124987;  
Best Local Similarity 86.8%; Pred. No. 1.6e-46;  
RESULT 456  
ID ADS88553 standard; cDNA; 124990 BP.  
DE Human housekeeping gene cDNA sequence SEQ ID NO:96.  
PN WO2004035785-A1.  
PD 29-APR-2004.  
PA (NIGA ) NGK INSULATORS LTD.  
Query Match 9.9%; Score 227.2; DB 13; Length 124990;  
Best Local Similarity 86.8%; Pred. No. 1.6e-46;  
RESULT 457  
ID ADU60195 standard; cDNA; 124990 BP.  
DE Housekeeping gene cDNA, SEQ ID 156.  
PN US2004229233-A1.  
PD 18-NOV-2004.  
PA (NIGA ) NGK INSULATORS LTD.  
Query Match 9.9%; Score 227.2; DB 13; Length 124990;  
Best Local Similarity 86.8%; Pred. No. 1.6e-46;  
RESULT 458  
ID ADQ59197 standard; DNA; 155225 BP.  
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:34.  
PN KR2004008012-A.  
PD 28-JAN-2004.  
PA (KIMH/) KIM H G.  
PA (KIMN/) KIM N G.  
PA (LEEJ/) LEE J S.  
PA (RHEE/) RHEE H S.  
Query Match 9.9%; Score 227.2; DB 12; Length 155225;  
Best Local Similarity 85.5%; Pred. No. 1.7e-46;  
RESULT 459  
ID ADL13748 standard; DNA; 169144 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #280.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.9%; Score 227.2; DB 10; Length 169144;  
Best Local Similarity 85.5%; Pred. No. 1.8e-46;  
RESULT 460  
ID ADL13719 standard; DNA; 199878 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #251.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.9%; Score 227.2; DB 10; Length 199878;  
Best Local Similarity 82.0%; Pred. No. 1.9e-46;  
RESULT 461  
ID ADA52974 standard; cDNA; 1960 BP.  
DE Human coding sequence, SEQ ID 542.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.9%; Score 227; DB 10; Length 1960;  
Best Local Similarity 86.2%; Pred. No. 2.7e-47;  
RESULT 462  
ID ADJ96582 standard; DNA; 7364 BP.  
DE Human Nim-A related protein kinase SK516 DNA SeqID 39.  
PN WO2004006838-A2.  
PD 22-JAN-2004.  
PA (SUGE-) SUGEN INC.  
Query Match 9.9%; Score 227; DB 12; Length 7364;  
Best Local Similarity 81.0%; Pred. No. 4.9e-47;  
RESULT 463  
ID ABA08132 standard; DNA; 32152 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 927.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 227; DB 4; Length 32152;  
Best Local Similarity 86.2%; Pred. No. 9.5e-47;  
RESULT 464

ID ABA17155 standard; DNA; 32249 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 9486.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 227; DB 5; Length 32249;  
Best Local Similarity 87.5%; Pred. No. 9.5e-47;  
RESULT 465  
ID ABK52612 standard; DNA; 58837 BP.  
DE Human Claspin genomic sequence.  
PN WO200233115-A2.  
PD 25-APR-2002.  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
Query Match 9.9%; Score 227; DB 6; Length 58837;  
Best Local Similarity 71.8%; Pred. No. 1.2e-46;  
RESULT 466  
ID AEG34296 standard; DNA; 67787 BP.  
DE DNA including human hypoxia-inducible factor 1-beta encoding DNA.  
PN WO2006026485-A2.  
PD 09-MAR-2006.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.9%; Score 227; DB 15; Length 67787;  
Best Local Similarity 85.0%; Pred. No. 1.3e-46;  
RESULT 467  
ID ACN44742 standard; DNA; 87731 BP.  
DE Human genomic sequence hCG1738334.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 227; DB 11; Length 87731;  
Best Local Similarity 85.0%; Pred. No. 1.5e-46;  
RESULT 468  
ID ADQ18615 standard; DNA; 104729 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1434.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 227; DB 12; Length 104729;  
Best Local Similarity 83.8%; Pred. No. 1.6e-46;  
RESULT 469  
ID ACN44210 standard; DNA; 238484 BP.  
DE Human genomic sequence hCG28803.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 227; DB 11; Length 238484;  
Best Local Similarity 86.2%; Pred. No. 2.3e-46;  
RESULT 470  
ID AEL18970 standard; DNA; 325775 BP.  
DE Human acetyl-CoA carboxylase-alpha (ACCI) gene SEQ ID NO:7.  
PN WO2006110775-A2.  
PD 19-OCT-2006.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.9%; Score 227; DB 15; Length 325775;  
Best Local Similarity 83.8%; Pred. No. 2.7e-46;  
RESULT 471  
ID AAK83997 standard; DNA; 603 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38809.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.8; DB 4; Length 603;  
Best Local Similarity 85.7%; Pred. No. 1.8e-47;  
RESULT 472  
ID ADB63769 standard; cDNA; 2643 BP.  
DE Human cDNA encoding clone UTERU20040390.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.9%; Score 226.8; DB 10; Length 2643;  
Best Local Similarity 84.5%; Pred. No. 3.5e-47;  
RESULT 473

ID ADS89013 standard; DNA; 11029 BP.  
DE Human ING4 gene SEQ ID NO:29.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 9.9%; Score 226.8; DB 13; Length 11029;  
Best Local Similarity 82.2%; Pred. No. 6.6e-47;  
RESULT 474  
ID AAK81690 standard; DNA; 13934 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36502.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.8; DB 4; Length 13934;  
Best Local Similarity 87.0%; Pred. No. 7.4e-47;  
RESULT 475  
ID AAK83283 standard; DNA; 21302 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38095.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.8; DB 4; Length 21302;  
Best Local Similarity 82.2%; Pred. No. 8.9e-47;  
RESULT 476  
ID ADT77137 standard; DNA; 24475 BP.  
DE Type II diabetes gene SEQ ID NO 14.  
PN WO2004084797-A2.  
PD 07-OCT-2004.  
PA (HUBI-) HUBIT GENOMIX INC.  
PA (DAIM-) DAIMON M.  
PA (KATO/) KATO T.  
Query Match 9.9%; Score 226.8; DB 13; Length 24475;  
Best Local Similarity 82.2%; Pred. No. 9.5e-47;  
RESULT 477  
ID AAK78746 standard; DNA; 33513 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33558.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.8; DB 4; Length 33513;  
Best Local Similarity 83.3%; Pred. No. 1.1e-46;  
RESULT 478  
ID ACN44314 standard; DNA; 60057 BP.  
DE Human genomic sequence hCG19476.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.8; DB 11; Length 60057;  
Best Local Similarity 83.3%; Pred. No. 1.4e-46;  
RESULT 479  
Query Match 9.9%; Score 226.8; DB 14; Length 110000;  
Best Local Similarity 80.2%; Pred. No. 1.9e-46;  
RESULT 480  
ID ACN43914 standard; DNA; 160482 BP.  
DE Human genomic sequence hCG26773.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.8; DB 11; Length 160482;  
Best Local Similarity 84.1%; Pred. No. 2.2e-46;  
RESULT 481  
ID ADQ97721 standard; DNA; 178024 BP.  
DE Human cancer associated sequence HD10-033, SEQ ID 698.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 226.8; DB 12; Length 178024;  
Best Local Similarity 85.7%; Pred. No. 2.3e-46;  
RESULT 482  
ID ABQ88146 standard; cDNA; 178896 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 53.  
PN WO200250301-A2.  
PD 27-JUN-2002.

PA (GENE-) GENE LOGIC INC.  
PA (PROC ) PROCTER & GAMBLE CO.  
Query Match 9.9%; Score 226.8; DB 6; Length 178896;  
Best Local Similarity 85.7%; Pred. No. 2.3e-46;  
RESULT 483  
ID ADQ97687 standard; DNA; 179487 BP.  
DE Human cancer associated sequence HD10-028, SEQ ID 664.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 226.8; DB 12; Length 179487;  
Best Local Similarity 80.2%; Pred. No. 2.3e-46;  
RESULT 484  
ID ACN44374 standard; DNA; 181684 BP.  
DE Human genomic sequence hCG16651.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.8; DB 11; Length 181684;  
Best Local Similarity 85.7%; Pred. No. 2.3e-46;  
RESULT 485  
ID ABN65477 standard; cDNA; 620 BP.  
DE Human cancer related polynucleotide SEQ ID NO 5444.  
PN WO200214500-A2.  
PD 21-FEB-2002.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.9%; Score 226.6; DB 6; Length 620;  
Best Local Similarity 81.8%; Pred. No. 2e-47;  
RESULT 486  
ID AAH04714 standard; cDNA; 772 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:1549.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.9%; Score 226.6; DB 4; Length 772;  
Best Local Similarity 84.0%; Pred. No. 2.3e-47;  
RESULT 487  
ID AAH18426 standard; cDNA; 1656 BP.  
DE Human cDNA sequence SEQ ID NO:18505.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.9%; Score 226.6; DB 4; Length 1656;  
Best Local Similarity 84.0%; Pred. No. 3.2e-47;  
RESULT 488  
ID ACC82887 standard; DNA; 7001 BP.  
DE Human thyroid hormone receptor interactor 6 (TRIP6) gene fragment.  
PN WO2003040328-A2.  
PD 15-MAY-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.9%; Score 226.6; DB 10; Length 7001;  
Best Local Similarity 81.8%; Pred. No. 6.1e-47;  
RESULT 489  
ID ABD13475 standard; DNA; 7001 BP.  
DE Human hormone receptor interactor 6 gene region SeqID10.  
PN US2005222073-A1.  
PD 06-OCT-2005.  
PA (BENN/) BENNETT C F.  
PA (MONI/) MONIA B P.  
PA (CROO/) CROOKE R M.  
PA (GRAH/) GRAHAM M J.  
PA (FREI/) FREIER S M.  
PA (NERO/) NERO P S.  
PA (WANC/) WANCEWICZ E.  
PA (DEAN/) DEAN N M.  
PA (COWS/) COWSERT L M.  
PA (DOBI/) DOBIE K W.  
Query Match 9.9%; Score 226.6; DB 14; Length 7001;  
Best Local Similarity 81.8%; Pred. No. 6.1e-47;  
RESULT 490  
ID ADZ12506 standard; DNA; 24244 BP.  
DE Human cancer-associated genomic DNA #4.

PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.9%; Score 226.6; DB 14; Length 24244;  
Best Local Similarity 85.2%; Pred. No. 1.1e-46;  
RESULT 491  
ID AEB96546 standard; DNA; 32704 BP.  
DE Human FGL1 gene, SEQ ID 30.  
Query Match 9.9%; Score 226.6; DB 14; Length 32704;  
Best Local Similarity 84.0%; Pred. No. 1.2e-46;  
RESULT 492  
ID AAK77216 standard; DNA; 43938 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32028.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.6; DB 4; Length 43938;  
Best Local Similarity 79.8%; Pred. No. 1.4e-46;  
RESULT 493  
ID AAK77217 standard; DNA; 45017 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32029.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.6; DB 4; Length 45017;  
Best Local Similarity 79.8%; Pred. No. 1.4e-46;  
RESULT 494  
ID ABL68647 standard; DNA; 49634 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:6984.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.9%; Score 226.6; DB 6; Length 49634;  
Best Local Similarity 84.0%; Pred. No. 1.5e-46;  
RESULT 495  
ID AEF74987 standard; DNA; 49634 BP.  
DE Human polynucleotide #501.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.9%; Score 226.6; DB 15; Length 49634;  
Best Local Similarity 84.0%; Pred. No. 1.5e-46;  
RESULT 496  
ID AEA61178 standard; DNA; 67253 BP.  
DE Human GPR105 gene genomic sequence SEQ ID NO:88.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB ) BAYER CORP.  
Query Match 9.9%; Score 226.6; DB 14; Length 67253;  
Best Local Similarity 84.0%; Pred. No. 1.7e-46;  
RESULT 497  
ID ACN44438 standard; DNA; 73967 BP.  
DE Human genomic sequence hCG27607.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.6; DB 11; Length 73967;  
Best Local Similarity 83.9%; Pred. No. 1.8e-46;  
RESULT 498  
ID AEB96528 standard; DNA; 87495 BP.  
DE Human APIB1 gene, SEQ ID 12.  
Query Match 9.9%; Score 226.6; DB 14; Length 87495;  
Best Local Similarity 86.5%; Pred. No. 1.9e-46;  
RESULT 499  
ID ACN44746 standard; DNA; 92117 BP.  
DE Human genomic sequence hCG29513.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.6; DB 11; Length 92117;  
Best Local Similarity 82.9%; Pred. No. 1.9e-46;  
RESULT 500

ID ADQ18808 standard; DNA; 111084 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1627.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 226.6; DB 12; Length 111084;  
Best Local Similarity 84.0%; Pred. No. 2.1e-46;  
RESULT 501  
ID AAD54480 standard; DNA; 117962 BP.  
DE Human CIP DNA #1.  
PN WO200299055-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 9.9%; Score 226.6; DB 8; Length 117962;  
Best Local Similarity 81.8%; Pred. No. 2.2e-46;  
RESULT 502  
ID AEI21870 standard; DNA; 181150 BP.  
DE Human repetitive element associated DNA SEQ ID NO 47.  
PN WO2006060308-A2.  
PD 08-JUN-2006.  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
Query Match 9.9%; Score 226.6; DB 15; Length 181150;  
Best Local Similarity 79.8%; Pred. No. 2.6e-46;  
RESULT 503  
ID AAT51258 standard; DNA; 2387 BP.  
DE Human AD4 gene genomic sequence stm.genE.  
PN WO9703192-A2..  
PD 30-JAN-1997.  
PA (DARW-) DARWIN MOLECULAR CORP.  
PA (VAME-) VA MEDICAL CENT.  
PA (GEHO ) GEN HOSPITAL CORP.  
Query Match 9.9%; Score 226.4; DB 2; Length 2387;  
Best Local Similarity 83.5%; Pred. No. 4.2e-47;  
RESULT 504  
ID ABA18607 standard; DNA; 2854 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 10938.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.4; DB 5; Length 2854;  
Best Local Similarity 87.2%; Pred. No. 4.6e-47;  
RESULT 505  
ID AAS32249 standard; DNA; 32187 BP.  
DE Human DNA repair and processing genomic DNA #35.  
PN WO200155204-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.4; DB 5; Length 32187;  
Best Local Similarity 85.9%; Pred. No. 1.4e-46;  
RESULT 506  
ID ABS67552 standard; DNA; 32187 BP.  
DE Novel human DNA repair protein, genomic sequence #35.  
PN US2002086353-A1.  
PD 04-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 226.4; DB 6; Length 32187;  
Best Local Similarity 85.9%; Pred. No. 1.4e-46;  
RESULT 507  
ID ADJ12398 standard; DNA; 43991 BP.  
DE DNA fragment of a BAC clone that encodes a human secreted protein Seq252.  
PN US2004010132-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (BREW/) BREWER L A.  
PA (DUAN/) DUAN R D.  
PA (RUBE/) RUBEN S M.  
PA (FLOR/) FLORENCE K A.  
PA (GREE/) GREENE J M.  
PA (YOUN/) YOUNG P E.  
PA (FERR/) FERRIE A M.  
PA (YUGG/) YU G.



PA (FLOR/) FLORENCE C.  
PA (EBNE/) EBNER R.  
PA (OLSE/) OLSEN H.  
Query Match 9.9%; Score 226.4; DB 12; Length 43991;  
Best Local Similarity 85.9%; Pred. No. 1.6e-46;  
RESULT 508  
ID ADQ97623 standard; DNA; 86764 BP.  
DE Human cancer associated sequence HD10-016, SEQ ID 600.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 226.4; DB 12; Length 86764;  
Best Local Similarity 87.2%; Pred. No. 2.1e-46;  
RESULT 509  
ID ACN44286 standard; DNA; 105219 BP.  
DE Human genomic sequence hCG36856.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.4; DB 11; Length 105219;  
Best Local Similarity 80.3%; Pred. No. 2.3e-46;  
RESULT 510  
ID AEA61160 standard; DNA; 354592 BP.  
DE Human NEDD4L gene genomic sequence SEQ ID NO:70.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB ) BAYER CORP.  
Query Match 9.9%; Score 226.4; DB 14; Length 110000;  
Best Local Similarity 79.4%; Pred. No. 2.4e-46;  
RESULT 511  
ID AED34666 standard; DNA; 458207 BP.  
DE ABL1 genomic DNA SEQ ID NO 2.  
PN WO2005094291-A2.  
PD 13-OCT-2005.  
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.  
Query Match 9.9%; Score 226.4; DB 14; Length 110000;  
Best Local Similarity 81.4%; Pred. No. 2.4e-46;  
RESULT 512  
ID AEF92730 standard; DNA; 163218 BP.  
DE Human chromosome 17 sequence, clone hRPK.318\_A\_15.  
PN WO2006020269-A2.  
PD 23-FEB-2006.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 9.9%; Score 226.4; DB 15; Length 163218;  
Best Local Similarity 85.9%; Pred. No. 2.8e-46;  
RESULT 513  
ID ABA18608 standard; DNA; 546 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 10939.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.2; DB 5; Length 546;  
Best Local Similarity 85.4%; Pred. No. 2.4e-47;  
RESULT 514  
ID ABN84129 standard; cDNA; 1615 BP.  
DE Human cytokine receptor 16.5 coding sequence.  
PN CN1331154-A.  
PD 16-JAN-2002.  
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
Query Match 9.9%; Score 226.2; DB 6; Length 1615;  
Best Local Similarity 84.2%; Pred. No. 4e-47;  
RESULT 515  
ID AAS26795 standard; DNA; 32248 BP.  
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1769.  
PN WO200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.2; DB 4; Length 32248;  
Best Local Similarity 86.7%; Pred. No. 1.5e-46;  
RESULT 516  
ID AAL37122 standard; DNA; 32248 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3487.  
PN WO200155367-A1.

PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.2; DB 4; Length 32248;  
Best Local Similarity 86.7%; Pred. No. 1.5e-46;  
RESULT 517  
ID ABA20412 standard; DNA; 32248 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12743.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.2; DB 5; Length 32248;  
Best Local Similarity 86.7%; Pred. No. 1.5e-46;  
RESULT 518  
ID ABX74144 standard; DNA; 32248 BP.  
DE Human novel polynucleotide #972.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 226.2; DB 8; Length 32248;  
Best Local Similarity 86.7%; Pred. No. 1.5e-46;  
RESULT 519  
ID ABX60110 standard; cDNA; 32248 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #2454.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 226.2; DB 8; Length 32248;  
Best Local Similarity 86.7%; Pred. No. 1.5e-46;  
RESULT 520  
ID ADJ30860 standard; DNA; 32248 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3487.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226.2; DB 12; Length 32248;  
Best Local Similarity 86.7%; Pred. No. 1.5e-46;  
RESULT 521  
ID AAD56075 standard; DNA; 32767 BP.  
DE Human SNL carcinoma associated (CA) gene.  
PN WO2003035837-A2.  
PD 01-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.2; DB 8; Length 32767;  
Best Local Similarity 78.1%; Pred. No. 1.5e-46;  
RESULT 522  
ID ADA02437 standard; DNA; 32767 BP.  
DE Human SNL carcinoma associated gene, SEQ ID NO:956.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.2; DB 9; Length 32767;  
Best Local Similarity 78.1%; Pred. No. 1.5e-46;  
RESULT 523  
ID ADB72176 standard; DNA; 32767 BP.  
DE Human SNL gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.2; DB 10; Length 32767;  
Best Local Similarity 78.1%; Pred. No. 1.5e-46;  
RESULT 524  
ID ADE82920 standard; DNA; 32767 BP.  
DE Human SNL genomic DNA sequence.  
PN WO2003080808-A2.  
PD 02-OCT-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 226.2; DB 10; Length 32767;  
Best Local Similarity 78.1%; Pred. No. 1.5e-46;  
RESULT 525

ID ABD33436 standard; DNA; 52710 BP.  
DE Human cancer-associated (CA) gene HD07-082.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 226.2; DB 13; Length 52710;  
Best Local Similarity 83.1%; Pred. No. 1.9e-46;  
RESULT 526  
ID AEJ13564 standard; DNA; 52710 BP.  
DE Cancer-associated gene sequence - SEQ ID 572.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.9%; Score 226.2; DB 15; Length 52710;  
Best Local Similarity 83.1%; Pred. No. 1.9e-46;  
RESULT 527  
ID AAD15256 standard; DNA; 74962 BP.  
DE Human phosphatase gene.  
PN WO200160992-A2.  
PD 23-AUG-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.9%; Score 226.2; DB 4; Length 74962;  
Best Local Similarity 84.2%; Pred. No. 2.2e-46;  
RESULT 528  
ID AEF92655 standard; cDNA; 174318 BP.  
DE Human Ras effector protein Rin3, cDNA.  
PN WO2006020269-A2.  
PD 23-FEB-2006.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 9.9%; Score 226.2; DB 15; Length 174318;  
Best Local Similarity 85.4%; Pred. No. 3.3e-46;  
RESULT 529  
ID ABQ75562 standard; DNA; 188888 BP.  
DE Human related CYP 27C1 clone RP11-30F3 SEQ ID NO:21.  
PN WO200264765-A2.  
PD 22-AUG-2002.  
PA (CYTO-) CYTOCHROMA INC.  
Query Match 9.9%; Score 226.2; DB 6; Length 188888;  
Best Local Similarity 73.5%; Pred. No. 3.4e-46;  
RESULT 530  
ID AAS27712 standard; DNA; 4087 BP.  
DE DNA encoding novel signal transduction pathway protein, Seq ID 1372.  
PN WO200154733-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 226; DB 4; Length 4087;  
Best Local Similarity 84.9%; Pred. No. 6.8e-47;  
RESULT 531  
ID ADB94515 standard; DNA; 4087 BP.  
DE Novel human protein DNA #124.  
PN US2002168711-A1.  
PD 14-NOV-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 226; DB 10; Length 4087;  
Best Local Similarity 84.9%; Pred. No. 6.8e-47;  
RESULT 532  
ID ABK83562 standard; cDNA; 139904 BP.  
DE Human cDNA differentially expressed in granulocytic cells #133.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.9%; Score 226; DB 6; Length 139904;  
Best Local Similarity 82.4%; Pred. No. 3.3e-46;  
RESULT 533  
ID AAD54634 standard; DNA; 142519 BP.  
DE Human chromodomain helicase DNA binding protein (CHD) encoding DNA #9.  
PN WO200298899-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC. 9.9%; Score 226; DB 10; Length 142519;  
Query Match

Best Local Similarity 84.9%; Pred. No. 3.4e-46;  
RESULT 534  
ID ABN83124 standard; DNA; 172637 BP.  
DE Human voltage-activated ion channel transporter protein gene.  
Query Match 9.9%; Score 226; DB 6; Length 172637;  
Best Local Similarity 78.6%; Pred. No. 3.7e-46;  
RESULT 535  
ID AEB80195 standard; DNA; 172637 BP.  
DE Human transporter genomic DNA.  
Query Match 9.9%; Score 226; DB 14; Length 172637;  
Best Local Similarity 78.6%; Pred. No. 3.7e-46;  
RESULT 536  
ID ACF62736 standard; DNA; 183610 BP.  
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:664.  
PN WO2003013534-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.9%; Score 226; DB 8; Length 183610;  
Best Local Similarity 77.7%; Pred. No. 3.8e-46;  
RESULT 537  
ID ADB20851 standard; DNA; 183610 BP.  
DE MRP1 based cancer related nucleic acid SEQ ID NO:664.  
PN WO2003013533-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.9%; Score 226; DB 8; Length 183610;  
Best Local Similarity 77.7%; Pred. No. 3.8e-46;  
RESULT 538  
ID ADB87940 standard; DNA; 183610 BP.  
DE Human UGT1A1 gene sequence SEQ ID NO:664.  
PN WO2003013536-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.9%; Score 226; DB 10; Length 183610;  
Best Local Similarity 77.7%; Pred. No. 3.8e-46;  
RESULT 539  
ID ADB96923 standard; DNA; 183610 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:664.  
PN WO2003013537-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.9%; Score 226; DB 10; Length 183610;  
Best Local Similarity 77.7%; Pred. No. 3.8e-46;  
RESULT 540  
ID ADB92114 standard; DNA; 183610 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:664.  
PN WO2003013535-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.9%; Score 226; DB 10; Length 183610;  
Best Local Similarity 77.7%; Pred. No. 3.8e-46;  
RESULT 541  
ID ABQ80552 standard; DNA; 237961 BP.  
DE Human CanIon gene fragment #2.  
PN WO200246404-A2.  
PD 13-JUN-2002.  
PA (GEST ) GENSET.  
Query Match 9.9%; Score 226; DB 6; Length 237961;  
Best Local Similarity 78.6%; Pred. No. 4.2e-46;  
RESULT 542  
ID AED76155 standard; DNA; 261108 BP.  
DE Human CA genomic DNA sequence-ID hD25-006.  
PN WO2005104810-A2.  
PD 10-NOV-2005.  
PA (SAGR-) SAGRES DISCOVERY INC.  
PA (LAIA/) LAI A.  
PA (FATT/) FATTAEY A.  
Query Match 9.9%; Score 226; DB 14; Length 261108;  
Best Local Similarity 88.9%; Pred. No. 4.4e-46;  
RESULT 543  
ID AAK67132 standard; DNA; 310 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21944.  
PN WO200157182-A2.

PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 4; Length 310;  
Best Local Similarity 87.0%; Pred. No. 2.4e-47;  
RESULT 544  
ID AAK67294 standard; DNA; 699 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22106.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 4; Length 699;  
Best Local Similarity 81.1%; Pred. No. 3.5e-47;  
RESULT 545  
ID AAS22674 standard; cDNA; 4385 BP.  
DE Human cDNA encoding a novel human protein #240.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.9%; Score 225.8; DB 4; Length 4385;  
Best Local Similarity 84.4%; Pred. No. 7.9e-47;  
RESULT 546  
ID AEE23807 standard; DNA; 4385 BP.  
DE Novel human protein coding sequence (contig) - SEQ ID 476.  
PN US2005266423-A1.  
PD 01-DEC-2005.  
PA (NUVE-) NUVELO INC.  
Query Match 9.9%; Score 225.8; DB 15; Length 4385;  
Best Local Similarity 84.4%; Pred. No. 7.9e-47;  
RESULT 547  
ID AAS30660 standard; DNA; 5530 BP.  
DE DNA encoding novel lung cancer antigen, Seq ID No 112.  
PN WO200155300-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 4; Length 5530;  
Best Local Similarity 87.0%; Pred. No. 8.8e-47;  
RESULT 548  
ID AAK66712 standard; DNA; 5530 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21524.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 4; Length 5530;  
Best Local Similarity 87.0%; Pred. No. 8.8e-47;  
RESULT 549  
ID AAS28733 standard; DNA; 5530 BP.  
DE Genomic sequence #573 encoding for novel human respiratory antigen.  
PN WO200155448-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 4; Length 5530;  
Best Local Similarity 87.0%; Pred. No. 8.8e-47;  
RESULT 550  
ID ACA03423 standard; DNA; 5530 BP.  
DE DNA encoding human lung cancer antigen HCLBW86.  
PN US2002173454-A1.  
PD 21-NOV-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 225.8; DB 8; Length 5530;  
Best Local Similarity 87.0%; Pred. No. 8.8e-47;  
RESULT 551  
ID ADB96771 standard; DNA; 5530 BP.  
DE Novel lung cancer antigen genomic DNA #42.  
PN US2003049703-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 9; Length 5530;  
Best Local Similarity 87.0%; Pred. No. 8.8e-47;  
RESULT 552  
ID ADG41929 standard; DNA; 5530 BP.  
DE Human respiratory system associated genomic DNA seq id 1167.

PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 10; Length 5530;  
Best Local Similarity 87.0%; Pred. No. 8.8e-47;  
RESULT 553  
ID ADI97703 standard; DNA; 5530 BP.  
DE Human respiratory system associated polypeptide-related DNA SeqID1167.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 11; Length 5530;  
Best Local Similarity 87.0%; Pred. No. 8.8e-47;  
RESULT 554  
ID ACC50871 standard; cDNA; 28215 BP.  
DE Human secreted protein BAC clone SEQ ID NO 1051.  
PN WO200295010-A2.  
PD 28-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 8; Length 28215;  
Best Local Similarity 83.3%; Pred. No. 1.8e-46;  
RESULT 555  
ID ABZ71493 standard; DNA; 28215 BP.  
DE Secreted protein gene 24 genomic fragment HCNDR47, SEQ ID NO:603.  
PN WO200276488-A1.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 8; Length 28215;  
Best Local Similarity 83.3%; Pred. No. 1.8e-46;  
RESULT 556  
ID ADB91849 standard; DNA; 28215 BP.  
DE Human secreted protein related DNA #SEQ ID 795.  
PN WO2003004622-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 9; Length 28215;  
Best Local Similarity 83.3%; Pred. No. 1.8e-46;  
RESULT 557  
ID ADC74632 standard; DNA; 28215 BP.  
DE Human secreted protein-related DNA - SEQ ID 1265.  
PN WO2003038063-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 10; Length 28215;  
Best Local Similarity 83.3%; Pred. No. 1.8e-46;  
RESULT 558  
ID AEL94875 standard; DNA; 28215 BP.  
DE Human secreted protein-related DNA sequence - SEQ ID 1057.  
PN US2006246483-A1.  
PD 02-NOV-2006.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 15; Length 28215;  
Best Local Similarity 83.3%; Pred. No. 1.8e-46;  
RESULT 559  
ID AAL35901 standard; DNA; 28818 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2266.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 4; Length 28818;  
Best Local Similarity 81.1%; Pred. No. 1.8e-46;  
RESULT 560  
ID ABX58889 standard; cDNA; 28818 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #1233.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 225.8; DB 8; Length 28818;  
Best Local Similarity 81.1%; Pred. No. 1.8e-46;  
RESULT 561  
ID ADJ29639 standard; DNA; 28818 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2266.



PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.8; DB 12; Length 28818;  
Best Local Similarity 81.1%; Pred. No. 1.8e-46;  
RESULT 562  
ID AAF54723 standard; DNA; 35465 BP.  
DE Nucleotide sequence of a human polynucleotide sequence.  
PN WO200105422-A2.  
PD 25-JAN-2001.  
PA (INMR ) BIOMERIEUX STELHYS.  
Query Match 9.9%; Score 225.8; DB 4; Length 35465;  
Best Local Similarity 83.3%; Pred. No. 2e-46;  
RESULT 563  
ID ABT17380 standard; DNA; 35465 BP.  
DE Human IG gene related nucleic acid SEQ ID No 6.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 9.9%; Score 225.8; DB 8; Length 35465;  
Best Local Similarity 83.3%; Pred. No. 2e-46;  
RESULT 564  
ID ABT17382 standard; DNA; 36991 BP.  
DE Human IG gene related nucleic acid SEQ ID No 8.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 9.9%; Score 225.8; DB 8; Length 36991;  
Best Local Similarity 83.3%; Pred. No. 2.1e-46;  
RESULT 565  
ID AED18110 standard; DNA; 36991 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 361.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 9.9%; Score 225.8; DB 14; Length 36991;  
Best Local Similarity 83.3%; Pred. No. 2.1e-46;  
RESULT 566  
ID AEF75130 standard; DNA; 36991 BP.  
DE Human polynucleotide #644.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS ) VISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.9%; Score 225.8; DB 15; Length 36991;  
Best Local Similarity 83.3%; Pred. No. 2.1e-46;  
RESULT 567  
ID ACN44494 standard; DNA; 60381 BP.  
DE Human genomic sequence hCG27935.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225.8; DB 11; Length 60381;  
Best Local Similarity 76.5%; Pred. No. 2.6e-46;  
RESULT 568  
ID ADO32260 standard; DNA; 106707 BP.  
DE Human chromosome 20 region containing type 2 diabetes mellitus genes.  
PN WO2004039954-A2.  
PD 13-MAY-2004.  
PA (JOSL-) JOSLIN DIABETES CENT INC.  
Query Match 9.9%; Score 225.8; DB 12; Length 106707;  
Best Local Similarity 85.7%; Pred. No. 3.3e-46;  
RESULT 569  
ID AEH93956 standard; DNA; 118899 BP.  
DE DNMT31 variant full length coding sequence.  
PN US2006115829-A1.  
PD 01-JUN-2006.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 9.9%; Score 225.8; DB 15; Length 118899;  
Best Local Similarity 87.1%; Pred. No. 3.5e-46;  
RESULT 570  
ID ADZ13043 standard; DNA; 140342 BP.  
DE Human cancer-associated genomic DNA #52.

PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.9%; Score 225.8; DB 14; Length 140342;  
Best Local Similarity 82.2%; Pred. No. 3.7e-46;  
RESULT 571  
ID AEF80130 standard; DNA; 162302 BP.  
DE Cancer-associated polypeptide genomic DNA sequence hD27-009 SEQ ID NO:26.  
PN US2006024677-A1.  
PD 02-FEB-2006.  
PA (MORR-) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
PA (LAIA/) LAI A.  
PA (TSEC/) TSE C.  
PA (FATT/) FATTAEY A.  
Query Match 9.9%; Score 225.8; DB 15; Length 162302;  
Best Local Similarity 79.2%; Pred. No. 4e-46;  
RESULT 572  
ID ADZ13735 standard; DNA; 187851 BP.  
DE Human cancer-associated genomic DNA #108.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.9%; Score 225.8; DB 14; Length 187851;  
Best Local Similarity 84.4%; Pred. No. 4.3e-46;  
RESULT 573  
ID ADB62640 standard; cDNA; 2946 BP.  
DE Human cDNA encoding clone KIDNE20150730.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.9%; Score 225.6; DB 10; Length 2946;  
Best Local Similarity 85.2%; Pred. No. 7.4e-47;  
RESULT 574  
ID AAL07337 standard; DNA; 4059 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 10025.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.6; DB 4; Length 4059;  
Best Local Similarity 85.2%; Pred. No. 8.6e-47;  
RESULT 575  
ID AAZ50904 standard; DNA; 17590 BP.  
DE Human TBC-1 partial genomic DNA comprising 5' end sequence.  
PN WO200008209-A2.  
PD 17-FEB-2000.  
PA (GEST ) GENSET.  
Query Match 9.9%; Score 225.6; DB 3; Length 17590;  
Best Local Similarity 86.4%; Pred. No. 1.7e-46;  
RESULT 576  
ID AEJ63934 standard; DNA; 17590 BP.  
DE Human TBC-1 genomic SEQ ID NO 1.  
PN US2006084073-A1.  
PD 20-APR-2006.  
PA (GEST ) GENSET SA.  
Query Match 9.9%; Score 225.6; DB 15; Length 17590;  
Best Local Similarity 86.4%; Pred. No. 1.7e-46;  
RESULT 577  
ID ADJ12398 standard; DNA; 43991 BP.  
DE DNA fragment of a BAC clone that encodes a human secreted protein seq252.  
PN US2004010132-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (BREW/) BREWER L A.  
PA (DUAN/) DUAN R D.  
PA (RUBE/) RUBEN S M.  
PA (FLOR/) FLORENCE K A.  
PA (GREE/) GREENE J M.  
PA (YOUN/) YOUNG P E.  
PA (FERR/) FERRIE A M.  
PA (YUGG/) YU G.  
PA (FLOR/) FLORENCE C.

PA (EBNE/) EBNER R.  
PA (OLSE/) OLSEN H.  
Query Match 9.9%; Score 225.6; DB 12; Length 43991;  
Best Local Similarity 84.2%; Pred. No. 2.5e-46;  
RESULT 578  
Query Match 9.9%; Score 225.6; DB 14; Length 110000;  
Best Local Similarity 82.8%; Pred. No. 3.8e-46;  
RESULT 579  
ID ADE82948 standard; DNA; 167163 BP.  
DE Human PVT1 genomic DNA sequence.  
PN WO2003080808-A2.  
PD 02-OCT-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225.6; DB 10; Length 167163;  
Best Local Similarity 82.8%; Pred. No. 4.6e-46;  
RESULT 580  
ID ABT10147 standard; cDNA; 185035 BP.  
DE Human breast cancer associated coding sequence SEQ ID NO: 281.  
PN WO200259271-A2.  
PD 01-AUG-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.9%; Score 225.6; DB 6; Length 185035;  
Best Local Similarity 87.8%; Pred. No. 4.8e-46;  
RESULT 581  
ID ACA64951 standard; DNA; 185035 BP.  
DE Human FEN1 DNA corresponding to AC004770.  
PN DE10127572-A1.  
PD 05-DEC-2002.  
PA (PATH-) PATHOARRAY GMBH.  
Query Match 9.9%; Score 225.6; DB 8; Length 185035;  
Best Local Similarity 87.8%; Pred. No. 4.8e-46;  
RESULT 582  
ID ADQ20284 standard; DNA; 185035 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3104.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 225.6; DB 12; Length 185035;  
Best Local Similarity 87.8%; Pred. No. 4.8e-46;  
RESULT 583  
ID AAK83109 standard; DNA; 2816 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37921.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.4; DB 4; Length 2816;  
Best Local Similarity 85.9%; Pred. No. 8.2e-47;  
RESULT 584  
ID ADR07011 standard; cDNA; 3847 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 517.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.9%; Score 225.4; DB 13; Length 3847;  
Best Local Similarity 81.7%; Pred. No. 9.4e-47;  
RESULT 585  
ID AAK79618 standard; DNA; 9510 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34430.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.4; DB 4; Length 9510;  
Best Local Similarity 82.7%; Pred. No. 1.4e-46;  
RESULT 586  
ID ABX13167 standard; DNA; 19650 BP.  
DE Human gene encoding a zinc metalloprotease.  
PN US6482629-B1.  
PD 19-NOV-2002.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 225.4; DB 8; Length 19650;  
Best Local Similarity 84.9%; Pred. No. 2e-46;  
RESULT 587  
ID AAD62720 standard; DNA; 19650 BP.

DE Human zinc metalloprotease genomic DNA.  
PN US2003129700-A1.  
PD 10-JUL-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 225.4; DB 10; Length 19650;  
Best Local Similarity 84.9%; Pred. No. 2e-46;  
RESULT 588  
ID ADQ88304 standard; DNA; 19650 BP.  
DE Human zinc metalloprotease genomic DNA.  
PN US2004142439-A1.  
PD 22-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 225.4; DB 13; Length 19650;  
Best Local Similarity 84.9%; Pred. No. 2e-46;  
RESULT 589  
ID ADY74758 standard; DNA; 19650 BP.  
DE Human zinc metalloprotease genomic DNA.  
PN US2005059075-A1.  
PD 17-MAR-2005.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 225.4; DB 14; Length 19650;  
Best Local Similarity 84.9%; Pred. No. 2e-46;  
RESULT 590  
ID AAK65309 standard; DNA; 19969 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20121.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.4; DB 4; Length 19969;  
Best Local Similarity 74.8%; Pred. No. 2e-46;  
RESULT 591  
ID AAP24851 standard; DNA; 20598 BP.  
DE Nucleotide sequence of a human helical cytokine designated Zalpha33.  
PN WO200077209-A1.  
PD 21-DEC-2000.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 9.9%; Score 225.4; DB 4; Length 20598;  
Best Local Similarity 74.8%; Pred. No. 2e-46;  
RESULT 592  
ID AAD42515 standard; DNA; 20598 BP.  
DE Human zalpha33 gene.  
PN US6406888-B1.  
PD 18-JUN-2002.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 9.9%; Score 225.4; DB 6; Length 20598;  
Best Local Similarity 74.8%; Pred. No. 2e-46;  
RESULT 593  
ID ACH00110 standard; DNA; 20598 BP.  
DE Human zalpha33 genomic DNA.  
PN US2003064479-A1.  
PD 03-APR-2003.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 9.9%; Score 225.4; DB 9; Length 20598;  
Best Local Similarity 74.8%; Pred. No. 2e-46;  
RESULT 594  
ID ABA20763 standard; DNA; 26427 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 13094.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.4; DB 5; Length 26427;  
Best Local Similarity 85.9%; Pred. No. 2.2e-46;  
RESULT 595  
ID ABA20762 standard; DNA; 26427 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 13093.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.4; DB 5; Length 26427;  
Best Local Similarity 85.9%; Pred. No. 2.2e-46;  
RESULT 596  
ID ADQ97657 standard; DNA; 32787 BP.  
DE Human cancer associated sequence HD10-022, SEQ ID 634.

PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 225.4; DB 12; Length 32787;  
Best Local Similarity 73.6%; Pred. No. 2.5e-46;  
RESULT 597  
ID ACN44490 standard; DNA; 32865 BP.  
DE Human genomic sequence hCG25375.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225.4; DB 11; Length 32865;  
Best Local Similarity 70.4%; Pred. No. 2.5e-46;  
RESULT 598  
ID ADJ10262 standard; DNA; 51001 BP.  
DE Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.  
PN US2004005570-A1.  
PD 08-JAN-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 12; Length 51001;  
Best Local Similarity 86.1%; Pred. No. 3e-46;  
RESULT 599  
ID ADQ97249 standard; DNA; 59575 BP.  
DE Human cancer associated sequence HD08-021, SEQ ID 225.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 225.4; DB 12; Length 59575;  
Best Local Similarity 81.5%; Pred. No. 3.2e-46;  
RESULT 600  
ID ABS52847 standard; DNA; 90541 BP.  
DE Human SR protein-specific kinase 2, SRPK2, genomic DNA.  
PN US2002094560-A1.  
PD 18-JUL-2002.  
PA (ABUT/) ABU-THREIDEH J.  
PA (GONG/) GONG F.  
PA (KETC/) KETCHUM K A.  
PA (DFRA/) DI FRANCESCO V.  
PA (BEAS/) BEASLEY E M.  
Query Match 9.9%; Score 225.4; DB 6; Length 90541;  
Best Local Similarity 85.9%; Pred. No. 3.9e-46;  
RESULT 601  
ID ADJ37690 standard; DNA; 90541 BP.  
DE Human kinase genomic DNA.  
PN US2003175927-A1.  
PD 18-SEP-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 225.4; DB 10; Length 90541;  
Best Local Similarity 85.9%; Pred. No. 3.9e-46;  
RESULT 602  
ID ADR31219 standard; DNA; 90541 BP.  
DE Human SRPK2 kinase protein alternative splice form genomic DNA.  
PN US2004157297-A1.  
PD 12-AUG-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 225.4; DB 13; Length 90541;  
Best Local Similarity 85.9%; Pred. No. 3.9e-46;  
RESULT 603  
ID ACC45150 standard; DNA; 96649 BP.  
DE Human NAC nucleotide sequence SEQ ID NO:10.  
PN WO2003024988-A1.  
PD 27-MAR-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 8; Length 96649;  
Best Local Similarity 83.5%; Pred. No. 4e-46;  
RESULT 604  
ID ADQ19183 standard; DNA; 110665 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2002.  
PN WO2004048938-A2.  
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 225.4; DB 12; Length 110665;  
Best Local Similarity 81.5%; Pred. No. 4.3e-46;  
RESULT 606  
ID AAL54213 standard; DNA; 113033 BP.  
DE SR protein-specific kinase-1 DNA, SEQ ID No 5.  
PN WO200299427-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 9.9%; Score 225.4; DB 8; Length 113033;  
Best Local Similarity 85.9%; Pred. No. 4.3e-46;  
RESULT 607  
ID ADQ21090 standard; DNA; 114411 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3910.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 225.4; DB 12; Length 114411;  
Best Local Similarity 81.3%; Pred. No. 4.3e-46;  
RESULT 608  
ID AAA34791 standard; DNA; 138169 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2480.  
PN WO200009525-A2.  
PD 24-FEB-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 9.9%; Score 225.4; DB 3; Length 138169;  
Best Local Similarity 82.7%; Pred. No. 4.7e-46;  
RESULT 609  
ID ABD20695 standard; DNA; 141586 BP.  
DE Human pulmonary and inflammatory target DNA #306.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 11; Length 141586;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 610  
ID AAA35005 standard; DNA; 141589 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2694.  
PN WO200009525-A2.  
PD 24-FEB-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 9.9%; Score 225.4; DB 3; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 611  
ID AAA35030 standard; DNA; 141589 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2719.  
PN WO200009525-A2.  
PD 24-FEB-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 9.9%; Score 225.4; DB 3; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 612  
ID AAF21152 standard; DNA; 141589 BP.  
DE Human low adenosine antisense oligonucleotide related sequence #2719.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
Query Match 9.9%; Score 225.4; DB 3; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 613  
ID AAF20913 standard; DNA; 141589 BP.  
DE Human ELAM-1 polynucleotide fragment #2480.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
Query Match 9.9%; Score 225.4; DB 3; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 614  
ID AAF21127 standard; DNA; 141589 BP.  
DE Human low adenosine antisense oligonucleotide related sequence #2694.  
PN WO200062736-A2.



PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
Query Match 9.9%; Score 225.4; DB 3; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 615  
ID ABZ96821 standard; DNA; 141589 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 10; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 616  
ID ABZ96607 standard; DNA; 141589 BP.  
DE Human ELAM-1 nucleic acid.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 10; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 617  
ID ABZ96846 standard; DNA; 141589 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 10; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 618  
ID ABD20670 standard; DNA; 141589 BP.  
DE Human pulmonary and inflammatory target DNA #281.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 11; Length 141589;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 619  
ID ABD19162 standard; DNA; 141601 BP.  
DE Human ELAM-1 DNA fragment #2.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 11; Length 141601;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 620  
ID AAF21442 standard; DNA; 146981 BP.  
DE Human ELAM-1 polynucleotide fragment #3009.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
Query Match 9.9%; Score 225.4; DB 3; Length 146981;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 621  
ID ABZ97136 standard; DNA; 146982 BP.  
DE Human ELAM-1 antisense fragment no.1738.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 10; Length 146982;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 622  
ID ABD19160 standard; DNA; 146984 BP.  
DE Human ELAM-1 DNA fragment 1738.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 11; Length 146984;  
Best Local Similarity 82.7%; Pred. No. 4.8e-46;  
RESULT 623  
ID ADS36467 standard; DNA; 154799 BP.  
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1681.

PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 225.4; DB 13; Length 154799;  
Best Local Similarity 82.4%; Pred. No. 5e-46;  
RESULT 624  
ID AEF92730 standard; DNA; 163218 BP.  
DE Human chromosome 17 sequence, clone hRPK.318\_A\_15.  
PN WO2006020269-A2.  
PD 23-FEB-2006.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 9.9%; Score 225.4; DB 15; Length 163218;  
Best Local Similarity 81.3%; Pred. No. 5.1e-46;  
RESULT 625  
ID ADL13501 standard; DNA; 167932 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #33.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.9%; Score 225.4; DB 10; Length 167932;  
Best Local Similarity 85.9%; Pred. No. 5.1e-46;  
RESULT 626  
ID ADL13752 standard; DNA; 190000 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #284.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.9%; Score 225.4; DB 10; Length 190000;  
Best Local Similarity 81.3%; Pred. No. 5.4e-46;  
RESULT 627  
ID AAF21437 standard; DNA; 209273 BP.  
DE Human factor-related antisense polynucleotide #3004.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
Query Match 9.9%; Score 225.4; DB 3; Length 209273;  
Best Local Similarity 82.7%; Pred. No. 5.7e-46;  
RESULT 628  
ID ABZ97131 standard; DNA; 209274 BP.  
DE Human enzyme-related antisense polynucleotide.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.9%; Score 225.4; DB 10; Length 209274;  
Best Local Similarity 82.7%; Pred. No. 5.7e-46;  
RESULT 629  
ID AAK67291 standard; DNA; 681 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22103.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.2; DB 4; Length 681;  
Best Local Similarity 81.9%; Pred. No. 4.9e-47;  
RESULT 630  
ID AAI96126 standard; cDNA; 811 BP.  
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2201.  
PN WO200166719-A1.  
PD 13-SEP-2001.  
PA (CHIB-) CHIBA PREFECTURE.  
PA (HISM ) HISAMITSU PHARM CO LTD.  
Query Match 9.9%; Score 225.2; DB 4; Length 811;  
Best Local Similarity 84.2%; Pred. No. 5.3e-47;  
RESULT 631  
ID ABT42918 standard; DNA; 811 BP.  
DE Human neuroblastoma-related DNA sequence, SEQ ID NO:199.  
PN WO2002103017-A1.  
PD 27-DEC-2002.  
PA (CHIB-) CHIBA PREFECTURE.  
PA (HISM ) HISAMITSU PHARM CO LTD.  
Query Match 9.9%; Score 225.2; DB 8; Length 811;  
Best Local Similarity 84.2%; Pred. No. 5.3e-47;  
RESULT 632

ID ADK67850 standard; cDNA; 1370 BP.  
DE Phosphoadenosine-phosphosulfate synthetase, modifier of AXIN pathway.  
PN WO2004013309-A2.  
PD 12-FEB-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 9.9%; Score 225.2; DB 12; Length 1370;  
Best Local Similarity 86.7%; Pred. No. 6.7e-47;  
RESULT 633  
ID AAL35996 standard; DNA; 1655 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2361.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.2; DB 4; Length 1655;  
Best Local Similarity 81.9%; Pred. No. 7.3e-47;  
RESULT 634  
ID ABX58984 standard; cDNA; 1655 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #1328.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 225.2; DB 8; Length 1655;  
Best Local Similarity 81.9%; Pred. No. 7.3e-47;  
RESULT 635  
ID ADJ29734 standard; DNA; 1655 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2361.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.2; DB 12; Length 1655;  
Best Local Similarity 81.9%; Pred. No. 7.3e-47;  
RESULT 636  
ID AEI44902 standard; DNA; 2177 BP.  
DE Human 3'-phosphoadenosine 5'-phosphosulfate synthetase 1 DNA SEQ ID: 1.  
PN US7067311-B1.  
PD 27-JUN-2006.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 9.9%; Score 225.2; DB 15; Length 2177;  
Best Local Similarity 86.7%; Pred. No. 8.2e-47;  
RESULT 637  
ID AEJ92460 standard; DNA; 2177 BP.  
DE Human 3'-phosphoadenosine-5'-phosphosulfate synthetase 1 exon 1 DNA.  
PN US2006188973-A1.  
PD 24-AUG-2006.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 9.9%; Score 225.2; DB 15; Length 2177;  
Best Local Similarity 86.7%; Pred. No. 8.2e-47;  
RESULT 638  
ID AAH17855 standard; cDNA; 2706 BP.  
DE Human cDNA sequence SEQ ID NO:17555.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.9%; Score 225.2; DB 4; Length 2706;  
Best Local Similarity 84.2%; Pred. No. 9.1e-47;  
RESULT 639  
ID ADR07592 standard; cDNA; 3877 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1098.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.9%; Score 225.2; DB 13; Length 3877;  
Best Local Similarity 83.0%; Pred. No. 1.1e-46;  
RESULT 640  
ID AAK74563 standard; DNA; 5283 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29375.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.2; DB 4; Length 5283;  
Best Local Similarity 85.4%; Pred. No. 1.2e-46;

RESULT 641  
ID AAS42014 standard; DNA; 6437 BP.  
DE Genomic sequence #330 encoding novel human enzyme polypeptide.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.2; DB 4; Length 6437;  
Best Local Similarity 80.9%; Pred. No. 1.3e-46;  
RESULT 642  
ID AAS42015 standard; DNA; 9742 BP.  
DE Genomic sequence #331 encoding novel human enzyme polypeptide.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225.2; DB 4; Length 9742;  
Best Local Similarity 80.9%; Pred. No. 1.6e-46;  
RESULT 643  
ID AEB96529 standard; DNA; 20001 BP.  
DE Human SULT2B1 gene, SEQ ID 13.  
PN JP2005204549-A.  
PD 04-AUG-2005.  
PA (HYUB-) HYUBITTO GENOMICS KK.  
PA (KAWA/) KAWADA Y.  
Query Match 9.9%; Score 225.2; DB 14; Length 20001;  
Best Local Similarity 84.2%; Pred. No. 2.2e-46;  
RESULT 644  
ID ADZ13548 standard; DNA; 38636 BP.  
DE Human cancer-associated genomic DNA #91.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.9%; Score 225.2; DB 14; Length 38636;  
Best Local Similarity 75.1%; Pred. No. 3e-46;  
RESULT 645  
ID ADZ13582 standard; DNA; 73702 BP.  
DE Human cancer-associated genomic DNA #94.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.9%; Score 225.2; DB 14; Length 73702;  
Best Local Similarity 83.0%; Pred. No. 4e-46;  
RESULT 646  
ID ABD33145 standard; DNA; 73723 BP.  
DE Human cancer-associated (CA) gene HD07-018.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 225.2; DB 13; Length 73723;  
Best Local Similarity 83.0%; Pred. No. 4e-46;  
RESULT 647  
ID AEJ13110 standard; DNA; 73723 BP.  
DE Cancer-associated gene sequence - SEQ ID 118.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.9%; Score 225.2; DB 15; Length 73723;  
Best Local Similarity 83.0%; Pred. No. 4e-46;  
RESULT 648  
ID ADC85284 standard; DNA; 92562 BP.  
DE Human Itk genomic sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225.2; DB 10; Length 92562;  
Best Local Similarity 71.0%; Pred. No. 4.4e-46;  
RESULT 649  
ID ADA02804 standard; DNA; 92563 BP.  
DE Human ITK carcinoma associated gene, SEQ ID NO:1322.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225.2; DB 9; Length 92563;

Best Local Similarity 71.0%; Pred. No. 4.4e-46;  
RESULT 650  
ID ADB72542 standard; DNA; 92563 BP.  
DE Human ITK gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225.2; DB 10; Length 92563;  
Best Local Similarity 71.0%; Pred. No. 4.4e-46;  
RESULT 651  
ID ADM74399 standard; DNA; 92563 BP.  
DE Human carcinoma associated (CA) nucleic acid #34.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.9%; Score 225.2; DB 12; Length 92563;  
Best Local Similarity 71.0%; Pred. No. 4.4e-46;  
RESULT 652  
Query Match 9.9%; Score 225.2; DB 6; Length 110000;  
Best Local Similarity 82.3%; Pred. No. 4.8e-46;  
RESULT 653  
Query Match 9.9%; Score 225.2; DB 6; Length 110000;  
Best Local Similarity 82.3%; Pred. No. 4.8e-46;  
RESULT 654  
Query Match 9.9%; Score 225.2; DB 8; Length 110000;  
Best Local Similarity 82.3%; Pred. No. 4.8e-46;  
RESULT 655  
Query Match 9.9%; Score 225.2; DB 10; Length 110000;  
Best Local Similarity 82.3%; Pred. No. 4.8e-46;  
RESULT 656  
Query Match 9.9%; Score 225.2; DB 12; Length 110000;  
Best Local Similarity 81.9%; Pred. No. 4.8e-46;  
RESULT 657  
ID ADC89520 standard; DNA; 139257 BP.  
DE Human COREST genomic DNA #SEQ ID 11.  
PN WO2003011890-A1.  
PD 13-FEB-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.9%; Score 225.2; DB 10; Length 139257;  
Best Local Similarity 83.0%; Pred. No. 5.3e-46;  
RESULT 658  
ID AAL35995 standard; DNA; 1647 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2360.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225; DB 4; Length 1647;  
Best Local Similarity 81.5%; Pred. No. 8.1e-47;  
RESULT 659  
ID ABX58983 standard; cDNA; 1647 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #1327.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.9%; Score 225; DB 8; Length 1647;  
Best Local Similarity 81.5%; Pred. No. 8.1e-47;  
RESULT 660  
ID ADJ29733 standard; DNA; 1647 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2360.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225; DB 12; Length 1647;  
Best Local Similarity 81.5%; Pred. No. 8.1e-47;  
RESULT 661  
ID AAK70585 standard; DNA; 5086 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25397.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.9%; Score 225; DB 4; Length 5086;  
Best Local Similarity 78.6%; Pred. No. 1.4e-46;  
RESULT 662  
ID AAK70584 standard; DNA; 5093 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25396.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225; DB 4; Length 5093;  
Best Local Similarity 78.6%; Pred. No. 1.4e-46;  
RESULT 663  
ID AAK70338 standard; DNA; 9481 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25150.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225; DB 4; Length 9481;  
Best Local Similarity 82.8%; Pred. No. 1.8e-46;  
RESULT 664  
ID ABD32562 standard; DNA; 21478 BP.  
DE Human cancer-associated genomic DNA HD14-034.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 225; DB 13; Length 21478;  
Best Local Similarity 81.3%; Pred. No. 2.6e-46;  
RESULT 665  
ID ADA02702 standard; DNA; 21666 BP.  
DE Human Nupr1 carcinoma associated gene, SEQ ID NO:1220.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225; DB 9; Length 21666;  
Best Local Similarity 83.7%; Pred. No. 2.6e-46;  
RESULT 666  
ID ADB72440 standard; DNA; 21666 BP.  
DE Human CA gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225; DB 10; Length 21666;  
Best Local Similarity 83.7%; Pred. No. 2.6e-46;  
RESULT 667  
ID ADE95950 standard; DNA; 21666 BP.  
DE Human hCG1745228 gene genomic DNA sequence.  
PN WO2003039484-A2.  
PD 15-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225; DB 10; Length 21666;  
Best Local Similarity 83.7%; Pred. No. 2.6e-46;  
RESULT 668  
ID AEK60221 standard; DNA; 21666 BP.  
DE Human NUPR1 genomic sequence, SEQ ID NO: 208.  
PN US2006204982-A1.  
PD 14-SEP-2006.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.9%; Score 225; DB 15; Length 21666;  
Best Local Similarity 83.7%; Pred. No. 2.6e-46;  
RESULT 669  
ID AAK86932 standard; DNA; 22465 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41744.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.9%; Score 225; DB 4; Length 22465;  
Best Local Similarity 82.6%; Pred. No. 2.6e-46;  
RESULT 670  
ID ACN45138 standard; DNA; 23694 BP.  
DE Human genomic sequence hCG17175.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.



Query Match 9.9%; Score 225; DB 11; Length 23694;  
Best Local Similarity 86.1%; Pred. No. 2.7e-46;  
RESULT 671  
ID ABD33540 standard; DNA; 25428 BP.  
DE Human cancer-associated (CA) gene HD07-107.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 225; DB 13; Length 25428;  
Best Local Similarity 81.3%; Pred. No. 2.8e-46;  
RESULT 672  
ID AEJ13722 standard; DNA; 25428 BP.  
DE Cancer-associated gene sequence - SEQ ID 730.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.9%; Score 225; DB 15; Length 25428;  
Best Local Similarity 81.3%; Pred. No. 2.8e-46;  
RESULT 673  
ID ABD33544 standard; DNA; 25899 BP.  
DE Human cancer-associated (CA) gene HD07-108.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 225; DB 13; Length 25899;  
Best Local Similarity 86.1%; Pred. No. 2.8e-46;  
RESULT 674  
ID AEJ13728 standard; DNA; 25899 BP.  
DE Cancer-associated gene sequence - SEQ ID 736.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.9%; Score 225; DB 15; Length 25899;  
Best Local Similarity 86.1%; Pred. No. 2.8e-46;  
RESULT 675  
ID ADS36474 standard; DNA; 40947 BP.  
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1688.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.9%; Score 225; DB 13; Length 40947;  
Best Local Similarity 81.5%; Pred. No. 3.5e-46;  
RESULT 676  
ID ABD33453 standard; DNA; 51837 BP.  
DE Human cancer-associated (CA) gene HD07-086.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 225; DB 13; Length 51837;  
Best Local Similarity 83.7%; Pred. No. 3.8e-46;  
RESULT 677  
ID AEJ13590 standard; DNA; 51837 BP.  
DE Cancer-associated gene sequence - SEQ ID 598.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.9%; Score 225; DB 15; Length 51837;  
Best Local Similarity 83.7%; Pred. No. 3.8e-46;  
RESULT 678  
ID ABD32769 standard; DNA; 100608 BP.  
DE Human cancer-associated genomic DNA HD16-031.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.9%; Score 225; DB 13; Length 100608;  
Best Local Similarity 87.5%; Pred. No. 5.2e-46;  
RESULT 679  
ID AED89397 standard; DNA; 150481 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 37.  
PN WO2005106044-A1.

PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.9%; Score 225; DB 14; Length 150481;  
Best Local Similarity 82.6%; Pred. No. 6.2e-46;  
RESULT 680  
ID ADQ20461 standard; DNA; 166181 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3281.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 225; DB 12; Length 166181;  
Best Local Similarity 81.7%; Pred. No. 6.5e-46;  
RESULT 681  
ID ADQ18633 standard; DNA; 166181 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.9%; Score 225; DB 12; Length 166181;  
Best Local Similarity 81.7%; Pred. No. 6.5e-46;  
RESULT 682  
ID AED89398 standard; DNA; 171162 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 38.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.9%; Score 225; DB 14; Length 171162;  
Best Local Similarity 82.6%; Pred. No. 6.6e-46;  
RESULT 683  
ID ACN44626 standard; DNA; 175077 BP.  
DE Human genomic sequence hCG19724.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.9%; Score 225; DB 11; Length 175077;  
Best Local Similarity 83.7%; Pred. No. 6.6e-46;  
RESULT 684  
ID ADQ22654 standard; DNA; 3820 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5474.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.8%; Score 224.8; DB 12; Length 3820;  
Best Local Similarity 78.5%; Pred. No. 1.3e-46;  
RESULT 685  
ID ADP13403 standard; DNA; 16689 BP.  
DE Renal cell carcinoma differentially expressed gene #139.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
Query Match 9.8%; Score 224.8; DB 12; Length 16689;  
Best Local Similarity 85.6%; Pred. No. 2.6e-46;  
RESULT 686  
ID AEA36261 standard; DNA; 16689 BP.  
DE Human nucleic acid sequence #193.  
PN WO2005054507-A2.  
PD 16-JUN-2005.  
PA (UYSH-) UNIV SHEFFIELD.  
Query Match 9.8%; Score 224.8; DB 14; Length 16689;  
Best Local Similarity 85.6%; Pred. No. 2.6e-46;  
RESULT 687  
ID ABG93507 standard; cDNA; 16689 BP.  
DE Human tumor cell cDNA SEQ ID NO:1003.  
PN WO2006036025-A1.  
PD 06-APR-2006.  
PA (EISA ) EISAI CO LTD.  
Query Match 9.8%; Score 224.8; DB 15; Length 16689;

Best Local Similarity 85.6%; Pred. No. 2.6e-46;  
RESULT 688  
ID ADO43240 standard; DNA; 37620 BP.  
DE Vacuolar protein sorting factor Vps4B gene, involved in HIV-1 budding.  
PN WO2004039311-A2.  
PD 13-MAY-2004.  
PA (UTAH ) UNIV UTAH RES FOUND.  
Query Match 9.8%; Score 224.8; DB 12; Length 37620;  
Best Local Similarity 85.8%; Pred. No. 3.7e-46;  
RESULT 689  
ID AEA61175 standard; DNA; 53779 BP.  
DE Human ENTPD5 gene genomic sequence SEQ ID NO:85.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB ) BAYER CORP.  
Query Match 9.8%; Score 224.8; DB 14; Length 53779;  
Best Local Similarity 81.1%; Pred. No. 4.4e-46;  
RESULT 690  
ID ADL13866 standard; DNA; 79597 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #398.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.8%; Score 224.8; DB 10; Length 79597;  
Best Local Similarity 85.6%; Pred. No. 5.2e-46;  
RESULT 691  
ID ABX14763 standard; DNA; 88191 BP.  
DE Genomic DNA encoding novel human ras-like protein.  
PN US2002132291-A1.  
PD 19-SEP-2002.  
PA (YEJJ/) YE J.  
PA (KETC/) KETCHUM K A.  
PA (DFRA/) DI FRANCESCO V.  
PA (BEAS/) BEASLEY E M.  
Query Match 9.8%; Score 224.8; DB 8; Length 88191;  
Best Local Similarity 81.1%; Pred. No. 5.5e-46;  
RESULT 692  
ID ABG03293 standard; DNA; 94000 BP.  
DE Human genomic nucleotide region of an ADCYAP1R1 region.  
PN WO2006022638-A1.  
PD 02-MAR-2006.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.8%; Score 224.8; DB 15; Length 94000;  
Best Local Similarity 84.4%; Pred. No. 5.6e-46;  
RESULT 693  
ID ABD33009 standard; DNA; 99918 BP.  
DE Human cancer-associated genomic DNA HD21-032.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 224.8; DB 13; Length 99918;  
Best Local Similarity 84.4%; Pred. No. 5.8e-46;  
RESULT 694  
ID ADQ17641 standard; DNA; 114771 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 458.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.8%; Score 224.8; DB 12; Length 114771;  
Best Local Similarity 71.4%; Pred. No. 6.2e-46;  
RESULT 695  
ID AAX90201 standard; DNA; 119950 BP.  
DE Human yes1 gene.  
PN WO9935290-A1.  
PD 15-JUL-1999.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 9.8%; Score 224.8; DB 2; Length 119950;  
Best Local Similarity 81.6%; Pred. No. 6.3e-46;  
RESULT 696  
ID AEB71426 standard; cDNA; 177556 BP.  
DE Human SGC alpha1 and beta1 subunit containing cDNA clone SEQ ID NO:6.  
PN US2005176043-A1.  
PD 11-AUG-2005.

PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 9.8%; Score 224.8; DB 14; Length 177556;  
Best Local Similarity 83.2%; Pred. No. 7.5e-46;  
RESULT 697  
ID ACD28257 standard; DNA; 177563 BP.  
DE Mouse soluble guanylyl cyclase SGC associated DNA #4.  
PN US2003096240-A1.  
PD 22-MAY-2003.  
PA (MURA/) MURAD F.  
PA (SHAR/) SHARINA I G.  
PA (KRUM/) KRUMENACKER J S.  
PA (MART/) MARTIN E.  
Query Match 9.8%; Score 224.8; DB 9; Length 177563;  
Best Local Similarity 83.2%; Pred. No. 7.5e-46;  
RESULT 698  
ID ABN64959 standard; cDNA; 525 BP.  
DE Human cancer related polynucleotide SEQ ID NO 4926.  
PN WO200214500-A2.  
PD 21-FEB-2002.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.8%; Score 224.6; DB 6; Length 525;  
Best Local Similarity 86.4%; Pred. No. 6.2e-47;  
RESULT 699  
ID ABD34711 standard; DNA; 1920 BP.  
DE ABL1 probe SEQ ID NO 47.  
PN WO2005094291-A2.  
PD 13-OCT-2005.  
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.  
Query Match 9.8%; Score 224.6; DB 14; Length 1920;  
Best Local Similarity 83.8%; Pred. No. 1.1e-46;  
RESULT 700  
ID ABK88737 standard; cDNA; 3053 BP.  
DE cDNA encoding methionyl tRNA synthetase 35.09.  
PN CN1341727-A.  
PD 27-MAR-2002.  
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.  
Query Match 9.8%; Score 224.6; DB 6; Length 3053;  
Best Local Similarity 81.7%; Pred. No. 1.4e-46;  
RESULT 701  
ID ADR07960 standard; cDNA; 4056 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1466.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.8%; Score 224.6; DB 13; Length 4056;  
Best Local Similarity 83.9%; Pred. No. 1.5e-46;  
RESULT 702  
ID ABA19375 standard; DNA; 25525 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 11706.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.6; DB 5; Length 25525;  
Best Local Similarity 83.9%; Pred. No. 3.5e-46;  
RESULT 703  
ID AAK89019 standard; DNA; 32204 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 2595.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.6; DB 4; Length 32204;  
Best Local Similarity 82.8%; Pred. No. 3.9e-46;  
RESULT 704  
ID AAK91533 standard; DNA; 32204 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 5109.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.6; DB 4; Length 32204;  
Best Local Similarity 82.8%; Pred. No. 3.9e-46;  
RESULT 705  
ID AAI57790 standard; DNA; 32204 BP.

DE Human colorectal cancer antigen coding sequence SEQ ID NO: 327.  
PN WO200155350-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.6; DB 4; Length 32204;  
Best Local Similarity 82.8%; Pred. No. 3.9e-46;  
RESULT 706  
ID AAS39620 standard; DNA; 32204 BP.  
DE Genomic sequence #39 encoding human colon associated polypeptide.  
PN WO200155302-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.6; DB 5; Length 32204;  
Best Local Similarity 82.8%; Pred. No. 3.9e-46;  
RESULT 707  
ID ABS99967 standard; DNA; 32204 BP.  
DE Genomic DNA #171 encoding human colorectal cancer related protein.  
PN US2002119919-A1.  
PD 29-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.8%; Score 224.6; DB 6; Length 32204;  
Best Local Similarity 82.8%; Pred. No. 3.9e-46;  
RESULT 708  
ID ADB32580 standard; DNA; 32204 BP.  
DE Human novel colon related polypeptide DNA SEQ ID NO 517.  
PN US2003050231-A1.  
PD 13-MAR-2003.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.8%; Score 224.6; DB 9; Length 32204;  
Best Local Similarity 82.8%; Pred. No. 3.9e-46;  
RESULT 709  
ID ADB93120 standard; DNA; 32204 BP.  
DE Human colorectal cancer related polypeptide DNA #171.  
PN US2003054420-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.6; DB 10; Length 32204;  
Best Local Similarity 82.8%; Pred. No. 3.9e-46;  
RESULT 710  
ID AAK71358 standard; DNA; 37314 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26170.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.6; DB 4; Length 37314;  
Best Local Similarity 82.8%; Pred. No. 4.2e-46;  
RESULT 711  
ID ABL64158 standard; DNA; 84539 BP.  
DE Stomach cancer related gene sequence SEQ ID NO:2495.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.8%; Score 224.6; DB 6; Length 84539;  
Best Local Similarity 83.8%; Pred. No. 6.1e-46;  
RESULT 712  
ID ADL13479 standard; DNA; 84539 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #11.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.8%; Score 224.6; DB 10; Length 84539;  
Best Local Similarity 83.8%; Pred. No. 6.1e-46;  
RESULT 713  
ID AEF73876 standard; DNA; 84539 BP.  
DE Human protein tyrosine kinase ABL-1 gene.  
PN WO2006015084-A2.  
PD 09-FEB-2006.  
PA (INVI-) INVITROGEN CORP.  
Query Match 9.8%; Score 224.6; DB 15; Length 84539;

Best Local Similarity 83.8%; Pred. No. 6.1e-46;  
RESULT 714  
ID AEF74626 standard; DNA; 84539 BP.  
DE Human polynucleotide #140.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.8%; Score 224.6; DB 15; Length 84539;  
Best Local Similarity 83.8%; Pred. No. 6.1e-46;  
RESULT 715  
ID ACN44154 standard; DNA; 101209 BP.  
DE Human genomic sequence hCG28567.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224.6; DB 11; Length 101209;  
Best Local Similarity 81.8%; Pred. No. 6.6e-46;  
RESULT 716  
Query Match 9.8%; Score 224.6; DB 11; Length 110000;  
Best Local Similarity 83.9%; Pred. No. 6.8e-46;  
RESULT 717  
Query Match 9.8%; Score 224.6; DB 14; Length 110000;  
Best Local Similarity 83.8%; Pred. No. 6.8e-46;  
RESULT 718  
ID ACN44262 standard; DNA; 168821 BP.  
DE Human genomic sequence hCG18035.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224.6; DB 11; Length 168821;  
Best Local Similarity 82.9%; Pred. No. 8.3e-46;  
RESULT 719  
ID AAD62832 standard; DNA; 180216 BP.  
DE Human BAC #1 containing formin (Fmn)-2 genomic DNA.  
PN US2003170683-A1.  
PD 11-SEP-2003.  
PA (LEDE/) LEDER P.  
PA (LEAD/) LEADER B.  
Query Match 9.8%; Score 224.6; DB 10; Length 180216;  
Best Local Similarity 80.6%; Pred. No. 8.5e-46;  
RESULT 720  
ID AAL54074 standard; DNA; 197997 BP.  
DE Human transporter protein encoding genomic DNA.  
Query Match 9.8%; Score 224.6; DB 10; Length 197997;  
Best Local Similarity 76.1%; Pred. No. 8.9e-46;  
RESULT 721  
ID ADL08109 standard; DNA; 247682 BP.  
DE Human gene associated with low HDL-C AT3.  
PN US2004043389-A1.  
PD 04-MAR-2004.  
PA (VITI-) VITIVITY INC.  
Query Match 9.8%; Score 224.6; DB 12; Length 247682;  
Best Local Similarity 84.0%; Pred. No. 9.8e-46;  
RESULT 722  
ID ADQ97433 standard; DNA; 295772 BP.  
DE Human cancer associated sequence HD08-047, SEQ ID 410.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 224.6; DB 12; Length 295772;  
Best Local Similarity 87.7%; Pred. No. 1.1e-45;  
RESULT 723  
ID AAH09299 standard; cDNA; 572 BP.  
DE Human cDNA clone (3'-primer) SEQ ID NO:6134.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.8%; Score 224.4; DB 4; Length 572;  
Best Local Similarity 82.3%; Pred. No. 7.2e-47;  
RESULT 724  
ID AAH15337 standard; cDNA; 1380 BP.  
DE Human cDNA sequence SEQ ID NO:13505.



PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.8%; Score 224.4; DB 4; Length 1380;  
Best Local Similarity 82.3%; Pred. No. 1.1e-46;  
RESULT 725  
ID AAK68489 standard; DNA; 1958 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23301.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.4; DB 4; Length 1958;  
Best Local Similarity 84.6%; Pred. No. 1.3e-46;  
RESULT 726  
ID ADJ94116 standard; DNA; 3577 BP.  
DE DLBCL tumour-associated antigen OX-TES-2 DNA.  
PN WO2003082916-A2.  
PD 09-OCT-2003.  
PA (ISIS-) ISIS INNOVATION LTD.  
Query Match 9.8%; Score 224.4; DB 10; Length 3577;  
Best Local Similarity 82.3%; Pred. No. 1.6e-46;  
RESULT 727  
ID AAK81191 standard; DNA; 5987 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36003.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.4; DB 4; Length 5987;  
Best Local Similarity 85.9%; Pred. No. 2.1e-46;  
RESULT 728  
ID AEE83905 standard; cDNA; 7224 BP.  
DE Human cDNA differentially expressed in asthma, SEQ ID NO:313.  
PN WO2005118403-A2.  
PD 15-DEC-2005.  
PA (LINK-) LINKAGENE LTD.  
Query Match 9.8%; Score 224.4; DB 15; Length 7224;  
Best Local Similarity 71.5%; Pred. No. 2.3e-46;  
RESULT 729  
ID AAS34684 standard; DNA; 9054 BP.  
DE Human DNA for a novel foetal antigen, SEQ ID No 2108.  
PN WO200155312-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.4; DB 5; Length 9054;  
Best Local Similarity 83.3%; Pred. No. 2.5e-46;  
RESULT 730  
ID AAI99373 standard; DNA; 9439 BP.  
DE Human excretory related polynucleotide SEQ ID NO 1137.  
PN WO200155313-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.4; DB 4; Length 9439;  
Best Local Similarity 82.3%; Pred. No. 2.5e-46;  
RESULT 731  
ID AAL35859 standard; DNA; 9439 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2224.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.4; DB 4; Length 9439;  
Best Local Similarity 82.3%; Pred. No. 2.5e-46;  
RESULT 732  
ID AAI63723 standard; DNA; 9439 BP.  
DE Human kidney related polynucleotide SEQ ID NO 1038.  
PN WO200155323-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.4; DB 5; Length 9439;  
Best Local Similarity 82.3%; Pred. No. 2.5e-46;  
RESULT 733  
ID ABX58847 standard; cDNA; 9439 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #1191.  
PN US2002147140-A1.

PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.8%; Score 224.4; DB 8; Length 9439;  
Best Local Similarity 82.3%; Pred. No. 2.5e-46;  
RESULT 734  
ID ADJ29597 standard; DNA; 9439 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2224.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.4; DB 12; Length 9439;  
Best Local Similarity 82.3%; Pred. No. 2.5e-46;  
RESULT 735  
ID ABA20516 standard; DNA; 14006 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12847.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.4; DB 5; Length 14006;  
Best Local Similarity 83.4%; Pred. No. 3e-46;  
RESULT 736  
ID ADA02966 standard; DNA; 31842 BP.  
DE Human LCK carcinoma associated gene, SEQ ID NO:1484.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224.4; DB 9; Length 31842;  
Best Local Similarity 82.3%; Pred. No. 4.4e-46;  
RESULT 737  
ID ADB72704 standard; DNA; 31842 BP.  
DE Human LCK gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224.4; DB 10; Length 31842;  
Best Local Similarity 82.3%; Pred. No. 4.4e-46;  
RESULT 738  
ID ADC85446 standard; DNA; 31842 BP.  
DE Human Lck genomic sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224.4; DB 10; Length 31842;  
Best Local Similarity 82.3%; Pred. No. 4.4e-46;  
RESULT 739  
ID ADM74561 standard; DNA; 31842 BP.  
DE Human carcinoma associated (CA) nucleic acid #115.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.8%; Score 224.4; DB 12; Length 31842;  
Best Local Similarity 82.3%; Pred. No. 4.4e-46;  
RESULT 740  
ID AEF80111 standard; DNA; 36911 BP.  
DE Cancer-associated polypeptide genomic DNA sequence hD22-022 SEQ ID NO:6.  
PN US2006024677-A1.  
PD 02-FEB-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
PA (LAIA/) LAI A.  
PA (TSEC/) TSE C.  
PA (FATT/) FATTAEY A.  
Query Match 9.8%; Score 224.4; DB 15; Length 36911;  
Best Local Similarity 85.9%; Pred. No. 4.7e-46;  
RESULT 741  
ID ADA02840 standard; DNA; 47573 BP.  
DE Human MAP3K8 carcinoma associated gene, SEQ ID NO:1358.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.

Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 9; Length 47573;  
RESULT 742  
ID ADB72578 standard; DNA; 47573 BP.  
DE Human MAP3K8 gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 10; Length 47573;  
RESULT 743  
ID ADC85319 standard; DNA; 47573 BP.  
DE Mouse Map3k8 coding sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 10; Length 47573;  
RESULT 744  
ID ADM74435 standard; DNA; 47573 BP.  
DE Human carcinoma associated (CA) nucleic acid #52.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 12; Length 47573;  
RESULT 745  
ID AEE04835 standard; DNA; 70803 BP.  
DE Cancer-associated gene SEQ ID NO:153.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 14; Length 70803;  
RESULT 746  
ID ACN43958 standard; DNA; 75839 BP.  
DE Human genomic sequence hCG1640505.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 11; Length 75839;  
RESULT 747  
ID ABD32806 standard; DNA; 653458 BP.  
DE Human cancer-associated genomic DNA HD16-059.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 13; Length 110000;  
RESULT 748  
ID ADL13931 standard; DNA; 180385 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #463.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 10; Length 180385;  
RESULT 749  
ID ADL13850 standard; DNA; 180550 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #382.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 10; Length 180550;  
RESULT 750  
ID ADQ20606 standard; DNA; 195917 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3426.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 12; Length 195917;  
RESULT 751  
ID AEE05008 standard; DNA; 246386 BP.  
DE Cancer-associated gene SEQ ID NO:326.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match  
Best Local Similarity 9.8%; Score 224.4; DB 14; Length 246386;  
RESULT 752  
ID AAK78073 standard; DNA; 1071 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32885.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.2; DB 4; Length 1071;  
RESULT 753  
ID AAK78077 standard; DNA; 1071 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32889.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.2; DB 4; Length 1071;  
RESULT 754  
ID AAK78075 standard; DNA; 1071 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32887.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.2; DB 4; Length 1071;  
RESULT 755  
ID ACN37326 standard; CDNA; 1810 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA323793, SEQ ID NO:133.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.2; DB 13; Length 1810;  
RESULT 756  
ID AAS36599 standard; DNA; 2687 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2099.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.2; DB 4; Length 2687;  
RESULT 757  
ID AAS36600 standard; DNA; 2687 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2100.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.2; DB 4; Length 2687;  
RESULT 758  
ID ADE47293 standard; DNA; 2687 BP.  
DE Human cardiovascular system related genomic DNA #859.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.2; DB 10; Length 2687;  
RESULT 759  
ID ADE47294 standard; DNA; 2687 BP.  
DE Human cardiovascular system related genomic DNA #860.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 9.8%; Score 224.2; DB 10; Length 2687;

Best Local Similarity 83.0%; Pred. No. 1.6e-46;  
RESULT 760  
ID ADJ08712 standard; DNA; 2687 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID2100.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.2; DB 13; Length 2687;  
Best Local Similarity 83.0%; Pred. No. 1.6e-46;  
RESULT 761  
ID ADJ08711 standard; DNA; 2687 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID2099.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.2; DB 13; Length 2687;  
Best Local Similarity 83.0%; Pred. No. 1.6e-46;  
RESULT 762  
ID ADA53076 standard; cDNA; 2850 BP.  
DE Human coding sequence, SEQ ID 644.  
PN EP1293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES. INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.8%; Score 224.2; DB 10; Length 2850;  
Best Local Similarity 85.3%; Pred. No. 1.7e-46;  
RESULT 763  
ID ABZ57227 standard; cDNA; 2981 BP.  
DE Human ATP dependent serine protein hydrolase 47.19-encoding cDNA.  
PN CN1364900-A.  
PD 21-AUG-2002.  
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
Query Match 9.8%; Score 224.2; DB 8; Length 2981;  
Best Local Similarity 85.3%; Pred. No. 1.7e-46;  
RESULT 764  
ID AAD46552 standard; DNA; 2984 BP.  
DE Human cMOAT gene #2.  
PN WO200272888-A2.  
PD 19-SEP-2002.  
PA (ASTR ) ASTRAZENECA AB.  
PA (ASTR ) ASTRAZENECA UK LTD.  
Query Match 9.8%; Score 224.2; DB 6; Length 29844;  
Best Local Similarity 83.3%; Pred. No. 4.8e-46;  
RESULT 765  
ID AAK89020 standard; DNA; 32152 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 2596.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.2; DB 4; Length 32152;  
Best Local Similarity 81.9%; Pred. No. 5e-46;  
RESULT 766  
ID AAK91534 standard; DNA; 32152 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 5110.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.2; DB 4; Length 32152;  
Best Local Similarity 81.9%; Pred. No. 5e-46;  
RESULT 767  
ID AAI57791 standard; DNA; 32152 BP.  
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 328.  
PN WO200155350-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.2; DB 4; Length 32152;  
Best Local Similarity 81.9%; Pred. No. 5e-46;  
RESULT 768  
ID AAS39621 standard; DNA; 32152 BP.  
DE Genomic sequence #40 encoding human colon associated polypeptide.  
PN WO200155302-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.8%; Score 224.2; DB 5; Length 32152;  
Best Local Similarity 81.9%; Pred. No. 5e-46;  
RESULT 769  
ID ABS99968 standard; DNA; 32152 BP.  
DE Genomic DNA #172 encoding human colorectal cancer related protein.  
PN US2002119919-A1.  
PD 29-AUG-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.8%; Score 224.2; DB 6; Length 32152;  
Best Local Similarity 81.9%; Pred. No. 5e-46;  
RESULT 770  
ID ADB32581 standard; DNA; 32152 BP.  
DE Human novel colon related polypeptide DNA SEQ ID NO 518.  
PN US2003050231-A1.  
PD 13-MAR-2003.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.8%; Score 224.2; DB 9; Length 32152;  
Best Local Similarity 81.9%; Pred. No. 5e-46;  
RESULT 771  
ID ADB93121 standard; DNA; 32152 BP.  
DE Human colorectal cancer related polypeptide DNA #172.  
PN US2003054420-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.2; DB 10; Length 32152;  
Best Local Similarity 81.9%; Pred. No. 5e-46;  
RESULT 772  
ID AAK67282 standard; DNA; 33147 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22094.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.2; DB 4; Length 33147;  
Best Local Similarity 80.8%; Pred. No. 5e-46;  
RESULT 773  
ID AAK66362 standard; DNA; 36933 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21174.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224.2; DB 4; Length 36933;  
Best Local Similarity 81.9%; Pred. No. 5.3e-46;  
RESULT 774  
ID ADQ97343 standard; DNA; 61739 BP.  
DE Human cancer associated sequence HD08-035, SEQ ID 320.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 224.2; DB 12; Length 61739;  
Best Local Similarity 84.2%; Pred. No. 6.7e-46;  
RESULT 775  
ID ADA03032 standard; DNA; 99957 BP.  
DE Human mCG10516 homologue carcinoma associated gene, SEQ ID NO:1550.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224.2; DB 9; Length 99957;  
Best Local Similarity 78.9%; Pred. No. 8.3e-46;  
RESULT 776  
ID ADB72770 standard; DNA; 99957 BP.  
DE Human CA gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224.2; DB 10; Length 99957;  
Best Local Similarity 78.9%; Pred. No. 8.3e-46;  
RESULT 777  
ID ADC85512 standard; DNA; 99957 BP.  
DE Human genomic sequence.

PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224.2; DB 10; Length 99957;  
Best Local Similarity 78.9%; Pred. No. 8.3e-46;  
RESULT 778  
ID ADM74627 standard; DNA; 99957 BP.  
DE Human carcinoma associated (CA) nucleic acid #148.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.8%; Score 224.2; DB 12; Length 99957;  
Best Local Similarity 78.9%; Pred. No. 8.3e-46;  
RESULT 779  
ID AEE03503 standard; DNA; 100097 BP.  
DE Acute myelogenous leukemia prognosis related DNA sequence SEQ ID NO: 165.  
PN JP2005333987-A.  
PD 08-DEC-2005.  
PA (VERI-) VERIDEX LLC.  
Query Match 9.8%; Score 224.2; DB 15; Length 100097;  
Best Local Similarity 74.5%; Pred. No. 8.3e-46;  
RESULT 780  
ID AEE03502 standard; DNA; 100097 BP.  
DE Acute myelogenous leukemia prognosis related DNA sequence SEQ ID NO: 164.  
PN JP2005333987-A.  
PD 08-DEC-2005.  
PA (VERI-) VERIDEX LLC.  
Query Match 9.8%; Score 224.2; DB 15; Length 100097;  
Best Local Similarity 74.5%; Pred. No. 8.3e-46;  
RESULT 781  
ID AEG70729 standard; CDNA; 100097 BP.  
DE Human p53 mutational status predicting gene SEQ ID NO: 203.  
PN US2006074565-A1.  
PD 06-APR-2006.  
PA (MILL/) MILLER L D.  
PA (GEOR/) GEORGE J.  
PA (VEGA/) VEGA V B.  
Query Match 9.8%; Score 224.2; DB 15; Length 100097;  
Best Local Similarity 74.5%; Pred. No. 8.3e-46;  
RESULT 782  
ID ABD33179 standard; DNA; 100445 BP.  
DE Human cancer-associated (CA) gene HD07-026.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 224.2; DB 13; Length 100445;  
Best Local Similarity 78.0%; Pred. No. 8.3e-46;  
RESULT 783  
ID AEJ13162 standard; DNA; 100445 BP.  
DE Cancer-associated gene sequence - SEQ ID 170.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.8%; Score 224.2; DB 15; Length 100445;  
Best Local Similarity 78.0%; Pred. No. 8.3e-46;  
RESULT 784  
ID ADQ17729 standard; DNA; 143239 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 546.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.8%; Score 224.2; DB 12; Length 143239;  
Best Local Similarity 83.0%; Pred. No. 9.7e-46;  
RESULT 785  
ID ABL64403 standard; DNA; 167343 BP.  
DE Stomach cancer related gene sequence SEQ ID NO: 2740.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.8%; Score 224.2; DB 6; Length 167343;  
Best Local Similarity 83.0%; Pred. No. 1e-45;

RESULT 786  
ID ABL67239 standard; DNA; 167343 BP.  
DE Thyroid cancer related gene sequence SEQ ID NO: 5576.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.8%; Score 224.2; DB 6; Length 167343;  
Best Local Similarity 83.0%; Pred. No. 1e-45;  
RESULT 787  
ID ADZ09671 standard; DNA; 224931 BP.  
DE Human breast cancer marker ZAP3 DNA.  
PN EP1522594-A2.  
PD 13-APR-2005.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 9.8%; Score 224.2; DB 14; Length 224931;  
Best Local Similarity 85.3%; Pred. No. 1.2e-45;  
RESULT 788  
ID AED76155 standard; DNA; 261108 BP.  
DE Human CA genomic DNA sequence-ID hd25-006.  
PN WO2005104810-A2.  
PD 10-NOV-2005.  
PA (SAGR-) SAGRES DISCOVERY INC.  
PA (LAI A.) LAI A.  
PA (FATT/) FATTAEY A.  
Query Match 9.8%; Score 224.2; DB 14; Length 261108;  
Best Local Similarity 83.0%; Pred. No. 1.3e-45;  
RESULT 789  
ID ABD33362 standard; DNA; 301477 BP.  
DE Human cancer-associated (CA) gene HD07-066.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 224.2; DB 13; Length 301477;  
Best Local Similarity 86.6%; Pred. No. 1.4e-45;  
RESULT 790  
ID AEJ13448 standard; DNA; 301477 BP.  
DE Cancer-associated gene sequence - SEQ ID 456.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.8%; Score 224.2; DB 15; Length 301477;  
Best Local Similarity 86.6%; Pred. No. 1.4e-45;  
RESULT 791  
ID AAS32547 standard; DNA; 2425 BP.  
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 501.  
PN WO200155319-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224; DB 4; Length 2425;  
Best Local Similarity 87.4%; Pred. No. 1.7e-46;  
RESULT 792  
ID AAK65546 standard; DNA; 8223 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 20358.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224; DB 4; Length 8223;  
Best Local Similarity 79.4%; Pred. No. 3e-46;  
RESULT 793  
ID ABT16305 standard; DNA; 22400 BP.  
DE Zinc finger protein 9 (ZNF9) DNA SEQ ID No 1.  
PN WO200292763-A2.  
PD 21-NOV-2002.  
PA (MINU) UNIV MINNESOTA.  
PA (RANU/) RANUM L P W.  
PA (DAYJ/) DAY J W.  
PA (LIQU/) LIQUORI C.  
Query Match 9.8%; Score 224; DB 8; Length 22400;  
Best Local Similarity 82.6%; Pred. No. 4.7e-46;  
RESULT 794  
ID AAK68575 standard; DNA; 32145 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 23387.



PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224; DB 4; Length 32145;  
Best Local Similarity 83.6%; Pred. No. 5.6e-46;  
RESULT 795  
ID AAK68491 standard; DNA; 32145 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23303.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 224; DB 4; Length 32145;  
Best Local Similarity 83.6%; Pred. No. 5.6e-46;  
RESULT 796  
ID ADQ97173 standard; DNA; 40783 BP.  
DE Human cancer associated sequence HD08-010, SEQ ID 149.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 224; DB 12; Length 40783;  
Best Local Similarity 80.4%; Pred. No. 6.2e-46;  
RESULT 797  
Query Match 9.8%; Score 224; DB 14; Length 75899;  
Best Local Similarity 84.8%; Pred. No. 8.2e-46;  
RESULT 798  
ID ADT77142 standard; DNA; 93500 BP.  
DE Type II diabetes gene SEQ ID NO 19.  
PN WO2004084797-A2.  
PD 07-OCT-2004.  
PA (HUBI-) HUBIT GENOMIX INC.  
PA (DAIM/) DAIMON M.  
PA (KATO/) KATO T.  
Query Match 9.8%; Score 224; DB 13; Length 93500;  
Best Local Similarity 83.6%; Pred. No. 9e-46;  
RESULT 799  
ID ADC85367 standard; DNA; 96593 BP.  
DE Mouse B1m coding sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224; DB 10; Length 96593;  
Best Local Similarity 81.4%; Pred. No. 9.2e-46;  
RESULT 800  
ID ADA02888 standard; DNA; 96594 BP.  
DE Human BLM carcinoma associated gene, SEQ ID NO:1406.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224; DB 9; Length 96594;  
Best Local Similarity 81.4%; Pred. No. 9.2e-46;  
RESULT 801  
ID ADB72626 standard; DNA; 96594 BP.  
DE Human BLM gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224; DB 10; Length 96594;  
Best Local Similarity 81.4%; Pred. No. 9.2e-46;  
RESULT 802  
ID ADM74483 standard; DNA; 96594 BP.  
DE Human carcinoma associated (CA) nucleic acid #76.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.8%; Score 224; DB 12; Length 96594;  
Best Local Similarity 81.4%; Pred. No. 9.2e-46;  
RESULT 803  
ID ADA03032 standard; DNA; 99957 BP.  
DE Human mCG10516 homologue carcinoma associated gene, SEQ ID NO:1550.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.

Query Match 9.8%; Score 224; DB 9; Length 99957;  
Best Local Similarity 80.4%; Pred. No. 9.3e-46;  
RESULT 804  
ID ADB72770 standard; DNA; 99957 BP.  
DE Human CA gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224; DB 10; Length 99957;  
Best Local Similarity 80.4%; Pred. No. 9.3e-46;  
RESULT 805  
ID ADC85512 standard; DNA; 99957 BP.  
DE Human genomic sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 224; DB 10; Length 99957;  
Best Local Similarity 80.4%; Pred. No. 9.3e-46;  
RESULT 806  
ID ADM74627 standard; DNA; 99957 BP.  
DE Human carcinoma associated (CA) nucleic acid #148.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.8%; Score 224; DB 12; Length 99957;  
Best Local Similarity 80.4%; Pred. No. 9.3e-46;  
RESULT 807  
ID ABD33163 standard; DNA; 138837 BP.  
DE Human cancer-associated (CA) gene HD07-022.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 224; DB 13; Length 138837;  
Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
RESULT 808  
ID AEJ13138 standard; DNA; 138837 BP.  
DE Cancer-associated gene sequence - SEQ ID 146.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.8%; Score 224; DB 15; Length 138837;  
Best Local Similarity 87.4%; Pred. No. 1.1e-45;  
RESULT 809  
ID ABD32694 standard; DNA; 252907 BP.  
DE Human cancer-associated genomic DNA HD14-012.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 224; DB 13; Length 252907;  
Best Local Similarity 86.1%; Pred. No. 1.4e-45;  
RESULT 810  
ID ACC46432 standard; cDNA; 608 BP.  
DE Human dithp membrane transport protein-encoding cDNA.  
PN WO200297031-A2.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.8%; Score 223.8; DB 8; Length 608;  
Best Local Similarity 80.0%; Pred. No. 1.1e-46;  
RESULT 811  
ID AAK65471 standard; DNA; 1275 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20283.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.8; DB 4; Length 1275;  
Best Local Similarity 88.2%; Pred. No. 1.5e-46;  
RESULT 812  
ID ACC50219 standard; cDNA; 2519 BP.  
DE Breast cancer associated cDNA sequence SEQ ID NO:281.  
PN WO2003004989-A2.  
PD 16-JAN-2003.

PA (MILL-) MILLENIUM PHARM INC.  
Query Match 9.8%; Score 223.8; DB 8; Length 2519;  
Best Local Similarity 85.6%; Pred. No. 2e-46;  
RESULT 813  
ID AEE83862 standard; cDNA; 3088 BP.  
DE Human cDNA differentially expressed in asthma, SEQ ID NO:270.  
PN WO2005118403-A2.  
PD 15-DEC-2005.  
PA (LINK-) LINKAGENE LTD.  
Query Match 9.8%; Score 223.8; DB 15; Length 3088;  
Best Local Similarity 85.6%; Pred. No. 2.2e-46;  
RESULT 814  
ID AAI58419 standard; cDNA; 6799 BP.  
DE Human polynucleotide SEQ ID NO 622.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.8%; Score 223.8; DB 4; Length 6799;  
Best Local Similarity 80.4%; Pred. No. 3.1e-46;  
RESULT 815  
ID ADQ98629 standard; cDNA; 6799 BP.  
DE DNA encoding human GPCR-like protein seqid 299.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.8%; Score 223.8; DB 5; Length 6799;  
Best Local Similarity 80.4%; Pred. No. 3.1e-46;  
RESULT 816  
ID ADB48389 standard; cDNA; 6799 BP.  
DE Novel human cDNA SEQ ID NO 299.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 9.8%; Score 223.8; DB 9; Length 6799;  
Best Local Similarity 80.4%; Pred. No. 3.1e-46;  
RESULT 817  
ID AAF97856 standard; DNA; 10097 BP.  
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:70.  
PN WO200116311-A1.  
PD 08-MAR-2001.  
PA (HISM) HISAMITSU PHARM CO LTD.  
PA (CHIB-) CHIBA PREFECTURE.  
Query Match 9.8%; Score 223.8; DB 5; Length 10097;  
Best Local Similarity 84.3%; Pred. No. 3.7e-46;  
RESULT 818  
ID AAL04059 standard; DNA; 10339 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 6747.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.8; DB 4; Length 10339;  
Best Local Similarity 84.3%; Pred. No. 3.8e-46;  
RESULT 819  
ID AAS40445 standard; DNA; 10339 BP.  
DE DNA encoding human prostate cancer antigen, Seq ID No 597.  
PN WO200155316-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.8; DB 5; Length 10339;  
Best Local Similarity 84.3%; Pred. No. 3.8e-46;  
RESULT 820  
ID ADJ09651 standard; DNA; 10339 BP.  
DE Human prostate cancer associated gene-related DNA SeqID597.  
PN US2003054373-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.8; DB 11; Length 10339;  
Best Local Similarity 84.3%; Pred. No. 3.8e-46;  
RESULT 821

ID AAK65305 standard; DNA; 22916 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20117.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.8; DB 4; Length 22916;  
Best Local Similarity 82.1%; Pred. No. 5.4e-46;  
RESULT 822  
ID ABE04693 standard; DNA; 65071 BP.  
DE Cancer-associated gene SEQ ID NO:11.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 9.8%; Score 223.8; DB 14; Length 65071;  
Best Local Similarity 79.1%; Pred. No. 8.6e-46;  
RESULT 823  
ID ACN44190 standard; DNA; 74183 BP.  
DE Human genomic sequence hCG27588.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.8; DB 11; Length 74183;  
Best Local Similarity 85.6%; Pred. No. 9.1e-46;  
RESULT 824  
ID ADN94799 standard; DNA; 91352 BP.  
DE DNA encoding human nidogen.  
PN US2004097451-A1.  
PD 20-MAY-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.8%; Score 223.8; DB 12; Length 91352;  
Best Local Similarity 81.2%; Pred. No. 1e-45;  
RESULT 825  
Query Match 9.8%; Score 223.8; DB 9; Length 110000;  
Best Local Similarity 85.6%; Pred. No. 1.1e-45;  
RESULT 826  
ID ADE11169 standard; DNA; 394191 BP.  
DE Human transporter protein encoding gene SEQ ID NO:1.  
Query Match 9.8%; Score 223.8; DB 10; Length 110000;  
Best Local Similarity 80.0%; Pred. No. 1.1e-45;  
RESULT 827  
Query Match 9.8%; Score 223.8; DB 12; Length 110000;  
Best Local Similarity 85.6%; Pred. No. 1.1e-45;  
RESULT 828  
Query Match 9.8%; Score 223.8; DB 14; Length 110000;  
Best Local Similarity 85.6%; Pred. No. 1.1e-45;  
RESULT 829  
Query Match 9.8%; Score 223.8; DB 14; Length 110000;  
Best Local Similarity 76.4%; Pred. No. 1.1e-45;  
RESULT 830  
ID ACN44586 standard; DNA; 118931 BP.  
DE Human genomic sequence hCG30014.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.8; DB 11; Length 118931;  
Best Local Similarity 82.1%; Pred. No. 1.1e-45;  
RESULT 831  
ID AAC66548 standard; DNA; 121162 BP.  
DE Human kinesin-like protein HKLP coding sequence contig SEQ ID NO: 1.  
PN WO200063375-A1.  
PD 26-OCT-2000.  
PA (GEST) GENSET.  
Query Match 9.8%; Score 223.8; DB 3; Length 121162;  
Best Local Similarity 84.3%; Pred. No. 1.1e-45;  
RESULT 832  
ID ADL13941 standard; DNA; 125515 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #473.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.8%; Score 223.8; DB 10; Length 125515;  
Best Local Similarity 85.6%; Pred. No. 1.2e-45;  
RESULT 833

ID ABD32872 standard; DNA; 130244 BP.  
DE Human cancer-associated genomic DNA HD17-083.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223.8; DB 13; Length 130244;  
Best Local Similarity 85.6%; Pred. No. 1.2e-45;  
RESULT 834  
ID ACN44890 standard; DNA; 131576 BP.  
DE Human genomic sequence hCG28994.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.8; DB 11; Length 131576;  
Best Local Similarity 85.6%; Pred. No. 1.2e-45;  
RESULT 835  
ID ABD32888 standard; DNA; 144068 BP.  
DE Human cancer-associated genomic DNA HD18-013.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223.8; DB 13; Length 144068;  
Best Local Similarity 83.2%; Pred. No. 1.2e-45;  
RESULT 836  
ID ACN44170 standard; DNA; 196686 BP.  
DE Human genomic sequence hCG39530.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.8; DB 11; Length 196686;  
Best Local Similarity 83.2%; Pred. No. 1.4e-45;  
RESULT 837  
ID ABD17970 standard; DNA; 209284 BP.  
DE Human factor-related antisense polynucleotide.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 9.8%; Score 223.8; DB 11; Length 209284;  
Best Local Similarity 82.4%; Pred. No. 1.5e-45;  
RESULT 838  
ID AAD58279 standard; DNA; 226475 BP.  
DE Human tumour suppressor gene, lmt reverse complement DNA.  
PN WO2003066869-A1.  
PD 14-AUG-2003.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
Query Match 9.8%; Score 223.8; DB 9; Length 226475;  
Best Local Similarity 83.2%; Pred. No. 1.5e-45;  
RESULT 839  
ID ADC86558 standard; DNA; 952 BP.  
DE Human GPCR gene SEQ ID NO:1011.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.8%; Score 223.6; DB 10; Length 952;  
Best Local Similarity 83.0%; Pred. No. 1.5e-46;  
RESULT 840  
ID ABZ74164 standard; DNA; 6404 BP.  
DE Secreted protein gene 200 genomic fragment HMQAI38, SEQ ID NO:1311.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.6; DB 8; Length 6404;  
Best Local Similarity 76.1%; Pred. No. 3.4e-46;  
RESULT 841  
ID ADC20801 standard; DNA; 6404 BP.  
DE Human secreted protein-related DNA sequence #219.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.6; DB 10; Length 6404;  
Best Local Similarity 76.1%; Pred. No. 3.4e-46;  
RESULT 842

ID AAK89070 standard; DNA; 11837 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 2646.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.6; DB 4; Length 11837;  
Best Local Similarity 82.7%; Pred. No. 4.5e-46;  
RESULT 843  
ID AAS33429 standard; DNA; 11837 BP.  
DE DNA encoding human secreted protein, Seq ID No 712.  
PN WO200155326-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.6; DB 4; Length 11837;  
Best Local Similarity 82.7%; Pred. No. 4.5e-46;  
RESULT 844  
ID AAK76413 standard; DNA; 21747 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31225.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.6; DB 4; Length 21747;  
Best Local Similarity 82.7%; Pred. No. 5.9e-46;  
RESULT 845  
ID ABD33071 standard; DNA; 24529 BP.  
DE Human cancer-associated (CA) gene HD07-001.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223.6; DB 13; Length 24529;  
Best Local Similarity 86.3%; Pred. No. 6.3e-46;  
RESULT 846  
ID AEJ12996 standard; DNA; 24529 BP.  
DE Cancer-associated gene sequence - SEQ ID 4.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.8%; Score 223.6; DB 15; Length 24529;  
Best Local Similarity 86.3%; Pred. No. 6.3e-46;  
RESULT 847  
ID ADL13819 standard; DNA; 41150 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #351.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.8%; Score 223.6; DB 10; Length 41150;  
Best Local Similarity 82.0%; Pred. No. 7.9e-46;  
RESULT 848  
ID AED18343 standard; DNA; 41150 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 594.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL) UNIV FLORIDA RES FOUND INC.  
Query Match 9.8%; Score 223.6; DB 14; Length 41150;  
Best Local Similarity 82.0%; Pred. No. 7.9e-46;  
RESULT 849  
ID ADN48556 standard; DNA; 44348 BP.  
DE Human Notch3 genomic DNA #2.  
PN US2004102390-A1.  
PD 27-MAY-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.8%; Score 223.6; DB 12; Length 44348;  
Best Local Similarity 82.0%; Pred. No. 8.2e-46;  
RESULT 850  
ID ACN44146 standard; DNA; 50602 BP.  
DE Human genomic sequence hCG28572.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.6; DB 11; Length 50602;  
Best Local Similarity 83.9%; Pred. No. 8.7e-46;  
RESULT 851

ID ACN45158 standard; DNA; 72705 BP.  
DE Human genomic sequence hCG25130.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.6; DB 11; Length 72705;  
Best Local Similarity 82.7%; Pred. No. 1e-45;  
RESULT 852  
ID ACN44438 standard; DNA; 73967 BP.  
DE Human genomic sequence hCG27607.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.6; DB 11; Length 73967;  
Best Local Similarity 85.3%; Pred. No. 1e-45;  
RESULT 853  
Query Match 9.8%; Score 223.6; DB 6; Length 91080;  
Best Local Similarity 83.9%; Pred. No. 1.1e-45;  
RESULT 854  
Query Match 9.8%; Score 223.6; DB 12; Length 91134;  
Best Local Similarity 83.9%; Pred. No. 1.1e-45;  
RESULT 855  
Query Match 9.8%; Score 223.6; DB 12; Length 91138;  
Best Local Similarity 83.9%; Pred. No. 1.1e-45;  
RESULT 856  
Query Match 9.8%; Score 223.6; DB 12; Length 91139;  
Best Local Similarity 83.9%; Pred. No. 1.1e-45;  
RESULT 857  
Query Match 9.8%; Score 223.6; DB 14; Length 91140;  
Best Local Similarity 83.9%; Pred. No. 1.1e-45;  
RESULT 858  
ID AED89413 standard; DNA; 191343 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 53.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.8%; Score 223.6; DB 14; Length 191343;  
Best Local Similarity 85.1%; Pred. No. 1.6e-45;  
RESULT 859  
ID AEL48676 standard; cDNA; 216498 BP.  
DE Peptidyl arginine deiminase, type II, cDNA.  
PN WO2006108135-A2.  
PD 12-OCT-2006.  
PA (YUJJ/) YU J.  
PA (JIAN/) JIANG Y.  
PA (YANG/) YANG F.  
PA (WANG/) WANG Y.  
PA (LEHN/) LEHNHARDT S.  
Query Match 9.8%; Score 223.6; DB 16; Length 216498;  
Best Local Similarity 82.7%; Pred. No. 1.7e-45;  
RESULT 860  
ID AAK81896 standard; DNA; 7794 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36708.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.4; DB 4; Length 7794;  
Best Local Similarity 83.7%; Pred. No. 4.2e-46;  
RESULT 861  
ID AAS28608 standard; DNA; 7794 BP.  
DE Genomic sequence #448 encoding for novel human respiratory antigen.  
PN WO200155448-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.4; DB 4; Length 7794;  
Best Local Similarity 83.7%; Pred. No. 4.2e-46;  
RESULT 862  
ID ADG41804 standard; DNA; 7794 BP.  
DE Human respiratory system associated genomic DNA seq id 1042.  
PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.4; DB 10; Length 7794;

Best Local Similarity 83.7%; Pred. No. 4.2e-46;  
RESULT 863  
ID ADI97578 standard; DNA; 7794 BP.  
DE Human respiratory system associated polypeptide-related DNA SeqID1042.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.4; DB 11; Length 7794;  
Best Local Similarity 83.7%; Pred. No. 4.2e-46;  
RESULT 864  
ID AEA61190 standard; DNA; 13989 BP.  
DE Human PDK4 gene genomic sequence SEQ ID NO:100.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB) BAYER CORP.  
Query Match 9.8%; Score 223.4; DB 14; Length 13989;  
Best Local Similarity 78.3%; Pred. No. 5.5e-46;  
RESULT 865  
ID AAK81246 standard; DNA; 26464 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36058.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.4; DB 4; Length 26464;  
Best Local Similarity 74.9%; Pred. No. 7.3e-46;  
RESULT 866  
ID AAS28363 standard; DNA; 32146 BP.  
DE Genomic sequence #203 encoding for novel human respiratory antigen.  
PN WO200155448-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.4; DB 4; Length 32146;  
Best Local Similarity 83.3%; Pred. No. 8e-46;  
RESULT 867  
ID ADG41559 standard; DNA; 32146 BP.  
DE Human respiratory system associated genomic DNA seq id 797.  
PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.4; DB 10; Length 32146;  
Best Local Similarity 83.3%; Pred. No. 8e-46;  
RESULT 868  
ID ADI97333 standard; DNA; 32146 BP.  
DE Human respiratory system associated polypeptide-related DNA SeqID797.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.4; DB 11; Length 32146;  
Best Local Similarity 83.3%; Pred. No. 8e-46;  
RESULT 869  
ID ADQ97910 standard; DNA; 44920 BP.  
DE Human cancer associated sequence HD11-022, SEQ ID 887.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223.4; DB 12; Length 44920;  
Best Local Similarity 82.1%; Pred. No. 9.2e-46;  
RESULT 870  
ID ABX85261 standard; DNA; 75899 BP.  
DE Human genomic DNA for protein phosphatase 1B, PTP1B.  
PN US2002055479-A1.  
PD 09-MAY-2002.  
PA (COWS/) COWSERT L M.  
PA (WYAT/) WYATT J.  
PA (FREI/) FREIER S M.  
PA (MONI/) MONIA B P.  
PA (BUTL/) BUTLER M M.  
PA (MCKA/) MCKAY R.  
Query Match 9.8%; Score 223.4; DB 6; Length 75899;  
Best Local Similarity 82.3%; Pred. No. 1.2e-45;  
RESULT 871  
ID ADI13990 standard; DNA; 75899 BP.  
DE Human protein phosphatase 1B (PTP1B) genomic DNA SeqID 243.



PN US2003220282-A1.  
PD 27-NOV-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.8%; Score 223.4; DB 12; Length 75899;  
Best Local Similarity 82.3%; Pred. No. 1.2e-45;  
RESULT 872  
ID ADZ56505 standard; DNA; 75899 BP.  
DE Human protein tyrosine phosphatase 1B genomic DNA SEQ ID NO:243.  
PN US2005095710-A1.  
PD 05-MAY-2005.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.8%; Score 223.4; DB 14; Length 75899;  
Best Local Similarity 82.3%; Pred. No. 1.2e-45;  
RESULT 873  
ID AEF59865 standard; DNA; 75899 BP.  
DE Human protein tyrosine phosphatase-1B DNA SEQ ID NO:243.  
PN US2006025372-A1.  
PD 02-FEB-2006.  
PA (BHAN/) BHANOT S.  
PA (COWS/) COWSERT L M.  
PA (WYAT/) WYATT J R.  
PA (MONI/) MONIA B P.  
PA (BUTL/) BUTLER M M.  
PA (MCKA/) MCKAY R.  
PA (FREI/) FREIER S M.  
PA (DOBI/) DOBIE K W.  
Query Match 9.8%; Score 223.4; DB 15; Length 75899;  
Best Local Similarity 82.3%; Pred. No. 1.2e-45;  
RESULT 874  
ID ACN44322 standard; DNA; 84073 BP.  
DE Human genomic sequence hCG28354.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.4; DB 11; Length 84073;  
Best Local Similarity 77.4%; Pred. No. 1.2e-45;  
RESULT 875  
ID ADQ97695 standard; DNA; 88892 BP.  
DE Human cancer associated sequence HD10-029, SEQ ID 672.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223.4; DB 12; Length 88892;  
Best Local Similarity 87.1%; Pred. No. 1.3e-45;  
RESULT 876  
ID ABQ88176 standard; cDNA; 100301 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 83.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC ) PROCTER & GAMBLE CO.  
Query Match 9.8%; Score 223.4; DB 6; Length 100301;  
Best Local Similarity 78.3%; Pred. No. 1.3e-45;  
RESULT 877  
ID ADQ20754 standard; DNA; 100301 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3574.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.8%; Score 223.4; DB 12; Length 100301;  
Best Local Similarity 78.3%; Pred. No. 1.3e-45;  
RESULT 878  
ID ACN44150 standard; DNA; 439892 BP.  
DE Human genomic sequence hCG27278.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.8%; Score 223.4; DB 11; Length 110000;  
Best Local Similarity 85.8%; Pred. No. 1.4e-45;  
RESULT 879  
Query Match 9.8%; Score 223.4; DB 13; Length 110000;  
Best Local Similarity 82.3%; Pred. No. 1.4e-45;  
RESULT 880

ID AEH93956 standard; DNA; 118899 BP.  
DE DNMT31 variant full length coding sequence.  
PN US2006115829-A1.  
PD 01-JUN-2006.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 9.8%; Score 223.4; DB 15; Length 118899;  
Best Local Similarity 85.8%; Pred. No. 1.4e-45;  
RESULT 881  
ID AEF74705 standard; DNA; 152037 BP.  
DE Human polynucleotide #219.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.8%; Score 223.4; DB 15; Length 152037;  
Best Local Similarity 82.1%; Pred. No. 1.6e-45;  
RESULT 882  
ID ADQ97433 standard; DNA; 295772 BP.  
DE Human cancer associated sequence HD08-047, SEQ ID 410.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223.4; DB 12; Length 295772;  
Best Local Similarity 80.2%; Pred. No. 2.2e-45;  
RESULT 883  
ID AAD00684 standard; cDNA; 1413 BP.  
DE Human Hydrolase protein-9 (HYDRL-9) encoding cDNA.  
PN WO200028045-A2.  
PD 18-MAY-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 9.8%; Score 223.2; DB 3; Length 1413;  
Best Local Similarity 81.0%; Pred. No. 2.2e-46;  
RESULT 884  
ID AAI59065 standard; cDNA; 2070 BP.  
DE Human polynucleotide SEQ ID NO 1268.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.8%; Score 223.2; DB 4; Length 2070;  
Best Local Similarity 71.8%; Pred. No. 2.6e-46;  
RESULT 885  
ID ADQ99288 standard; cDNA; 2070 BP.  
DE DNA encoding human GPCR-like protein seqid 958.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.8%; Score 223.2; DB 5; Length 2070;  
Best Local Similarity 71.8%; Pred. No. 2.6e-46;  
RESULT 886  
ID ADB49048 standard; cDNA; 2070 BP.  
DE Novel human cDNA SEQ ID NO 958.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 9.8%; Score 223.2; DB 9; Length 2070;  
Best Local Similarity 71.8%; Pred. No. 2.6e-46;  
RESULT 887  
ID AAK89399 standard; DNA; 10316 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 2975.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 4; Length 10316;  
Best Local Similarity 85.5%; Pred. No. 5.4e-46;  
RESULT 888  
ID AAK73166 standard; DNA; 19965 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27978.  
PN WO200157182-A2.  
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 4; Length 19965;  
Best Local Similarity 86.6%; Pred. No. 7.2e-46;  
RESULT 889  
ID ABK69932 standard; DNA; 19965 BP.  
DE Human secreted protein gene 68 genomic DNA fragment #20.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 6; Length 19965;  
Best Local Similarity 86.6%; Pred. No. 7.2e-46;  
RESULT 890  
ID AAK73165 standard; DNA; 20420 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27977.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 4; Length 20420;  
Best Local Similarity 86.6%; Pred. No. 7.3e-46;  
RESULT 891  
ID ABK69933 standard; DNA; 20420 BP.  
DE Human secreted protein gene 68 genomic DNA fragment #21.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 6; Length 20420;  
Best Local Similarity 86.6%; Pred. No. 7.3e-46;  
RESULT 892  
ID AAL35943 standard; DNA; 32132 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2308.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 4; Length 32132;  
Best Local Similarity 70.6%; Pred. No. 8.9e-46;  
RESULT 893  
ID AAL07060 standard; DNA; 32132 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9748.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 4; Length 32132;  
Best Local Similarity 70.6%; Pred. No. 8.9e-46;  
RESULT 894  
ID ABX58931 standard; cDNA; 32132 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #1275.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.8%; Score 223.2; DB 8; Length 32132;  
Best Local Similarity 70.6%; Pred. No. 8.9e-46;  
RESULT 895  
ID ADJ29681 standard; DNA; 32132 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2308.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 12; Length 32132;  
Best Local Similarity 70.6%; Pred. No. 8.9e-46;  
RESULT 896  
Query Match 9.8%; Score 223.2; DB 12; Length 40684;  
Best Local Similarity 82.9%; Pred. No. 9.9e-46;  
RESULT 897  
ID AEE04771 standard; DNA; 44633 BP.  
DE Cancer-associated gene SEQ ID NO:89.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.8%; Score 223.2; DB 14; Length 44633;  
Best Local Similarity 86.5%; Pred. No. 1e-45;  
RESULT 898

ID ABZ74619 standard; DNA; 58181 BP.  
DE Secreted protein gene 372 genomic fragment HWBCN36, SEQ ID NO:1766.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 8; Length 58181;  
Best Local Similarity 70.6%; Pred. No. 1.2e-45;  
RESULT 899  
ID ADC21010 standard; DNA; 58181 BP.  
DE Human secreted protein-related DNA sequence #428.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 10; Length 58181;  
Best Local Similarity 70.6%; Pred. No. 1.2e-45;  
RESULT 900  
ID ABZ68140 standard; DNA; 58181 BP.  
DE Human secreted protein encoding genomic DNA SEQ ID NO 1663.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223.2; DB 10; Length 58181;  
Best Local Similarity 70.6%; Pred. No. 1.2e-45;  
RESULT 901  
ID AAD58282 standard; DNA; 62782 BP.  
DE Human tumour suppressor gene, Lmt intron 3 DNA.  
PN WO2003066869-A1.  
PD 14-AUG-2003.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
Query Match 9.8%; Score 223.2; DB 9; Length 62782;  
Best Local Similarity 78.8%; Pred. No. 1.2e-45;  
RESULT 902  
ID AAD58281 standard; DNA; 62782 BP.  
DE Human tumour suppressor gene, Lmt intron 2 DNA.  
PN WO2003066869-A1.  
PD 14-AUG-2003.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
Query Match 9.8%; Score 223.2; DB 9; Length 62782;  
Best Local Similarity 78.8%; Pred. No. 1.2e-45;  
RESULT 903  
ID ADJ53477 standard; DNA; 70000 BP.  
DE Human PPP3CB genomic DNA #3.  
PN US2004023382-A1.  
PD 05-FEB-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.8%; Score 223.2; DB 12; Length 70000;  
Best Local Similarity 85.3%; Pred. No. 1.3e-45;  
RESULT 904  
ID AAF30035 standard; DNA; 81001 BP.  
DE Human apolipoprotein A-IV-related protein (AA4RP) gene.  
PN WO200100803-A2.  
PD 04-JAN-2001.  
PA (GEST ) GENSET.  
Query Match 9.8%; Score 223.2; DB 4; Length 81001;  
Best Local Similarity 85.5%; Pred. No. 1.4e-45;  
RESULT 905  
ID AEB77360 standard; DNA; 89014 BP.  
DE Human TGF beta receptor II complete antisense sequence SEQ ID NO 1.  
PN WO2005074981-A2.  
PD 18-AUG-2005.  
PA (BOGD/) BOGDH N U.  
Query Match 9.8%; Score 223.2; DB 14; Length 89014;  
Best Local Similarity 86.6%; Pred. No. 1.4e-45;  
RESULT 906  
Query Match 9.8%; Score 223.2; DB 12; Length 110000;  
Best Local Similarity 82.9%; Pred. No. 1.6e-45;  
RESULT 907  
ID AEG92754 standard; cDNA; 113681 BP.  
DE Human tumor cell cDNA SEQ ID NO:250.  
PN WO2006036025-A1.  
PD 06-APR-2006.  
PA (EISA ) EISAI CO LTD.  
Query Match 9.8%; Score 223.2; DB 15; Length 113681;

Best Local Similarity 86.6%; Pred. No. 1.6e-45;  
RESULT 908  
ID AEH15864 standard; DNA; 114001 BP.  
DE Human estrogen reactivity gene, GREB1, SEQ ID 19.  
PN JP2006101790-A.  
PD 20-APR-2006.  
PA (HUMA-) ZH HUMAN SCI SHINKO ZAIDAN.  
Query Match 9.8%; Score 223.2; DB 15; Length 114001;  
Best Local Similarity 82.9%; Pred. No. 1.6e-45;  
RESULT 909  
ID AEB32396 standard; DNA; 119226 BP.  
DE Human genomic DNA #37.  
PN US2005147987-A1.  
PD 07-JUL-2005.  
PA (APPL-) APPLERA CORP NY.  
Query Match 9.8%; Score 223.2; DB 14; Length 119226;  
Best Local Similarity 81.8%; Pred. No. 1.6e-45;  
RESULT 910  
ID AEB32401 standard; DNA; 119313 BP.  
DE Human genomic DNA #42.  
PN US2005147987-A1.  
PD 07-JUL-2005.  
PA (APPL-) APPLERA CORP NY.  
Query Match 9.8%; Score 223.2; DB 14; Length 119313;  
Best Local Similarity 81.8%; Pred. No. 1.6e-45;  
RESULT 911  
ID ABD33616 standard; DNA; 122656 BP.  
DE Human cancer-associated (CA) gene HD07-125.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223.2; DB 13; Length 122656;  
Best Local Similarity 85.3%; Pred. No. 1.6e-45;  
RESULT 912  
ID AEJ13838 standard; DNA; 122656 BP.  
DE Cancer-associated gene sequence - SEQ ID 846.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.8%; Score 223.2; DB 15; Length 122656;  
Best Local Similarity 85.3%; Pred. No. 1.6e-45;  
RESULT 913  
ID ADH77370 standard; DNA; 137000 BP.  
DE Human PTPN12 polynucleotide #1.  
PN US2003232434-A1.  
PD 18-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.8%; Score 223.2; DB 12; Length 137000;  
Best Local Similarity 85.3%; Pred. No. 1.7e-45;  
RESULT 914  
ID AEE96219 standard; DNA; 137000 BP.  
DE Human PTPN12 genomic DNA.  
PN US2005282760-A1.  
PD 22-DEC-2005.  
PA (COWS/) COWSERT L M.  
PA (DOBI/) DOBIE K W.  
Query Match 9.8%; Score 223.2; DB 15; Length 137000;  
Best Local Similarity 85.3%; Pred. No. 1.7e-45;  
RESULT 915  
ID AAL38336 standard; DNA; 143899 BP.  
DE Genomic sequence encoding a human Ngr2 protein.  
PN WO200229059-A2.  
PD 11-APR-2002.  
PA (UYYA ) UNIV YALE.  
PA (BIOJ ) BIOGEN INC.  
Query Match 9.8%; Score 223.2; DB 6; Length 143899;  
Best Local Similarity 84.1%; Pred. No. 1.8e-45;  
RESULT 916  
ID AAD02697 standard; DNA; 160552 BP.  
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.  
PN WO200106015-A1.  
PD 25-JAN-2001.

PA (REGC ) UNIV CALIFORNIA.  
Query Match 9.8%; Score 223.2; DB 4; Length 160552;  
Best Local Similarity 83.2%; Pred. No. 1.8e-45;  
RESULT 917  
ID AEE49487 standard; DNA; 180000 BP.  
DE Marfans' syndrome diagnosis associated DNA SEQ ID NO 1.  
PN WO2005116253-A1.  
PD 08-DEC-2005.  
PA (UYNA-) UNIV NAGASAKI.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match 9.8%; Score 223.2; DB 15; Length 180000;  
Best Local Similarity 86.6%; Pred. No. 1.9e-45;  
RESULT 918  
ID AAD62832 standard; DNA; 180216 BP.  
DE Human BAC #1 containing formin (Fmn)-2 genomic DNA.  
PN US2003170683-A1.  
PD 11-SEP-2003.  
PA (LEDE/) LEDER P.  
PA (LEAD/) LEADER B.  
Query Match 9.8%; Score 223.2; DB 10; Length 180216;  
Best Local Similarity 81.8%; Pred. No. 1.9e-45;  
RESULT 919  
ID ADL08108 standard; DNA; 188971 BP.  
DE Human gene associated with low HDL-C APOA1.  
PN US2004043389-A1.  
PD 04-MAR-2004.  
PA (VITI-) VITIVITY INC.  
Query Match 9.8%; Score 223.2; DB 12; Length 188971;  
Best Local Similarity 85.5%; Pred. No. 2e-45;  
RESULT 920  
ID ADC87619 standard; DNA; 349981 BP.  
DE Human GPCR related polynucleotide SEQ ID NO:2072.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.8%; Score 223.2; DB 10; Length 349981;  
Best Local Similarity 84.1%; Pred. No. 2.6e-45;  
RESULT 921  
ID ADC86916 standard; DNA; 349989 BP.  
DE Human GPCR gene SEQ ID NO:1369.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.8%; Score 223.2; DB 10; Length 349989;  
Best Local Similarity 84.1%; Pred. No. 2.6e-45;  
RESULT 922  
ID ADQ63518 standard; cDNA; 3708 BP.  
DE Novel human cDNA sequence #679.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.8%; Score 223; DB 12; Length 3708;  
Best Local Similarity 81.4%; Pred. No. 3.8e-46;  
RESULT 923  
ID AAS36855 standard; DNA; 15714 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2355.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223; DB 4; Length 15714;  
Best Local Similarity 72.0%; Pred. No. 7.3e-46;  
RESULT 924  
ID ADE47549 standard; DNA; 15714 BP.  
DE Human cardiovascular system related genomic DNA #1115.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223; DB 10; Length 15714;  
Best Local Similarity 72.0%; Pred. No. 7.3e-46;  
RESULT 925  
ID ADJ08967 standard; DNA; 15714 BP.

DE Human cardiovascular system associated polypeptide-related DNA SeqID2355.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.8%; Score 223; DB 13; Length 15714;  
Best Local Similarity 72.0%; Pred. No. 7.3e-46;  
RESULT 926  
ID ADQ59185 standard; DNA; 38504 BP.  
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:22.  
PN KR2004008012-A.  
PD 28-JAN-2004.  
PA (KIMH/) KIM H G.  
PA (KIMN/) KIM N G.  
PA (LEEJ/) LEE J S.  
PA (RHEE/) RHEE H S.  
Query Match 9.8%; Score 223; DB 12; Length 38504;  
Best Local Similarity 86.0%; Pred. No. 1.1e-45;  
RESULT 927  
ID AEG17800 standard; cDNA; 52280 BP.  
DE Human plasminogen genomic cDNA.  
PN US2006051780-A1.  
PD 09-MAR-2006.  
PA (UYDU-) UNIV DUKE.  
PA (ROCH-) ROCHE PALO ALTO LLC.  
Query Match 9.8%; Score 223; DB 15; Length 52280;  
Best Local Similarity 75.9%; Pred. No. 1.3e-45;  
RESULT 928  
ID AAS20588 standard; DNA; 84495 BP.  
DE Human methionine aminopeptidase protease genomic DNA.  
PN US6329188-B1.  
PD 11-DEC-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 9.8%; Score 223; DB 6; Length 84495;  
Best Local Similarity 81.4%; Pred. No. 1.6e-45;  
RESULT 929  
ID ADQ97846 standard; DNA; 94911 BP.  
DE Human cancer associated sequence HD11-010, SEQ ID 823.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223; DB 12; Length 94911;  
Best Local Similarity 83.6%; Pred. No. 1.6e-45;  
RESULT 930  
ID AAA10225 standard; DNA; 106746 BP.  
DE Human PCTA-1 genomic DNA, SEQ ID NO:1.  
PN WO9964590-A1.  
PD 16-DEC-1999.  
PA (GEST ) GENSET.  
Query Match 9.8%; Score 223; DB 3; Length 106746;  
Best Local Similarity 83.6%; Pred. No. 1.7e-45;  
RESULT 931  
ID ABD32653 standard; DNA; 117750 BP.  
DE Human cancer-associated genomic DNA HD13-060.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.8%; Score 223; DB 13; Length 117750;  
Best Local Similarity 79.4%; Pred. No. 1.8e-45;  
RESULT 932  
ID AED18413 standard; DNA; 152811 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 664.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 9.8%; Score 223; DB 14; Length 152811;  
Best Local Similarity 82.5%; Pred. No. 2e-45;  
RESULT 933  
ID ACL56842 standard; cDNA; 573 BP.  
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:2977.  
PN WO2005000087-A2.  
PD 06-JAN-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.8%; Score 222.8; DB 14; Length 573;

Best Local Similarity 82.0%; Pred. No. 1.9e-46;  
RESULT 934  
ID ADB82525 standard; cDNA; 714 BP.  
DE Human cDNA sequence useful for the treatment of cancer (SeqID 837).  
PN WO2003050236-A2.  
PD 19-JUN-2003.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.8%; Score 222.8; DB 9; Length 714;  
Best Local Similarity 82.0%; Pred. No. 2e-46;  
RESULT 935  
ID ABQ89583 standard; cDNA; 738 BP.  
DE Human prostate expressed polynucleotide SEQ ID NO 839.  
PN WO200255700-A2.  
PD 18-JUL-2002.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.8%; Score 222.8; DB 6; Length 738;  
Best Local Similarity 82.0%; Pred. No. 2.1e-46;  
RESULT 936  
ID ABK12093 standard; cDNA; 1380 BP.  
DE cDNA encoding Phytochrome 9\_9 protein.  
PN WO200212309-A1.  
PD 14-FEB-2002.  
PA (BIOW-) BOWINDOW GENE DEV INC SHANGHAI.  
Query Match 9.8%; Score 222.8; DB 6; Length 1380;  
Best Local Similarity 82.0%; Pred. No. 2.8e-46;  
RESULT 937  
ID AAF97866 standard; DNA; 5301 BP.  
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:80.  
PN WO200116311-A1.  
PD 08-MAR-2001.  
PA (HISM ) HISAMITSU PHARM CO LTD.  
PA (CHIB-) CHIBA PREFECTURE.  
Query Match 9.8%; Score 222.8; DB 5; Length 5301;  
Best Local Similarity 79.0%; Pred. No. 5e-46;  
RESULT 938  
ID ABK50893 standard; DNA; 7920 BP.  
DE Human chromosome 19 bases 117001-124920, clone CTD-3093.  
PN WO200220718-A2.  
PD 14-MAR-2002.  
PA (UYRQ ) UNIV ROCKEFELLER.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Query Match 9.8%; Score 222.8; DB 6; Length 7920;  
Best Local Similarity 79.7%; Pred. No. 6e-46;  
RESULT 939  
ID ADS89069 standard; DNA; 15355 BP.  
DE Human FGF1 gene SEQ ID NO:85.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 9.8%; Score 222.8; DB 13; Length 15355;  
Best Local Similarity 81.0%; Pred. No. 8.1e-46;  
RESULT 940  
ID ADZ59511 standard; DNA; 37034 BP.  
DE Secondary hyperparathyroidism detection human polymorphic gene, FGF1.  
PN JP2005102601-A.  
PD 21-APR-2005.  
PA (HYUB-) HYUBITTO GENOMICS KK.  
PA (JIKE-) UNIV JIKEI.  
Query Match 9.8%; Score 222.8; DB 14; Length 37034;  
Best Local Similarity 81.0%; Pred. No. 1.2e-45;  
RESULT 941  
ID ADL13662 standard; DNA; 76416 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #194.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.8%; Score 222.8; DB 10; Length 76416;  
Best Local Similarity 81.0%; Pred. No. 1.7e-45;  
RESULT 942  
ID ADS36495 standard; DNA; 77522 BP.  
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1709.



PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP. 9.8%; Score 222.8; DB 13; Length 77522;  
Query Match 81.0%; Pred. No. 1.7e-45;  
Best Local Similarity 81.0%; Pred. No. 1.7e-45;  
RESULT 943  
ID AAL57571 standard; cDNA; 83120 BP.  
DE Human CGI-51 protein cDNA.  
PN WO2003059148-A2.  
PD 24-JUL-2003.  
PA (GENE-) GENE LOGIC INC.  
PA (LGBI-) LG BIOMEDICAL INST.  
Query Match 9.8%; Score 222.8; DB 9; Length 83120;  
Best Local Similarity 85.5%; Pred. No. 1.7e-45;  
RESULT 944  
Query Match 9.8%; Score 222.8; DB 14; Length 110000;  
Best Local Similarity 83.1%; Pred. No. 2e-45;  
RESULT 945  
ID ABN95044 standard; DNA; 110096 BP.  
DE Gene #1542 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.8%; Score 222.8; DB 6; Length 110096;  
Best Local Similarity 83.0%; Pred. No. 2e-45;  
RESULT 946  
ID AED18046 standard; DNA; 110096 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 297.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL) UNIV FLORIDA RES FOUND INC.  
Query Match 9.8%; Score 222.8; DB 14; Length 110096;  
Best Local Similarity 83.0%; Pred. No. 2e-45;  
RESULT 947  
ID AEF74649 standard; DNA; 110096 BP.  
DE Human polynucleotide #163.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.8%; Score 222.8; DB 15; Length 110096;  
Best Local Similarity 83.0%; Pred. No. 2e-45;  
RESULT 948  
ID AEF74540 standard; DNA; 110096 BP.  
DE Human polynucleotide #54.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.8%; Score 222.8; DB 15; Length 110096;  
Best Local Similarity 83.0%; Pred. No. 2e-45;  
RESULT 949  
ID AEF74955 standard; DNA; 110096 BP.  
DE Human polynucleotide #469.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.8%; Score 222.8; DB 15; Length 110096;  
Best Local Similarity 83.0%; Pred. No. 2e-45;  
RESULT 950  
ID AEF74955 standard; DNA; 134000 BP.  
DE Human proline rich 4, PROL4, genomic sequence.  
PN WO2006074061-A2.  
PD 13-JUL-2006.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.8%; Score 222.8; DB 15; Length 134000;  
Best Local Similarity 71.3%; Pred. No. 2.2e-45;  
RESULT 951  
ID AAD55694 standard; DNA; 175561 BP.  
DE Human THBS4 reference gene (GI 14916146).  
PD WO2003020120-A2.  
PD 13-MAR-2003.

PA (VITI-) VITIVITY INC.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 9.8%; Score 222.8; DB 8; Length 175561;  
Best Local Similarity 85.5%; Pred. No. 2.4e-45;  
RESULT 952  
ID ADL08129 standard; DNA; 175561 BP.  
DE Human gene associated with low HDL-C THBS4.  
PN US2004043389-A1.  
PD 04-MAR-2004.  
PA (VITI-) VITIVITY INC.  
Query Match 9.8%; Score 222.8; DB 12; Length 175561;  
Best Local Similarity 85.5%; Pred. No. 2.4e-45;  
RESULT 953  
ID AAH16931 standard; cDNA; 556 BP.  
DE Human cDNA clone (3'-primer) SEQ ID NO:16208.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.7%; Score 222.6; DB 4; Length 556;  
Best Local Similarity 86.3%; Pred. No. 2.1e-46;  
RESULT 954  
ID ADB62815 standard; cDNA; 2477 BP.  
DE Human cDNA encoding clone NTONG200005310.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 222.6; DB 10; Length 2477;  
Best Local Similarity 82.7%; Pred. No. 4e-46;  
RESULT 955  
ID AAH17838 standard; cDNA; 2504 BP.  
DE Human cDNA sequence SEQ ID NO:17524.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.7%; Score 222.6; DB 4; Length 2504;  
Best Local Similarity 86.3%; Pred. No. 4.1e-46;  
RESULT 956  
ID AAK68368 standard; DNA; 5969 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23180.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 5969;  
Best Local Similarity 85.0%; Pred. No. 6e-46;  
RESULT 957  
ID AAK73167 standard; DNA; 11746 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27979.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 11746;  
Best Local Similarity 86.3%; Pred. No. 8.1e-46;  
RESULT 958  
ID ABK69935 standard; DNA; 11746 BP.  
DE Human secreted protein gene 68 genomic DNA fragment #23.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 6; Length 11746;  
Best Local Similarity 86.3%; Pred. No. 8.1e-46;  
RESULT 959  
ID ABK42245 standard; DNA; 12932 BP.  
DE Genomic sequence #144 encoding novel human connective tissue polypeptide.  
PN WO200155343-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 12932;  
Best Local Similarity 83.8%; Pred. No. 8.5e-46;  
RESULT 960  
ID ADB60401 standard; DNA; 12932 BP.  
DE Connective tissue related genomic DNA #144.  
PN US2003054375-A1.

PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 9; Length 12932;  
Best Local Similarity 83.8%; Pred. No. 8.5e-46;  
RESULT 961  
ID AAL05850 standard; DNA; 32184 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8538.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 32184;  
Best Local Similarity 79.0%; Pred. No. 1.3e-45;  
RESULT 962  
ID ABL98414 standard; DNA; 32184 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3066.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 32184;  
Best Local Similarity 79.0%; Pred. No. 1.3e-45;  
RESULT 963  
ID AAL36806 standard; DNA; 32185 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3171.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 32185;  
Best Local Similarity 86.5%; Pred. No. 1.3e-45;  
RESULT 964  
ID ABX59794 standard; cDNA; 32185 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #2138.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.7%; Score 222.6; DB 8; Length 32185;  
Best Local Similarity 86.5%; Pred. No. 1.3e-45;  
RESULT 965  
ID ADJ30544 standard; DNA; 32185 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3171.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 12; Length 32185;  
Best Local Similarity 86.5%; Pred. No. 1.3e-45;  
RESULT 966  
ID AAL05849 standard; DNA; 32204 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8537.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 32204;  
Best Local Similarity 79.0%; Pred. No. 1.3e-45;  
RESULT 967  
ID ABL98413 standard; DNA; 32204 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3065.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 32204;  
Best Local Similarity 79.0%; Pred. No. 1.3e-45;  
RESULT 968  
ID AEK79131 standard; DNA; 35320 BP.  
DE Human DGK zeta gene, SEQ ID NO: 4.  
Query Match 9.7%; Score 222.6; DB 15; Length 35320;  
Best Local Similarity 81.6%; Pred. No. 1.3e-45;  
RESULT 969  
ID AAK84729 standard; DNA; 48037 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39541.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.7%; Score 222.6; DB 4; Length 48037;  
Best Local Similarity 74.4%; Pred. No. 1.5e-45;  
RESULT 970  
ID AAK85983 standard; DNA; 48037 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40795.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 48037;  
Best Local Similarity 74.4%; Pred. No. 1.5e-45;  
RESULT 971  
ID AAK84730 standard; DNA; 48045 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39542.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 48045;  
Best Local Similarity 74.4%; Pred. No. 1.5e-45;  
RESULT 972  
ID AAK85984 standard; DNA; 48045 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40796.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 48045;  
Best Local Similarity 74.4%; Pred. No. 1.5e-45;  
RESULT 973  
ID AAK67426 standard; DNA; 55235 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22238.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.6; DB 4; Length 55235;  
Best Local Similarity 85.0%; Pred. No. 1.6e-45;  
RESULT 974  
ID ADV09374 standard; DNA; 62520 BP.  
DE Human helicase-like transcription factor (HLTF) genomic DNA.  
PN US2004242510-A1.  
PD 02-DEC-2004.  
PA (MARK/) MARKOWITZ S D.  
Query Match 9.7%; Score 222.6; DB 14; Length 62520;  
Best Local Similarity 80.9%; Pred. No. 1.7e-45;  
RESULT 975  
ID AAV83940 standard; DNA; 80240 BP.  
DE NC-contig derived from mardel(10) on chromosome 10q25.2.  
PN WO9851790-A1.  
PD 19-NOV-1998.  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
Query Match 9.7%; Score 222.6; DB 2; Length 80240;  
Best Local Similarity 85.0%; Pred. No. 1.9e-45;  
RESULT 976  
ID AAV83939 standard; DNA; 80595 BP.  
DE HC-contig derived from normal human chromosome 10q25.2 region.  
PN WO9851790-A1.  
PD 19-NOV-1998.  
PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
Query Match 9.7%; Score 222.6; DB 2; Length 80595;  
Best Local Similarity 85.0%; Pred. No. 1.9e-45;  
RESULT 977  
ID ADP08388 standard; DNA; 95400 BP.  
DE Human laminin alpha 4 (LAMA4) genomic DNA.  
Query Match 9.7%; Score 222.6; DB 12; Length 95400;  
Best Local Similarity 83.8%; Pred. No. 2.1e-45;  
RESULT 978  
ID AEK50257 standard; DNA; 95400 BP.  
DE Human laminin, alpha 4 - LAMA4 genomic DNA.  
Query Match 9.7%; Score 222.6; DB 15; Length 95400;  
Best Local Similarity 83.8%; Pred. No. 2.1e-45;  
RESULT 979  
ID ADY70791 standard; DNA; 104424 BP.  
DE Human soluble adenylyl cyclase (SAC) gene SEQ ID NO:21.  
PN CN1548557-A.  
PD 24-NOV-2004.

PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.  
Query Match 9.7%; Score 222.6; DB 14; Length 104424;  
Best Local Similarity 86.3%; Pred. No. 2.2e-45;  
RESULT 980  
ID ADZ46659 standard; DNA; 104424 BP.  
DE Type-II diabetes susceptibility gene SAC, SEQ ID 27.  
PN CN1548553-A.  
PD 24-NOV-2004.  
PA (PREC-) INST PRECLINICAL MEDICINE CHINESE ACAD M.  
Query Match 9.7%; Score 222.6; DB 14; Length 104424;  
Best Local Similarity 86.3%; Pred. No. 2.2e-45;  
RESULT 981  
ID ABK83569 standard; cDNA; 122888 BP.  
DE Human cDNA differentially expressed in granulocytic cells #140.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 222.6; DB 6; Length 122888;  
Best Local Similarity 81.6%; Pred. No. 2.3e-45;  
RESULT 982  
ID ABK49450 standard; DNA; 147309 BP.  
DE Human transporter genomic DNA sequence.  
Query Match 9.7%; Score 222.6; DB 6; Length 147309;  
Best Local Similarity 86.3%; Pred. No. 2.5e-45;  
RESULT 983  
ID ADQ97721 standard; DNA; 178024 BP.  
DE Human cancer associated sequence HD10-033, SEQ ID 698.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 222.6; DB 12; Length 178024;  
Best Local Similarity 80.5%; Pred. No. 2.8e-45;  
RESULT 984  
ID AEE04958 standard; DNA; 212235 BP.  
DE Cancer-associated gene SEQ ID NO:276.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 222.6; DB 14; Length 212235;  
Best Local Similarity 86.3%; Pred. No. 3e-45;  
RESULT 985  
ID ACN44514 standard; DNA; 256493 BP.  
DE Human genomic sequence hCG17361.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 222.6; DB 11; Length 256493;  
Best Local Similarity 86.3%; Pred. No. 3.2e-45;  
RESULT 986  
ID ADP69744 standard; DNA; 312477 BP.  
DE Human ROCK 1 DNA #2.  
PN US2004115641-A1.  
PD 17-JUN-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.7%; Score 222.6; DB 12; Length 312477;  
Best Local Similarity 77.7%; Pred. No. 3.5e-45;  
RESULT 987  
ID ABZ74324 standard; DNA; 518 BP.  
DE Secreted protein gene 236 genomic fragment HNTMH79, SEQ ID NO:1471.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 8; Length 518;  
Best Local Similarity 81.1%; Pred. No. 2.2e-46;  
RESULT 988  
ID ABZ67892 standard; DNA; 518 BP.  
DE Human secreted protein encoding genomic DNA SEQ ID NO 1415.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 10; Length 518;  
Best Local Similarity 81.1%; Pred. No. 2.2e-46;  
RESULT 989

ID ABL37980 standard; cDNA; 577 BP.  
DE Human colon tumour antigen polynucleotide SEQ ID NO:1569.  
PN WO200196388-A2.  
PD 20-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.7%; Score 222.4; DB 6; Length 577;  
Best Local Similarity 87.1%; Pred. No. 2.4e-46;  
RESULT 990  
ID ABV57704 standard; cDNA; 608 BP.  
DE Human prostate expression marker cDNA 57695.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 9.7%; Score 222.4; DB 5; Length 608;  
Best Local Similarity 80.1%; Pred. No. 2.4e-46;  
RESULT 991  
ID AAH16959 standard; cDNA; 1503 BP.  
DE Human cDNA sequence SEQ ID NO:16245.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.7%; Score 222.4; DB 4; Length 1503;  
Best Local Similarity 75.2%; Pred. No. 3.6e-46;  
RESULT 992  
ID ACA54696 standard; cDNA; 2842 BP.  
DE Human NF-kappaB associated polynucleotide sequence #136.  
PN WO200286076-A2.  
PD 31-OCT-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 9.7%; Score 222.4; DB 10; Length 2842;  
Best Local Similarity 78.2%; Pred. No. 4.8e-46;  
RESULT 993  
ID ADU83314 standard; cDNA; 2842 BP.  
DE Human NFKappaB-associated gene 40, cDNA #2.  
PN WO2004100886-A2.  
PD 25-NOV-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 9.7%; Score 222.4; DB 14; Length 2842;  
Best Local Similarity 78.2%; Pred. No. 4.8e-46;  
RESULT 994  
ID ADQ87646 standard; cDNA; 2924 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4524.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 9.7%; Score 222.4; DB 12; Length 2924;  
Best Local Similarity 87.1%; Pred. No. 4.9e-46;  
RESULT 995  
ID ACN37302 standard; cDNA; 2924 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA323769, SEQ ID NO:95.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 222.4; DB 13; Length 2924;  
Best Local Similarity 87.1%; Pred. No. 4.9e-46;  
RESULT 996  
ID ADP54897 standard; cDNA; 2924 BP.  
DE Human PRO cDNA sequence SEQ ID NO:873.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.7%; Score 222.4; DB 13; Length 2924;  
Best Local Similarity 87.1%; Pred. No. 4.9e-46;  
RESULT 997  
ID AAS92457 standard; cDNA; 7487 BP.  
DE DNA encoding novel human diagnostic protein #28261.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.7%; Score 222.4; DB 5; Length 7487;  
Best Local Similarity 81.1%; Pred. No. 7.5e-46;

RESULT 998  
ID ABA20857 standard; DNA; 11234 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 13188.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 5; Length 11234;  
Best Local Similarity 77.3%; Pred. No. 8.9e-46;  
RESULT 999  
ID AAK73037 standard; DNA; 12834 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27849.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 4; Length 12834;  
Best Local Similarity 84.6%; Pred. No. 9.5e-46;  
RESULT 1000  
ID AAD16553 standard; DNA; 13021 BP.  
DE Human novel protein-encoding gene 6 genomic DNA, SEQ ID NO:55.  
PN WO200155311-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 4; Length 13021;  
Best Local Similarity 83.3%; Pred. No. 9.6e-46;  
RESULT 1001  
ID AAS35084 standard; DNA; 13021 BP.  
DE DNA #34 encoding human neoplastic disease associated polypeptide.  
PN WO200155163-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 4; Length 13021;  
Best Local Similarity 83.3%; Pred. No. 9.6e-46;  
RESULT 1002  
ID ABS64143 standard; DNA; 13021 BP.  
DE Human apoptosis related protein genomic DNA clone HOHBY04 #1.  
PN US2002086811-A1.  
PD 04-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.7%; Score 222.4; DB 6; Length 13021;  
Best Local Similarity 83.3%; Pred. No. 9.6e-46;  
RESULT 1003  
ID ADC46526 standard; DNA; 13021 BP.  
DE Human neoplastic disease-associated gene 61 DNA #1.  
PN US2003082758-A1.  
PD 01-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 10; Length 13021;  
Best Local Similarity 83.3%; Pred. No. 9.6e-46;  
RESULT 1004  
ID AAD60452 standard; DNA; 13021 BP.  
DE Human secreted protein-encoding genomic DNA, SEQ ID NO:55.  
PN US2003092615-A1.  
PD 15-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 10; Length 13021;  
Best Local Similarity 83.3%; Pred. No. 9.6e-46;  
RESULT 1005  
ID AAF97862 standard; DNA; 22081 BP.  
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:76.  
PN WO200116311-A1.  
PD 08-MAR-2001.  
PA (HISM) HISAMITSU PHARM CO LTD.  
PA (CHIB-) CHIBA PREFECTURE.  
Query Match 9.7%; Score 222.4; DB 5; Length 22081;  
Best Local Similarity 84.5%; Pred. No. 1.2e-45;  
RESULT 1006  
ID AEE04761 standard; DNA; 22659 BP.  
DE Cancer-associated gene SEQ ID NO:79.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR) CHIRON CORP.

Query Match 9.7%; Score 222.4; DB 14; Length 22659;  
Best Local Similarity 82.2%; Pred. No. 1.2e-45;  
RESULT 1007  
ID AAL56668 standard; DNA; 23324 BP.  
DE Human G-CSF stimulated clone 1 (hGC-1) genomic DNA.  
PN WO2003050293-A2.  
PD 19-JUN-2003.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 9.7%; Score 222.4; DB 9; Length 23324;  
Best Local Similarity 78.2%; Pred. No. 1.2e-45;  
RESULT 1008  
ID AAK75632 standard; DNA; 23802 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30444.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.4; DB 4; Length 23802;  
Best Local Similarity 68.5%; Pred. No. 1.3e-45;  
RESULT 1009  
ID ACN43922 standard; DNA; 45864 BP.  
DE Human genomic sequence hCG27363.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 222.4; DB 11; Length 45864;  
Best Local Similarity 82.4%; Pred. No. 1.7e-45;  
RESULT 1010  
ID ABN89533 standard; DNA; 48436 BP.  
DE Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.  
PN US2002061562-A1.  
PD 23-MAY-2002.  
PA (FUKU/) FUKUDA M N.  
PA (AKAM/) AKAMA T O.  
Query Match 9.7%; Score 222.4; DB 6; Length 48436;  
Best Local Similarity 78.6%; Pred. No. 1.7e-45;  
RESULT 1011  
ID ABS98185 standard; DNA; 53099 BP.  
DE Human multidrug resistance gene exons 4-28 sequence.  
PN WO200257410-A2.  
PD 25-JUL-2002.  
PA (DNAS-) DNA SCI LAB INC.  
Query Match 9.7%; Score 222.4; DB 6; Length 53099;  
Best Local Similarity 74.6%; Pred. No. 1.8e-45;  
RESULT 1012  
ID ADH56439 standard; DNA; 95001 BP.  
DE Human hypothetical tumour endothelial marker DNA.  
PN US2003232770-A1.  
PD 18-DEC-2003.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.7%; Score 222.4; DB 12; Length 95001;  
Best Local Similarity 83.3%; Pred. No. 2.3e-45;  
RESULT 1013  
ID ABD32669 standard; DNA; 106544 BP.  
DE Human cancer-associated genomic DNA HD13-073.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 222.4; DB 13; Length 106544;  
Best Local Similarity 85.8%; Pred. No. 2.5e-45;  
RESULT 1014  
Query Match 9.7%; Score 222.4; DB 14; Length 110000;  
Best Local Similarity 84.6%; Pred. No. 2.5e-45;  
RESULT 1015  
ID ADH99063 standard; DNA; 118518 BP.  
DE Human NF-kappa-B p50 subunit full length DNA.  
PN US2004005569-A1.  
PD 08-JAN-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 9.7%; Score 222.4; DB 12; Length 118518;  
Best Local Similarity 68.5%; Pred. No. 2.6e-45;  
RESULT 1016  
ID ACF62749 standard; DNA; 128993 BP.  
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:681.



PN WO2003013534-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 222.4; DB 8; Length 128993;  
Best Local Similarity 74.6%; Pred. No. 2.7e-45;  
RESULT 1017  
ID ADB20868 standard; DNA; 128993 BP.  
DE MRP1 based cancer related nucleic acid SEQ ID NO:681.  
PN WO2003013533-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 222.4; DB 8; Length 128993;  
Best Local Similarity 74.6%; Pred. No. 2.7e-45;  
RESULT 1018  
ID ADB87957 standard; DNA; 128993 BP.  
DE Human UGT1A1 gene sequence SEQ ID NO:681.  
PN WO2003013536-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 222.4; DB 10; Length 128993;  
Best Local Similarity 74.6%; Pred. No. 2.7e-45;  
RESULT 1019  
ID ADB96940 standard; DNA; 128993 BP.  
DE Human MDRI related DNA sequence SEQ ID NO:681.  
PN WO2003013537-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 222.4; DB 10; Length 128993;  
Best Local Similarity 74.6%; Pred. No. 2.7e-45;  
RESULT 1020  
ID ADB21131 standard; DNA; 128993 BP.  
DE Human MDRI related DNA sequence SEQ ID NO:681.  
PN WO2003013535-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 222.4; DB 10; Length 128993;  
Best Local Similarity 74.6%; Pred. No. 2.7e-45;  
RESULT 1021  
ID ABD33163 standard; DNA; 138837 BP.  
DE Human cancer-associated (CA) gene HD07-022.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 222.4; DB 13; Length 138837;  
Best Local Similarity 85.8%; Pred. No. 2.8e-45;  
RESULT 1022  
ID AEJ13138 standard; DNA; 138837 BP.  
DE Cancer-associated gene sequence - SEQ ID 146.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.7%; Score 222.4; DB 15; Length 138837;  
Best Local Similarity 85.8%; Pred. No. 2.8e-45;  
RESULT 1023  
ID AED89419 standard; DNA; 168656 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 59.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 222.4; DB 14; Length 168656;  
Best Local Similarity 83.3%; Pred. No. 3e-45;  
RESULT 1024  
ID AED89418 standard; DNA; 170285 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 58.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 222.4; DB 14; Length 170285;  
Best Local Similarity 83.3%; Pred. No. 3e-45;  
RESULT 1025  
ID ABK83571 standard; cDNA; 175737 BP.  
DE Human cDNA differentially expressed in granulocytic cells #142.

PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 222.4; DB 6; Length 175737;  
Best Local Similarity 81.1%; Pred. No. 3.1e-45;  
RESULT 1026  
ID ADL13596 standard; DNA; 175737 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #128.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.7%; Score 222.4; DB 10; Length 175737;  
Best Local Similarity 81.1%; Pred. No. 3.1e-45;  
RESULT 1027  
ID ADQ18934 standard; DNA; 175737 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1753.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.7%; Score 222.4; DB 12; Length 175737;  
Best Local Similarity 81.1%; Pred. No. 3.1e-45;  
RESULT 1028  
ID AEC32799 standard; DNA; 175737 BP.  
DE Breast cancer detection expression profile gene, SEQ ID 34.  
PN US2005186577-A1.  
PD 25-AUG-2005.  
PA (WANG/) WANG Y.  
Query Match 9.7%; Score 222.4; DB 14; Length 175737;  
Best Local Similarity 81.1%; Pred. No. 3.1e-45;  
RESULT 1029  
ID AEC82466 standard; cDNA; 175737 BP.  
DE Breast cancer associated cDNA SEQ ID NO 34.  
PN WO2005083429-A2.  
PD 09-SEP-2005.  
PA (VERI-) VERIDEX LLC.  
Query Match 9.7%; Score 222.4; DB 14; Length 175737;  
Best Local Similarity 81.1%; Pred. No. 3.1e-45;  
RESULT 1030  
ID AED18210 standard; DNA; 175737 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 461.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL) UNIV FLORIDA RES FOUND INC.  
Query Match 9.7%; Score 222.4; DB 14; Length 175737;  
Best Local Similarity 81.1%; Pred. No. 3.1e-45;  
RESULT 1031  
ID AEK17570 standard; DNA; 242981 BP.  
DE Cell/tissue epigenetic characterization human gene, SEQ ID NO:22.  
PN WO2006094836-A2.  
PD 14-SEP-2006.  
PA (EPIO-) EPIONTIS GMBH.  
Query Match 9.7%; Score 222.4; DB 15; Length 242981;  
Best Local Similarity 84.5%; Pred. No. 3.6e-45;  
RESULT 1032  
ID ABD33276 standard; DNA; 256190 BP.  
DE Human cancer-associated (CA) gene HD07-048.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 222.4; DB 13; Length 256190;  
Best Local Similarity 84.6%; Pred. No. 3.6e-45;  
RESULT 1033  
ID AEJ13312 standard; DNA; 256190 BP.  
DE Cancer-associated gene sequence - SEQ ID 320.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.7%; Score 222.4; DB 15; Length 256190;  
Best Local Similarity 84.6%; Pred. No. 3.6e-45;  
RESULT 1034  
ID AAH71089 standard; cDNA; 366 BP.  
DE Human cervical cancer marker nucleic acid 2363.

PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 9.7%; Score 222.2; DB 4; Length 366;  
Best Local Similarity 85.2%; Pred. No. 2.2e-46;  
RESULT 1035  
ID ABN65466 standard; cDNA; 509 BP.  
DE Human cancer related polynucleotide SEQ ID NO 5433.  
PN WO200214500-A2.  
PD 21-FEB-2002.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.7%; Score 222.2; DB 6; Length 509;  
Best Local Similarity 71.8%; Pred. No. 2.5e-46;  
RESULT 1036  
ID AAH98536 standard; cDNA; 859 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 393.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.7%; Score 222.2; DB 4; Length 859;  
Best Local Similarity 83.9%; Pred. No. 3.2e-46;  
RESULT 1037  
ID AAD34114 standard; cDNA; 921 BP.  
DE Human secreted protein-encoding gene 9 cDNA clone HE8NQ42, SEQ ID NO:19.  
PN WO200222654-A1.  
PD 21-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.2; DB 6; Length 921;  
Best Local Similarity 85.2%; Pred. No. 3.3e-46;  
RESULT 1038  
ID AAH17382 standard; cDNA; 2835 BP.  
DE Human cDNA sequence SEQ ID NO:16817.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.7%; Score 222.2; DB 4; Length 2835;  
Best Local Similarity 81.8%; Pred. No. 5.4e-46;  
RESULT 1039  
ID ADQ63525 standard; cDNA; 3871 BP.  
DE Novel human cDNA sequence #686.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 222.2; DB 12; Length 3871;  
Best Local Similarity 84.0%; Pred. No. 6.2e-46;  
RESULT 1040  
ID AAH18205 standard; cDNA; 3877 BP.  
DE Human cDNA sequence SEQ ID NO:18124.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.7%; Score 222.2; DB 4; Length 3877;  
Best Local Similarity 85.2%; Pred. No. 6.2e-46;  
RESULT 1041  
ID AAK80271 standard; DNA; 6418 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35083.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.2; DB 4; Length 6418;  
Best Local Similarity 84.1%; Pred. No. 7.8e-46;  
RESULT 1042  
ID ADH10009 standard; DNA; 8949 BP.  
DE Human FUS II exon A and A1 DNA.  
PN WO2003093310-A1.  
PD 13-NOV-2003.  
PA (UYBR-) UNIV BREMEN.  
Query Match 9.7%; Score 222.2; DB 10; Length 8949;  
Best Local Similarity 85.2%; Pred. No. 9.1e-46;  
RESULT 1043  
ID ADL13829 standard; DNA; 12414 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #361.

PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.7%; Score 222.2; DB 10; Length 12414;  
Best Local Similarity 81.8%; Pred. No. 1.1e-45;  
RESULT 1044  
ID AAK67239 standard; DNA; 30393 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22051.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.2; DB 4; Length 30393;  
Best Local Similarity 81.9%; Pred. No. 1.6e-45;  
RESULT 1045  
ID AAI99255 standard; DNA; 32127 BP.  
DE Human excretory related polynucleotide SEQ ID NO 1019.  
PN WO200155313-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.2; DB 4; Length 32127;  
Best Local Similarity 84.0%; Pred. No. 1.6e-45;  
RESULT 1046  
ID AAI63605 standard; DNA; 32127 BP.  
DE Human kidney related polynucleotide SEQ ID NO 920.  
PN WO200155323-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.2; DB 5; Length 32127;  
Best Local Similarity 84.0%; Pred. No. 1.6e-45;  
RESULT 1047  
ID AAK82338 standard; DNA; 48908 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37150.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.2; DB 4; Length 48908;  
Best Local Similarity 84.0%; Pred. No. 1.9e-45;  
RESULT 1048  
ID ADC86870 standard; DNA; 69770 BP.  
DE Human GPCR gene SEQ ID NO:1323.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.7%; Score 222.2; DB 10; Length 69770;  
Best Local Similarity 78.8%; Pred. No. 2.3e-45;  
RESULT 1049  
ID AAK86832 standard; DNA; 72215 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41644.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222.2; DB 4; Length 72215;  
Best Local Similarity 84.0%; Pred. No. 2.3e-45;  
RESULT 1050  
ID ADP08387 standard; DNA; 94400 BP.  
DE Human glycoprotein VI (platelet) (GP6;GPV;GPVI) genomic DNA.  
Query Match 9.7%; Score 222.2; DB 12; Length 94400;  
Best Local Similarity 84.0%; Pred. No. 2.6e-45;  
RESULT 1051  
ID AEK50256 standard; DNA; 94400 BP.  
DE Human glycoprotein VI (platelet) - GP6 genomic DNA.  
PN US2006204967-A1.  
PD 14-SEP-2006.  
PA (ROTH/) ROTH R B.  
PA (BRAU/) BRAUN A.  
PA (KAMM/) KAMMERER S M.  
PA (NELS/) NELSON M R.  
PA (RENE/) RENELAND R H.  
Query Match 9.7%; Score 222.2; DB 15; Length 94400;  
Best Local Similarity 84.0%; Pred. No. 2.6e-45;  
RESULT 1052  
ID ADX98574 standard; DNA; 95050 BP.

DE Human LOC145197 genomic DNA.  
Query Match 9.7%; Score 222.2; DB 14; Length 95050;  
Best Local Similarity 81.8%; Pred. No. 2.6e-45;  
RESULT 1053  
ID AEG24777 standard; DNA; 98800 BP.  
DE Human TRPS1 DNA.  
PN WO2006022636-A1.  
PD 02-MAR-2006.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222.2; DB 15; Length 98800;  
Best Local Similarity 70.5%; Pred. No. 2.7e-45;  
RESULT 1054  
ID AEI93841 standard; DNA; 100000 BP.  
DE Human glutathione peroxidase 3, GPX3, genomic sequence.  
PN WO2006074061-A2.  
PD 13-JUL-2006.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222.2; DB 15; Length 100000;  
Best Local Similarity 75.8%; Pred. No. 2.7e-45;  
RESULT 1055  
ID ADE43582 standard; DNA; 128034 BP.  
DE Polymorphic human IDE genomic sequence, SEQ ID 187.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 9.7%; Score 222.2; DB 10; Length 128034;  
Best Local Similarity 85.2%; Pred. No. 3e-45;  
RESULT 1056  
ID ADE43581 standard; DNA; 128034 BP.  
DE Human IDE genomic sequence, SEQ ID 186.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 9.7%; Score 222.2; DB 10; Length 128034;  
Best Local Similarity 85.2%; Pred. No. 3e-45;  
RESULT 1057  
ID ADH54059 standard; DNA; 128034 BP.  
DE Human IDE gene DNA sequence SeqID186.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 9.7%; Score 222.2; DB 12; Length 128034;  
Best Local Similarity 85.2%; Pred. No. 3e-45;  
RESULT 1058  
ID ADH54060 standard; DNA; 128034 BP.  
DE Human IDE gene variant DNA sequence SeqID187.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 9.7%; Score 222.2; DB 12; Length 128034;  
Best Local Similarity 85.2%; Pred. No. 3e-45;  
RESULT 1059  
ID ABZ35015 standard; cDNA; 136328 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 127.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.  
Query Match 9.7%; Score 222.2; DB 6; Length 136328;  
Best Local Similarity 87.9%; Pred. No. 3.1e-45;  
RESULT 1060  
ID ABT10718 standard; cDNA; 185371 BP.  
DE Human breast cancer associated coding sequence SEQ ID NO: 852.  
PN WO200259271-A2.  
PD 01-AUG-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 222.2; DB 6; Length 185371;  
Best Local Similarity 81.8%; Pred. No. 3.5e-45;  
RESULT 1061  
ID ADM69029 standard; DNA; 191150 BP.  
DE Human platelet derived growth factor receptor alpha wild-type gDNA.  
PN WO2003105773-A2.

PD 24-DEC-2003.  
PA (UYOR-) UNIV OREGON HEALTH SCI.  
PA (DAND) DANA FARBER CANCER INST INC.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
PA (USGO) US DEPT VETERANS AFFAIRS.  
Query Match 9.7%; Score 222.2; DB 12; Length 191150;  
Best Local Similarity 82.1%; Pred. No. 3.6e-45;  
RESULT 1062  
ID ADL13719 standard; DNA; 199878 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #251.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.7%; Score 222.2; DB 10; Length 199878;  
Best Local Similarity 73.1%; Pred. No. 3.7e-45;  
RESULT 1063  
ID ADE43315 standard; DNA; 202100 BP.  
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 9.7%; Score 222.2; DB 10; Length 202100;  
Best Local Similarity 85.2%; Pred. No. 3.7e-45;  
RESULT 1064  
ID ADH54357 standard; DNA; 202100 BP.  
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 9.7%; Score 222.2; DB 12; Length 202100;  
Best Local Similarity 85.2%; Pred. No. 3.7e-45;  
RESULT 1065  
ID ACN44070 standard; DNA; 344548 BP.  
DE Human genomic sequence hCG36954.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 222.2; DB 11; Length 344548;  
Best Local Similarity 87.9%; Pred. No. 4.7e-45;  
RESULT 1066  
ID AAK78857 standard; DNA; 358 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33669.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 4; Length 358;  
Best Local Similarity 78.4%; Pred. No. 2.4e-46;  
RESULT 1067  
ID AAK78858 standard; DNA; 358 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33670.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 4; Length 358;  
Best Local Similarity 78.4%; Pred. No. 2.4e-46;  
RESULT 1068  
ID ACN40083 standard; cDNA; 2417 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326241, SEQ ID NO:4645.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 9.7%; Score 222; DB 13; Length 2417;  
Best Local Similarity 84.8%; Pred. No. 5.7e-46;  
RESULT 1069  
ID ADM20191 standard; cDNA; 6491 BP.  
DE Alternative nucleotide for novel channel/transporter cDNA #212.  
PN WO200154472-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 5; Length 6491;  
Best Local Similarity 82.4%; Pred. No. 8.9e-46;  
RESULT 1070

ID ADC20800 standard; DNA; 10115 BP.  
DE Human secreted protein-related DNA sequence #218.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 10; Length 10115;  
Best Local Similarity 83.5%; Pred. No. 1.1e-45;  
RESULT 1071  
ID ABZ74163 standard; DNA; 10116 BP.  
DE Secreted protein gene 200 genomic fragment HMQA138, SEQ ID NO:1310.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 8; Length 10116;  
Best Local Similarity 83.5%; Pred. No. 1.1e-45;  
RESULT 1072  
ID ABZ74318 standard; DNA; 11168 BP.  
DE Secreted protein gene 236 genomic fragment HNTMH79, SEQ ID NO:1465.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 8; Length 11168;  
Best Local Similarity 82.4%; Pred. No. 1.1e-45;  
RESULT 1073  
ID ABZ67886 standard; DNA; 11168 BP.  
DE Human secreted protein encoding genomic DNA SEQ ID NO 1409.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 10; Length 11168;  
Best Local Similarity 82.4%; Pred. No. 1.1e-45;  
RESULT 1074  
ID AAI99007 standard; DNA; 11992 BP.  
DE Human excretory related polynucleotide SEQ ID NO 771.  
PN WO200155313-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 4; Length 11992;  
Best Local Similarity 80.3%; Pred. No. 1.2e-45;  
RESULT 1075  
ID AAK80050 standard; DNA; 11992 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34862.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 4; Length 11992;  
Best Local Similarity 80.3%; Pred. No. 1.2e-45;  
RESULT 1076  
ID AAI63357 standard; DNA; 11992 BP.  
DE Human kidney related polynucleotide SEQ ID NO 672.  
PN WO200155323-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 5; Length 11992;  
Best Local Similarity 80.3%; Pred. No. 1.2e-45;  
RESULT 1077  
ID ABZ74319 standard; DNA; 12212 BP.  
DE Secreted protein gene 236 genomic fragment HNTMH79, SEQ ID NO:1466.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 8; Length 12212;  
Best Local Similarity 82.4%; Pred. No. 1.2e-45;  
RESULT 1078  
ID ABZ67887 standard; DNA; 12212 BP.  
DE Human secreted protein encoding genomic DNA SEQ ID NO 1410.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 10; Length 12212;  
Best Local Similarity 82.4%; Pred. No. 1.2e-45;  
RESULT 1079  
ID AAS42069 standard; DNA; 17687 BP.

DE Genomic sequence #385 encoding novel human enzyme polypeptide.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 4; Length 17687;  
Best Local Similarity 68.6%; Pred. No. 1.4e-45;  
RESULT 1080  
ID AAS42064 standard; DNA; 19815 BP.  
DE Genomic sequence #380 encoding novel human enzyme polypeptide.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 4; Length 19815;  
Best Local Similarity 68.6%; Pred. No. 1.5e-45;  
RESULT 1081  
ID ABD33582 standard; DNA; 21823 BP.  
DE Human cancer-associated (CA) gene HD07-117.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 222; DB 13; Length 21823;  
Best Local Similarity 84.7%; Pred. No. 1.5e-45;  
RESULT 1082  
ID AEJ13786 standard; DNA; 21823 BP.  
DE Cancer-associated gene sequence - SEQ ID 794.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.7%; Score 222; DB 15; Length 21823;  
Best Local Similarity 84.7%; Pred. No. 1.5e-45;  
RESULT 1083  
ID AAL05336 standard; DNA; 32249 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8024.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 4; Length 32249;  
Best Local Similarity 72.6%; Pred. No. 1.8e-45;  
RESULT 1084  
ID ABL98205 standard; DNA; 32249 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2857.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 222; DB 4; Length 32249;  
Best Local Similarity 72.6%; Pred. No. 1.8e-45;  
RESULT 1085  
ID ACN44094 standard; DNA; 35236 BP.  
DE Human genomic sequence hCG23314.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 222; DB 11; Length 35236;  
Best Local Similarity 82.4%; Pred. No. 1.9e-45;  
RESULT 1086  
ID ADQ97207 standard; DNA; 56181 BP.  
DE Human cancer associated sequence HD08-013, SEQ ID 183.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 222; DB 12; Length 56181;  
Best Local Similarity 82.4%; Pred. No. 2.3e-45;  
RESULT 1087  
ID AAC89559 standard; DNA; 80331 BP.  
DE Human histone deacetylase HDAC-C coding sequence.  
PN WO200071703-A2.  
PD 30-NOV-2000.  
PA (METH-) METHYLGENE INC.  
Query Match 9.7%; Score 222; DB 4; Length 80331;  
Best Local Similarity 70.9%; Pred. No. 2.7e-45;  
RESULT 1088  
ID ADQ97846 standard; DNA; 94911 BP.



DE Human cancer associated sequence HD11-010, SEQ ID 823.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 222; DB 12; Length 94911;  
Best Local Similarity 83.5%; Pred. No. 3e-45;  
RESULT 1089  
ID ABQ88125 standard; cDNA; 109201 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 32.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC ) PROCTER & GAMBLE CO.  
Query Match 9.7%; Score 222; DB 6; Length 109201;  
Best Local Similarity 83.5%; Pred. No. 3.1e-45;  
RESULT 1090  
ID ACN44674 standard; DNA; 129042 BP.  
DE Human genomic sequence hCG27276.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 222; DB 11; Length 129042;  
Best Local Similarity 86.0%; Pred. No. 3.4e-45;  
RESULT 1091  
ID AED18548 standard; DNA; 150147 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 799.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 9.7%; Score 222; DB 14; Length 150147;  
Best Local Similarity 85.0%; Pred. No. 3.6e-45;  
RESULT 1092  
ID AAD28763 standard; DNA; 154465 BP.  
DE Human AKAP allelic variant (AKAP10-1) gene.  
PN WO200204489-A2.  
PD 17-JAN-2002.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 6; Length 154465;  
Best Local Similarity 81.3%; Pred. No. 3.7e-45;  
RESULT 1093  
ID AAD28762 standard; DNA; 158245 BP.  
DE Human AKAP allelic variant (AKAP10) gene.  
PN WO200204489-A2.  
PD 17-JAN-2002.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 6; Length 158245;  
Best Local Similarity 81.3%; Pred. No. 3.7e-45;  
RESULT 1094  
ID AED89421 standard; DNA; 159497 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 61.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 222; DB 14; Length 159497;  
Best Local Similarity 82.4%; Pred. No. 3.7e-45;  
RESULT 1095  
ID AAH02340 standard; DNA; 161425 BP.  
DE Human AKAP10 gene SEQ ID NO: 36.  
PN WO200127857-A2.  
PD 19-APR-2001.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 4; Length 161425;  
Best Local Similarity 81.3%; Pred. No. 3.7e-45;  
RESULT 1096  
ID AAH02339 standard; DNA; 162025 BP.  
DE Human AKAP10 gene SEQ ID NO: 35.  
PN WO200127857-A2.  
PD 19-APR-2001.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 4; Length 162025;  
Best Local Similarity 81.3%; Pred. No. 3.8e-45;  
RESULT 1097  
ID AAD28758 standard; DNA; 162025 BP.

DE Human AKAP allelic variant (AKAP10-6) gene.  
PN WO200204489-A2.  
PD 17-JAN-2002.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 6; Length 162025;  
Best Local Similarity 81.3%; Pred. No. 3.8e-45;  
RESULT 1098  
ID AAD28759 standard; DNA; 162025 BP.  
DE Human AKAP allelic variant (AKAP10-7) gene.  
PN WO200204489-A2.  
PD 17-JAN-2002.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 6; Length 162025;  
Best Local Similarity 81.3%; Pred. No. 3.8e-45;  
RESULT 1099  
ID ADS75958 standard; DNA; 162025 BP.  
DE Human A-kinase anchoring protein 10 allele AKAP10-6 genomic sequence.  
PN WO2004081576-A2.  
PD 23-SEP-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 13; Length 162025;  
Best Local Similarity 81.3%; Pred. No. 3.8e-45;  
RESULT 1100  
ID ADS75959 standard; DNA; 162025 BP.  
DE Human A-kinase anchoring protein 10 allele AKAP10-7 genomic sequence.  
PN WO2004081576-A2.  
PD 23-SEP-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 13; Length 162025;  
Best Local Similarity 81.3%; Pred. No. 3.8e-45;  
RESULT 1101  
ID ADS75963 standard; DNA; 162025 BP.  
DE Human A-kinase anchoring protein 10 allele AKAP10-1 genomic sequence.  
PN WO2004081576-A2.  
PD 23-SEP-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 13; Length 162025;  
Best Local Similarity 81.3%; Pred. No. 3.8e-45;  
RESULT 1102  
ID ADS75962 standard; DNA; 162025 BP.  
DE Human A-kinase anchoring protein 10 wild type genomic sequence.  
PN WO2004081576-A2.  
PD 23-SEP-2004.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 222; DB 13; Length 162025;  
Best Local Similarity 81.3%; Pred. No. 3.8e-45;  
RESULT 1103  
ID AEE05008 standard; DNA; 246386 BP.  
DE Cancer-associated gene SEQ ID NO:326.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 222; DB 14; Length 246386;  
Best Local Similarity 84.7%; Pred. No. 4.5e-45;  
RESULT 1104  
ID ADQ97557 standard; DNA; 254396 BP.  
DE Human cancer associated sequence HD09-013, SEQ ID 534.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 222; DB 12; Length 254396;  
Best Local Similarity 75.0%; Pred. No. 4.6e-45;  
RESULT 1105  
ID ADP65796 standard; DNA; 270150 BP.  
DE Human 16p133 sequence section 7 of 8 DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 9.7%; Score 222; DB 11; Length 270150;  
Best Local Similarity 68.6%; Pred. No. 4.7e-45;  
RESULT 1106  
ID ABQ92014 standard; cDNA; 4236 BP.  
DE Human polynucleotide SEQ ID NO 11.

PN US2002065394-A1.  
PD 30-MAY-2002.  
PA (JACO/) JACOBS K.  
PA (MCCO/) MCCOY J M.  
PA (LAVA/) LAVALLIE E R.  
PA (COLL/) COLLINS-RACIE L A.  
PA (EVAN/) EVANS C.  
PA (MERB/) MERBERG D.  
PA (TREA/) TREACY M.  
PA (SPAU/) SPAULDING V.  
Query Match 9.7%; Score 221.8; DB 6; Length 4236;  
Best Local Similarity 83.0%; Pred. No. 8.2e-46;  
RESULT 1107  
ID AAV61487 standard; cDNA; 4237 BP.  
DE Human secreted protein fe366\_1 cDNA.  
PN WO9841539-A2.  
PD 24-SEP-1998.  
PA (GEMY ) GENETICS INST INC.  
Query Match 9.7%; Score 221.8; DB 2; Length 4237;  
Best Local Similarity 83.0%; Pred. No. 8.2e-46;  
RESULT 1108  
ID AAK66570 standard; DNA; 10708 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21382.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 4; Length 10708;  
Best Local Similarity 83.1%; Pred. No. 1.2e-45;  
RESULT 1109  
ID ABA16244 standard; DNA; 11715 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 8575.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 5; Length 11715;  
Best Local Similarity 84.2%; Pred. No. 1.3e-45;  
RESULT 1110  
ID ADG20558 standard; DNA; 15620 BP.  
DE Human RNASEL nucleotide sequence SEQ ID NO:2.  
PN WO2003106617-A2.  
PD 24-DEC-2003.  
PA (TELA-) TEL AVIV MEDICAL CENT RES DEV FUND.  
Query Match 9.7%; Score 221.8; DB 12; Length 15620;  
Best Local Similarity 83.1%; Pred. No. 1.5e-45;  
RESULT 1111  
ID AAS36927 standard; DNA; 20869 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2427.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 4; Length 20869;  
Best Local Similarity 84.2%; Pred. No. 1.7e-45;  
RESULT 1112  
ID AAK85001 standard; DNA; 20869 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39813.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 4; Length 20869;  
Best Local Similarity 84.2%; Pred. No. 1.7e-45;  
RESULT 1113  
ID ABA16245 standard; DNA; 20869 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 8576.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 5; Length 20869;  
Best Local Similarity 84.2%; Pred. No. 1.7e-45;  
RESULT 1114  
ID ADE47621 standard; DNA; 20869 BP.  
DE Human cardiovascular system related genomic DNA #1187.  
PN US2003059908-A1.  
PD 27-MAR-2003.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 10; Length 20869;  
Best Local Similarity 84.2%; Pred. No. 1.7e-45;  
RESULT 1115  
ID ADJ09039 standard; DNA; 20869 BP.  
DE Human cardiovascular system associated polypeptide-related DNA SeqID2427.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 13; Length 20869;  
Best Local Similarity 84.2%; Pred. No. 1.7e-45;  
RESULT 1116  
ID AAL03917 standard; DNA; 22299 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 6605.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 4; Length 22299;  
Best Local Similarity 75.5%; Pred. No. 1.7e-45;  
RESULT 1117  
ID AAS40317 standard; DNA; 22299 BP.  
DE DNA encoding human prostate cancer antigen, Seq ID No 469.  
PN WO200155316-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 5; Length 22299;  
Best Local Similarity 75.5%; Pred. No. 1.7e-45;  
RESULT 1118  
ID ADJ09523 standard; DNA; 22299 BP.  
DE Human prostate cancer associated gene-related DNA SeqID469.  
PN US2003054373-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 11; Length 22299;  
Best Local Similarity 75.5%; Pred. No. 1.7e-45;  
RESULT 1119  
ID ACN44866 standard; DNA; 27204 BP.  
DE Human genomic sequence hCG23376.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221.8; DB 11; Length 27204;  
Best Local Similarity 82.1%; Pred. No. 1.9e-45;  
RESULT 1120  
ID ABK86948 standard; DNA; 28444 BP.  
DE Human glutathione synthetase (GSS) gene sequence.  
PN WO200238585-A2.  
PD 16-MAY-2002.  
PA (GENA-) GENAISSANCE PHARM INC.  
Query Match 9.7%; Score 221.8; DB 6; Length 28444;  
Best Local Similarity 82.0%; Pred. No. 1.9e-45;  
RESULT 1121  
ID AEB31548 standard; DNA; 29764 BP.  
DE Glutathione synthetase (GSS) DNA.  
PN WO2005068649-A1.  
PD 28-JUL-2005.  
PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG.  
Query Match 9.7%; Score 221.8; DB 14; Length 29764;  
Best Local Similarity 82.0%; Pred. No. 2e-45;  
RESULT 1122  
ID AAK69758 standard; DNA; 32986 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24570.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 4; Length 32986;  
Best Local Similarity 84.3%; Pred. No. 2.1e-45;  
RESULT 1123  
ID AAK84629 standard; DNA; 32986 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39441.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.7%; Score 221.8; DB 4; Length 32986;  
Best Local Similarity 84.3%; Pred. No. 2.1e-45;  
RESULT 1124  
ID AAK87512 standard; DNA; 41488 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42324.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.8; DB 4; Length 41488;  
Best Local Similarity 76.6%; Pred. No. 2.3e-45;  
RESULT 1125  
ID ADC86998 standard; DNA; 43419 BP.  
DE Human GPCR gene SEQ ID NO:1451.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.7%; Score 221.8; DB 10; Length 43419;  
Best Local Similarity 82.0%; Pred. No. 2.3e-45;  
RESULT 1126  
ID AED18692 standard; DNA; 59102 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 943.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL) UNIV FLORIDA RES FOUND INC.  
Query Match 9.7%; Score 221.8; DB 14; Length 59102;  
Best Local Similarity 82.0%; Pred. No. 2.7e-45;  
RESULT 1127  
ID AED18692 standard; DNA; 59102 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 943.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL) UNIV FLORIDA RES FOUND INC.  
Query Match 9.7%; Score 221.8; DB 14; Length 59102;  
Best Local Similarity 82.0%; Pred. No. 2.7e-45;  
RESULT 1128  
ID ABK90695 standard; DNA; 73467 BP.  
DE DNA encoding human transporter protein.  
Query Match 9.7%; Score 221.8; DB 6; Length 73467;  
Best Local Similarity 83.1%; Pred. No. 3e-45;  
RESULT 1129  
ID ABX95843 standard; DNA; 73467 BP.  
DE Genomic DNA encoding novel human transporter protein.  
Query Match 9.7%; Score 221.8; DB 8; Length 73467;  
Best Local Similarity 83.1%; Pred. No. 3e-45;  
RESULT 1130  
ID AEC00670 standard; DNA; 73467 BP.  
DE Human sodium/glucose cotransporter related genomic DNA, SEQ ID NO: 3.  
Query Match 9.7%; Score 221.8; DB 14; Length 73467;  
Best Local Similarity 83.1%; Pred. No. 3e-45;  
RESULT 1131  
ID ABD33179 standard; DNA; 100445 BP.  
DE Human cancer-associated (CA) gene HD07-026.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 221.8; DB 13; Length 100445;  
Best Local Similarity 84.5%; Pred. No. 3.4e-45;  
RESULT 1132  
ID AEJ13162 standard; DNA; 100445 BP.  
DE Cancer-associated gene sequence - SEQ ID 170.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.7%; Score 221.8; DB 15; Length 100445;  
Best Local Similarity 84.5%; Pred. No. 3.4e-45;  
RESULT 1133  
ID ABD32988 standard; DNA; 115611 BP.  
DE Human cancer-associated genomic DNA HD21-012.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.

Query Match 9.7%; Score 221.8; DB 13; Length 115611;  
Best Local Similarity 85.5%; Pred. No. 3.6e-45;  
RESULT 1134  
ID ADZ12550 standard; DNA; 117730 BP.  
DE Human cancer-associated genomic DNA #8.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 9.7%; Score 221.8; DB 14; Length 117730;  
Best Local Similarity 83.1%; Pred. No. 3.7e-45;  
RESULT 1135  
ID ADS36461 standard; DNA; 158417 BP.  
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.7%; Score 221.8; DB 13; Length 158417;  
Best Local Similarity 77.6%; Pred. No. 4.2e-45;  
RESULT 1136  
ID ABK83497 standard; cDNA; 227968 BP.  
DE Human cDNA differentially expressed in granulocytic cells #68.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 221.8; DB 6; Length 227968;  
Best Local Similarity 83.1%; Pred. No. 4.9e-45;  
RESULT 1137  
ID ADQ18538 standard; DNA; 227968 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.7%; Score 221.8; DB 12; Length 227968;  
Best Local Similarity 83.1%; Pred. No. 4.9e-45;  
RESULT 1138  
ID AED17856 standard; DNA; 227968 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 107.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL) UNIV FLORIDA RES FOUND INC.  
Query Match 9.7%; Score 221.8; DB 14; Length 227968;  
Best Local Similarity 83.1%; Pred. No. 4.9e-45;  
RESULT 1139  
ID AEF51726 standard; DNA; 304486 BP.  
DE Human p21-activated kinase 5 (PAK5) encoding DNA.  
PN EP1619504-A1.  
PD 25-JAN-2006.  
PA (FRAU-) FRAUNHOFER INST TOXIKOLOGIE & EXPERIMENT.  
Query Match 9.7%; Score 221.8; DB 15; Length 304486;  
Best Local Similarity 85.5%; Pred. No. 5.6e-45;  
RESULT 1140  
ID ADW81937 standard; DNA; 408 BP.  
DE MAP3K9 marker amplicon #182.  
PN WO2005007144-A2.  
PD 27-JAN-2005.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 9.7%; Score 221.6; DB 14; Length 408;  
Best Local Similarity 78.2%; Pred. No. 3.2e-46;  
RESULT 1141  
ID AEK86105 standard; DNA; 408 BP.  
DE Human chromosome-14 microsatellite, SEQ ID NO:1278.  
PN WO2006081555-A2.  
PD 03-AUG-2006.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 9.7%; Score 221.6; DB 15; Length 408;  
Best Local Similarity 78.2%; Pred. No. 3.2e-46;  
RESULT 1142  
ID ABN65219 standard; cDNA; 602 BP.  
DE Human cancer related polynucleotide SEQ ID NO 5186.  
PN WO200214500-A2.  
PD 21-FEB-2002.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.

Query Match 9.7%; Score 221.6; DB 6; Length 602;  
Best Local Similarity 81.5%; Pred. No. 3.9e-46;  
RESULT 1143  
ID ACL58593 standard; cDNA; 602 BP.  
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:4728.  
PN WO200500087-A2.  
PD 06-JAN-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 221.6; DB 14; Length 602;  
Best Local Similarity 81.5%; Pred. No. 3.9e-46;  
RESULT 1144  
ID AAI59074 standard; cDNA; 1426 BP.  
DE Human polynucleotide SEQ ID NO 1277.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.7%; Score 221.6; DB 4; Length 1426;  
Best Local Similarity 80.7%; Pred. No. 5.7e-46;  
RESULT 1145  
ID ADQ99297 standard; cDNA; 1426 BP.  
DE DNA encoding human GPCR-like protein seqid 967.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.7%; Score 221.6; DB 5; Length 1426;  
Best Local Similarity 80.7%; Pred. No. 5.7e-46;  
RESULT 1146  
ID ADB49057 standard; cDNA; 1426 BP.  
DE Novel human cDNA SEQ ID NO 967.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 9.7%; Score 221.6; DB 9; Length 1426;  
Best Local Similarity 80.7%; Pred. No. 5.7e-46;  
RESULT 1147  
ID ADM01487 standard; cDNA; 2345 BP.  
DE Human cDNA of the invention SEQ ID NO:172.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 221.6; DB 11; Length 2345;  
Best Local Similarity 85.0%; Pred. No. 7.1e-46;  
RESULT 1148  
ID AEC84417 standard; cDNA; 2345 BP.  
DE Human cDNA clone BRACE20228480, SEQ ID 172.  
PN EP1580263-A1.  
PD 28-SEP-2005.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 221.6; DB 14; Length 2345;  
Best Local Similarity 85.0%; Pred. No. 7.1e-46;  
RESULT 1149  
ID ADB63298 standard; cDNA; 2405 BP.  
DE Human cDNA encoding clone TESTI20057200.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 221.6; DB 10; Length 2405;  
Best Local Similarity 82.6%; Pred. No. 7.2e-46;  
RESULT 1150  
ID AAH14554 standard; cDNA; 2918 BP.  
DE Human cDNA sequence SEQ ID NO:12123.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.7%; Score 221.6; DB 4; Length 2918;  
Best Local Similarity 86.2%; Pred. No. 7.8e-46;  
RESULT 1151  
ID AEG92703 standard; cDNA; 2921 BP.

DE Human tumor cell cDNA SEQ ID NO:199.  
PN WO2006036025-A1.  
PD 06-APR-2006.  
PA (EISA ) EISAI CO LTD.  
Query Match 9.7%; Score 221.6; DB 15; Length 2921;  
Best Local Similarity 86.2%; Pred. No. 7.8e-46;  
RESULT 1152  
ID AEG55422 standard; DNA; 3102 BP..  
DE Human Kir6.2 genomic DNA.  
PN WO2006027128-A1.  
PD 16-MAR-2006.  
PA (SNFI ) SANOFI-AVENTIS DEUT GMBH.  
Query Match 9.7%; Score 221.6; DB 15; Length 3102;  
Best Local Similarity 82.6%; Pred. No. 8e-46;  
RESULT 1153  
ID AEE83655 standard; cDNA; 3807 BP.  
DE Human cDNA differentially expressed in asthma, SEQ ID NO:63.  
PN WO2005118403-A2.  
PD 15-DEC-2005.  
PA (LINK-) LINKAGENE LTD.  
Query Match 9.7%; Score 221.6; DB 15; Length 3807;  
Best Local Similarity 76.8%; Pred. No. 8.8e-46;  
RESULT 1154  
ID ABZ20987 standard; DNA; 5278 BP.  
DE Human thyroid tumour associated CAT-A genomic sequence SEQ ID NO: 12.  
PN WO200283727-A2.  
PD 24-OCT-2002.  
PA (BULL/) BULLERDIEK J.  
Query Match 9.7%; Score 221.6; DB 10; Length 5278;  
Best Local Similarity 81.5%; Pred. No. 1e-45;  
RESULT 1155  
ID ADX08890 standard; DNA; 7639 BP.  
DE Human matrix metalloproteinase 9 gene.  
PN WO2005017113-A2.  
PD 24-FEB-2005.  
PA (LOVE-) LOVEFACE RESPIRATORY RES INST.  
Query Match 9.7%; Score 221.6; DB 14; Length 7639;  
Best Local Similarity 85.0%; Pred. No. 1.2e-45;  
RESULT 1156  
ID AAK81565 standard; DNA; 14897 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:363377.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.6; DB 4; Length 14897;  
Best Local Similarity 76.8%; Pred. No. 1.6e-45;  
RESULT 1157  
ID AAK81510 standard; DNA; 15651 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:363322.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.6; DB 4; Length 15651;  
Best Local Similarity 86.2%; Pred. No. 1.7e-45;  
RESULT 1158  
ID ABN89476 standard; cDNA; 19806 BP.  
DE Human dehydrogenase genomic DNA SEQ ID NO:3.  
PN WO200250255-A2.  
PD 27-JUN-2002.  
PA (PEKE ) PE CORP NY.  
Query Match 9.7%; Score 221.6; DB 6; Length 19806;  
Best Local Similarity 86.2%; Pred. No. 1.8e-45;  
RESULT 1159  
ID ABD33092 standard; DNA; 21602 BP.  
DE Human cancer-associated (CA) gene HD07-006.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 221.6; DB 13; Length 21602;  
Best Local Similarity 76.3%; Pred. No. 1.9e-45;  
RESULT 1160  
ID AEJ13028 standard; DNA; 21602 BP.  
DE Cancer-associated gene sequence - SEQ ID 36.



PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.7%; Score 221.6; DB 15; Length 21602;  
Best Local Similarity 76.3%; Pred. No. 1.9e-45;  
RESULT 1161  
ID AAK89452 standard; DNA; 32192 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 3028.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.6; DB 4; Length 32192;  
Best Local Similarity 78.1%; Pred. No. 2.3e-45;  
RESULT 1162  
ID AED83346 standard; DNA; 38703 BP.  
DE Human cosmid clone cg/ml DNA, SEQ ID NO: 28.  
PN US2005255504-A1.  
PD 17-NOV-2005.  
PA (PARL/) PARL F F.  
Query Match 9.7%; Score 221.6; DB 14; Length 38703;  
Best Local Similarity 79.7%; Pred. No. 2.5e-45;  
RESULT 1163  
ID ABK84756 standard; cDNA; 81800 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1327.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 221.6; DB 6; Length 81800;  
Best Local Similarity 80.5%; Pred. No. 3.5e-45;  
RESULT 1164  
ID ADA02576 standard; DNA; 87878 BP.  
DE Human FKBP5 carcinoma associated gene, SEQ ID NO:1094.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221.6; DB 9; Length 87878;  
Best Local Similarity 82.6%; Pred. No. 3.6e-45;  
RESULT 1165  
ID ADB72314 standard; DNA; 87878 BP.  
DE Human FKBP5 gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221.6; DB 10; Length 87878;  
Best Local Similarity 82.6%; Pred. No. 3.6e-45;  
RESULT 1166  
ID ADE95824 standard; DNA; 87878 BP.  
DE Human FKBP5 gene genomic DNA sequence.  
PN WO2003039484-A2.  
PD 15-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221.6; DB 10; Length 87878;  
Best Local Similarity 82.6%; Pred. No. 3.6e-45;  
RESULT 1167  
ID AEK60095 standard; DNA; 87878 BP.  
DE Human FKBP5 genomic sequence, SEQ ID NO: 82.  
PN US2006204982-A1.  
PD 14-SEP-2006.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.7%; Score 221.6; DB 15; Length 87878;  
Best Local Similarity 82.6%; Pred. No. 3.6e-45;  
RESULT 1168  
ID ADX06943 standard; DNA; 103738 BP.  
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1508.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 9.7%; Score 221.6; DB 14; Length 103738;  
Best Local Similarity 78.1%; Pred. No. 3.9e-45;  
RESULT 1169  
Query Match 9.7%; Score 221.6; DB 14; Length 110000;

Best Local Similarity 81.5%; Pred. No. 4e-45;  
RESULT 1170  
ID ADS36461 standard; DNA; 158417 BP.  
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.7%; Score 221.6; DB 13; Length 158417;  
Best Local Similarity 83.8%; Pred. No. 4.7e-45;  
RESULT 1171  
ID ADL08127 standard; DNA; 166043 BP.  
DE Human gene associated with low HDL-C PDARG.  
PN US2004043389-A1.  
PD 04-MAR-2004.  
PA (VITI-) VITIVITY INC.  
Query Match 9.7%; Score 221.6; DB 12; Length 166043;  
Best Local Similarity 83.8%; Pred. No. 4.8e-45;  
RESULT 1172  
ID ADL13775 standard; DNA; 173805 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #307.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.7%; Score 221.6; DB 10; Length 173805;  
Best Local Similarity 82.7%; Pred. No. 4.9e-45;  
RESULT 1173  
ID ACC44402 standard; DNA; 1933 BP.  
DE Gene encoding human molecule for disease detection and treatment MDDT-15.  
PN WO2003031595-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.7%; Score 221.4; DB 8; Length 1933;  
Best Local Similarity 85.7%; Pred. No. 7.3e-46;  
RESULT 1174  
ID AEF03331 standard; cDNA; 1949 BP.  
DE KCNJ11 coding sequence.  
PN WO2005124343-A2.  
PD 29-DEC-2005.  
PA (GALA-) GALAPAGOS GENOMICS NV.  
Query Match 9.7%; Score 221.4; DB 15; Length 1949;  
Best Local Similarity 83.3%; Pred. No. 7.3e-46;  
RESULT 1175  
ID ADR10439 standard; cDNA; 3513 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 3945.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 221.4; DB 13; Length 3513;  
Best Local Similarity 83.3%; Pred. No. 9.6e-46;  
RESULT 1176  
ID ADX07495 standard; DNA; 5654 BP.  
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 2060.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 9.7%; Score 221.4; DB 14; Length 5654;  
Best Local Similarity 83.3%; Pred. No. 1.2e-45;  
RESULT 1177  
ID ABQ93471 standard; cDNA; 6170 BP.  
DE Human cDNA SEQ ID NO 184.  
PN WO200218424-A2.  
PD 07-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 9.7%; Score 221.4; DB 6; Length 6170;  
Best Local Similarity 83.3%; Pred. No. 1.2e-45;  
RESULT 1178  
ID AEI63044 standard; DNA; 6458 BP.  
DE Type-II diabetes susceptibility gene KCNJ11 - SEQ ID 30.  
PN CN1721549-A.  
PD 18-JAN-2006.  
PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.  
Query Match 9.7%; Score 221.4; DB 15; Length 6458;  
Best Local Similarity 83.3%; Pred. No. 1.3e-45;

RESULT 1179  
 ID AEI78937 standard; DNA; 6458 BP.  
 DE Type-II diabetes susceptibility gene KCNJ11.  
 PN CNI721550-A.  
 PD 18-JAN-2006.  
 PA (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.  
 Query Match 9.7%; Score 221.4; DB 15; Length 6458;  
 Best Local Similarity 83.3%; Pred. No. 1.3e-45;  
 RESULT 1180  
 ID ABA07082 standard; DNA; 9721 BP.  
 DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 401.  
 PN WO200155206-A1.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.7%; Score 221.4; DB 4; Length 9721;  
 Best Local Similarity 84.5%; Pred. No. 1.5e-45;  
 RESULT 1181  
 ID AAK89292 standard; DNA; 9721 BP.  
 DE Human digestive system antigen genomic sequence SEQ ID NO: 2868.  
 PN WO200155314-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.7%; Score 221.4; DB 4; Length 9721;  
 Best Local Similarity 84.5%; Pred. No. 1.5e-45;  
 RESULT 1182  
 ID AAK65483 standard; DNA; 11127 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20295.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.7%; Score 221.4; DB 4; Length 11127;  
 Best Local Similarity 82.2%; Pred. No. 1.6e-45;  
 RESULT 1183  
 ID AAL05506 standard; DNA; 11127 BP.  
 DE Human reproductive system related antigen DNA SEQ ID NO: 8194.  
 PN WO200155320-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.7%; Score 221.4; DB 4; Length 11127;  
 Best Local Similarity 82.2%; Pred. No. 1.6e-45;  
 RESULT 1184  
 ID AAA50353 standard; DNA; 12482 BP.  
 DE Human Goodpasture antigen binding protein gene.  
 PN WO200050607-A2.  
 PD 31-AUG-2000.  
 PA (SAUS/) SAUS J.  
 Query Match 9.7%; Score 221.4; DB 3; Length 12482;  
 Best Local Similarity 77.6%; Pred. No. 1.7e-45;  
 RESULT 1185  
 ID ABS64477 standard; DNA; 12482 BP.  
 DE Human Goodpasture binding protein, GPBP, genomic DNA.  
 PN WO200261430-A2.  
 PD 08-AUG-2002.  
 PA (SAUS/) SAUS J.  
 Query Match 9.7%; Score 221.4; DB 6; Length 12482;  
 Best Local Similarity 77.6%; Pred. No. 1.7e-45;  
 RESULT 1186  
 ID ADF69350 standard; DNA; 12482 BP.  
 DE Human Goodpasture antigen binding protein (GPBP) genomic DNA.  
 PN US2003054488-A1.  
 PD 20-MAR-2003.  
 PA (SAUS/) SAUS J.  
 Query Match 9.7%; Score 221.4; DB 10; Length 12482;  
 Best Local Similarity 77.6%; Pred. No. 1.7e-45;  
 RESULT 1187  
 ID AAK69721 standard; DNA; 16086 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24533.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.7%; Score 221.4; DB 4; Length 16086;  
 Best Local Similarity 84.5%; Pred. No. 1.9e-45;  
 RESULT 1188

ID AAL36020 standard; DNA; 16086 BP.  
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2385.  
 PN WO200155367-A1.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.7%; Score 221.4; DB 4; Length 16086;  
 Best Local Similarity 84.5%; Pred. No. 1.9e-45;  
 RESULT 1189  
 ID ABX59008 standard; CDNA; 16086 BP.  
 DE cDNA encoding novel human musculoskeletal system antigen #1352.  
 PN US2002147140-A1.  
 PD 10-OCT-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 9.7%; Score 221.4; DB 8; Length 16086;  
 Best Local Similarity 84.5%; Pred. No. 1.9e-45;  
 RESULT 1190  
 ID ADJ29758 standard; DNA; 16086 BP.  
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2385.  
 PN US2004009488-A1.  
 PD 15-JAN-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.7%; Score 221.4; DB 12; Length 16086;  
 Best Local Similarity 84.5%; Pred. No. 1.9e-45;  
 RESULT 1191  
 ID ABD33005 standard; DNA; 31840 BP.  
 DE Human cancer-associated genomic DNA HD21-026.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 9.7%; Score 221.4; DB 13; Length 31840;  
 Best Local Similarity 82.2%; Pred. No. 2.6e-45;  
 RESULT 1192  
 ID ABK84372 standard; CDNA; 37160 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #943.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 9.7%; Score 221.4; DB 6; Length 37160;  
 Best Local Similarity 87.0%; Pred. No. 2.8e-45;  
 RESULT 1193  
 ID AAL57448 standard; DNA; 39726 BP.  
 DE Human NSD1 genomic DNA sequence.  
 PN EP1321533-A2.  
 PD 25-JUN-2003.  
 PA (UYNA-) UNIV NAGASAKI.  
 Query Match 9.7%; Score 221.4; DB 9; Length 39726;  
 Best Local Similarity 79.1%; Pred. No. 2.8e-45;  
 RESULT 1194  
 ID ADB16926 standard; DNA; 50000 BP.  
 DE Human DYXC1 DNA, chromosomal gene region nucleotides 1-50000.  
 PN WO2003068814-A1.  
 PD 21-AUG-2003.  
 PA (LICN) LICENTIA LTD.  
 Query Match 9.7%; Score 221.4; DB 9; Length 50000;  
 Best Local Similarity 83.4%; Pred. No. 3.2e-45;  
 RESULT 1195  
 ID ADQ97986 standard; DNA; 86899 BP.  
 DE Human cancer associated sequence HD11-036, SEQ ID 963.  
 PN WO2004060304-A2.  
 PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 9.7%; Score 221.4; DB 12; Length 86899;  
 Best Local Similarity 82.3%; Pred. No. 4e-45;  
 RESULT 1196  
 ID ADQ19501 standard; DNA; 135005 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 9.7%; Score 221.4; DB 12; Length 135005;  
 Best Local Similarity 84.5%; Pred. No. 4.9e-45;

RESULT 1197  
ID AED89414 standard; DNA; 150450 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 54.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 221.4; DB 14; Length 150450;  
Best Local Similarity 84.5%; Pred. No. 5.2e-45;  
RESULT 1198  
ID AEF19127 standard; DNA; 188056 BP.  
DE Human NIPBL genomic sequence.  
PN US2006003354-A1.  
PD 05-JAN-2006.  
PA (KRAN/) KRANTZ I D.  
PA (JACK/) JACKSON L G.  
Query Match 9.7%; Score 221.4; DB 15; Length 188056;  
Best Local Similarity 88.0%; Pred. No. 5.7e-45;  
RESULT 1199  
ID AEA17302 standard; DNA; 197140 BP.  
DE Human GNAL gene locus Seq 12.  
PN WO2005047318-A1.  
PD 26-MAY-2005.  
PA (ASTR ) ASTRAZENECA AB.  
PA (ASTR ) ASTRAZENECA UK LTD.  
Query Match 9.7%; Score 221.4; DB 14; Length 197140;  
Best Local Similarity 84.5%; Pred. No. 5.8e-45;  
RESULT 1200  
ID AED89381 standard; DNA; 207908 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 21.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 221.4; DB 14; Length 207908;  
Best Local Similarity 85.7%; Pred. No. 6e-45;  
RESULT 1201  
ID AAH17100 standard; cDNA; 1803 BP.  
DE Human cDNA sequence SEQ ID NO:16426.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.7%; Score 221.2; DB 4; Length 1803;  
Best Local Similarity 85.4%; Pred. No. 8e-46;  
RESULT 1202  
ID AAS21879 standard; DNA; 1867 BP.  
DE Human collagen gene COL9A1 5' UTR.  
PN US6265157-B1.  
PD 24-JUL-2001.  
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
PA (UYOU-) UNIV OULU.  
Query Match 9.7%; Score 221.2; DB 5; Length 1867;  
Best Local Similarity 81.7%; Pred. No. 8.1e-46;  
RESULT 1203  
ID ABA14499 standard; DNA; 2229 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 6830.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 5; Length 2229;  
Best Local Similarity 85.2%; Pred. No. 8.8e-46;  
RESULT 1204  
ID AAK69791 standard; DNA; 2784 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24603.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 2784;  
Best Local Similarity 80.7%; Pred. No. 9.7e-46;  
RESULT 1205  
ID AAK69792 standard; DNA; 2787 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24604.  
PN WO200157182-A2.  
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 2787;  
Best Local Similarity 80.7%; Pred. No. 9.7e-46;  
RESULT 1206  
ID AAL05661 standard; DNA; 2787 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8349.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 2787;  
Best Local Similarity 80.7%; Pred. No. 9.7e-46;  
RESULT 1207  
ID ABA07987 standard; DNA; 2787 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 782.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 2787;  
Best Local Similarity 80.7%; Pred. No. 9.7e-46;  
RESULT 1208  
ID AAL36019 standard; DNA; 5930 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2384.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 5930;  
Best Local Similarity 85.2%; Pred. No. 1.4e-45;  
RESULT 1209  
ID ABX59007 standard; cDNA; 5930 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #1351.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.7%; Score 221.2; DB 8; Length 5930;  
Best Local Similarity 85.2%; Pred. No. 1.4e-45;  
RESULT 1210  
ID ADJ29757 standard; DNA; 5930 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2384.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 12; Length 5930;  
Best Local Similarity 85.2%; Pred. No. 1.4e-45;  
RESULT 1211  
ID ABZ09913 standard; DNA; 6289 BP.  
DE Human 5' and/or regulatory region of RBL2 DNA SEQ ID NO:53.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 9.7%; Score 221.2; DB 8; Length 6289;  
Best Local Similarity 86.5%; Pred. No. 1.4e-45;  
RESULT 1212  
ID ADE84033 standard; DNA; 9289 BP.  
DE 5' regulatory region of human gene RBL2.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 9.7%; Score 221.2; DB 10; Length 9289;  
Best Local Similarity 86.5%; Pred. No. 1.7e-45;  
RESULT 1213  
ID AAL05679 standard; DNA; 10680 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8367.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 10680;  
Best Local Similarity 80.4%; Pred. No. 1.8e-45;  
RESULT 1214  
ID AAK68712 standard; DNA; 11482 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23524.  
PN WO200157182-A2.

PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 11482;  
Best Local Similarity 78.7%; Pred. No. 1.8e-45;  
RESULT 1215  
ID AAK71246 standard; DNA; 11482 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26058.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 11482;  
Best Local Similarity 78.7%; Pred. No. 1.8e-45;  
RESULT 1216  
ID AEG35806 standard; DNA; 23880 BP.  
DE Human calcium channel 1D subunit G16155 allele DNA sequence SEQ ID NO: 4.  
PN JP2006067886-A.  
PD 16-MAR-2006.  
PA (HUMA-) ZH HUMAN SCI SHINKO ZAIDAN.  
Query Match 9.7%; Score 221.2; DB 15; Length 23880;  
Best Local Similarity 85.2%; Pred. No. 2.5e-45;  
RESULT 1217  
ID AEG35818 standard; DNA; 23880 BP.  
DE Human calcium channel 1D subunit A16155 allele DNA sequence.  
PN JP2006067886-A.  
PD 16-MAR-2006.  
PA (HUMA-) ZH HUMAN SCI SHINKO ZAIDAN.  
Query Match 9.7%; Score 221.2; DB 15; Length 23880;  
Best Local Similarity 85.2%; Pred. No. 2.5e-45;  
RESULT 1218  
ID AAS21771 standard; DNA; 24183 BP.  
DE Human gene for collagen COL9A1.  
PN US6265157-B1.  
PD 24-JUL-2001.  
PA (UYAL-) UNIV ALLEGHENY HEALTH SCI.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
PA (UYOU-) UNIV OULU.  
Query Match 9.7%; Score 221.2; DB 5; Length 24183;  
Best Local Similarity 81.7%; Pred. No. 2.6e-45;  
RESULT 1219  
ID ACN44954 standard; DNA; 31116 BP.  
DE Human genomic sequence hCG38622.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221.2; DB 11; Length 31116;  
Best Local Similarity 80.9%; Pred. No. 2.9e-45;  
RESULT 1220  
ID ADZ13255 standard; DNA; 31279 BP.  
DE Human cancer-associated genomic DNA #63.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 221.2; DB 14; Length 31279;  
Best Local Similarity 80.9%; Pred. No. 2.9e-45;  
RESULT 1221  
ID AAK77458 standard; DNA; 44196 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32270.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221.2; DB 4; Length 44196;  
Best Local Similarity 82.9%; Pred. No. 3.4e-45;  
RESULT 1222  
ID AEE05072 standard; DNA; 50244 BP.  
DE Cancer-associated gene SEQ ID NO:390.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 221.2; DB 14; Length 50244;  
Best Local Similarity 84.3%; Pred. No. 3.6e-45;  
RESULT 1223  
ID ADC87618 standard; DNA; 58366 BP.  
DE Human GPCR related polynucleotide SEQ ID NO:2071.

PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.7%; Score 221.2; DB 10; Length 58366;  
Best Local Similarity 86.5%; Pred. No. 3.8e-45;  
RESULT 1224  
ID ADA02540 standard; DNA; 58822 BP.  
DE Human TCOF1 carcinoma associated gene, SEQ ID NO:1058.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221.2; DB 9; Length 58822;  
Best Local Similarity 80.9%; Pred. No. 3.8e-45;  
RESULT 1225  
ID ADB72278 standard; DNA; 58822 BP.  
DE Human TCOF1 gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221.2; DB 10; Length 58822;  
Best Local Similarity 80.9%; Pred. No. 3.8e-45;  
RESULT 1226  
ID ADE95788 standard; DNA; 58822 BP.  
DE Human TCOF1 gene genomic DNA sequence.  
PN WO2003039484-A2.  
PD 15-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221.2; DB 10; Length 58822;  
Best Local Similarity 80.9%; Pred. No. 3.8e-45;  
RESULT 1227  
ID AEK60059 standard; DNA; 58822 BP.  
DE Human TCOF1 genomic sequence, SEQ ID NO:46.  
PN US2006204982-A1.  
PD 14-SEP-2006.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.7%; Score 221.2; DB 15; Length 58822;  
Best Local Similarity 80.9%; Pred. No. 3.8e-45;  
RESULT 1228  
ID ABQ88096 standard; cDNA; 92638 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 3.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC ) PROCTER & GAMBLE CO.  
Query Match 9.7%; Score 221.2; DB 6; Length 92638;  
Best Local Similarity 80.4%; Pred. No. 4.7e-45;  
RESULT 1229  
ID ADQ97313 standard; DNA; 121062 BP.  
DE Human cancer associated sequence HD08-030, SEQ ID 290.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 221.2; DB 12; Length 121062;  
Best Local Similarity 82.8%; Pred. No. 5.3e-45;  
RESULT 1230  
ID ADX06911 standard; DNA; 131078 BP.  
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1476.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 9.7%; Score 221.2; DB 14; Length 131078;  
Best Local Similarity 80.7%; Pred. No. 5.5e-45;  
RESULT 1231  
ID AEE04699 standard; DNA; 151790 BP.  
DE Cancer-associated gene SEQ ID NO:17.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 221.2; DB 14; Length 151790;  
Best Local Similarity 84.3%; Pred. No. 5.8e-45;  
RESULT 1232



ID ADQ59422 standard; DNA; 246940 BP.  
DE Human cancer-associated (CA) gene sequence SEQ ID NO:58.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 221.2; DB 12; Length 246940;  
Best Local Similarity 80.7%; Pred. No. 7.3e-45;  
RESULT 1233  
ID ADQ59416 standard; DNA; 337022 BP.  
DE Human cancer-associated (CA) gene sequence SEQ ID NO:52.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 221.2; DB 12; Length 337022;  
Best Local Similarity 85.2%; Pred. No. 8.4e-45;  
RESULT 1234  
ID ADZ13691 standard; DNA; 338780 BP.  
DE Human cancer-associated genomic DNA #105.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 221.2; DB 14; Length 338780;  
Best Local Similarity 85.2%; Pred. No. 8.4e-45;  
RESULT 1235  
ID ADC86642 standard; DNA; 349881 BP.  
DE Human GPCR gene SEQ ID NO:1095.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.7%; Score 221.2; DB 10; Length 349881;  
Best Local Similarity 86.5%; Pred. No. 8.5e-45;  
RESULT 1236  
ID ADQ64631 standard; cDNA; 1955 BP.  
DE Novel human cDNA sequence #1792.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 221; DB 12; Length 1955;  
Best Local Similarity 83.5%; Pred. No. 9.3e-46;  
RESULT 1237  
ID AAA40727 standard; DNA; 2561 BP.  
DE Wild type human CD36 nucleic acid sequence SEQ ID NO:101.  
PN WO200019883-A2.  
PD 13-APR-2000.  
PA (MEDI-) MEDICAL RES COUNCIL.  
PA (SCIO-) SCIOS INC.  
PA (AITM/) AITMAN T J.  
PA (SCOT/) SCOTT J.  
PA (STAN/) STANTON L W.  
Query Match 9.7%; Score 221; DB 3; Length 2561;  
Best Local Similarity 84.7%; Pred. No. 1.1e-45;  
RESULT 1238  
ID AAA40745 standard; DNA; 2561 BP.  
DE Wild type human CD36 nucleic acid sequence SEQ ID NO:119.  
PN WO200019883-A2.  
PD 13-APR-2000.  
PA (MEDI-) MEDICAL RES COUNCIL.  
PA (SCIO-) SCIOS INC.  
PA (AITM/) AITMAN T J.  
PA (SCOT/) SCOTT J.  
PA (STAN/) STANTON L W.  
Query Match 9.7%; Score 221; DB 3; Length 2561;  
Best Local Similarity 84.7%; Pred. No. 1.1e-45;  
RESULT 1239  
ID ADL13540 standard; DNA; 2561 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #72.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.7%; Score 221; DB 10; Length 2561;  
Best Local Similarity 84.7%; Pred. No. 1.1e-45;  
RESULT 1240

ID ADO15852 standard; DNA; 3442 BP.  
DE 4 synthesis-period of neuroblastoma related DNA, SEQ ID 114.  
PN WO2004039975-A1.  
PD 13-MAY-2004.  
PA (HISM ) HISAMITSU PHARM CO LTD.  
PA (CHIB-) CHIBA PREFECTURE.  
Query Match 9.7%; Score 221; DB 12; Length 3442;  
Best Local Similarity 82.4%; Pred. No. 1.2e-45;  
RESULT 1241  
ID ADQ63041 standard; cDNA; 4161 BP.  
DE Novel human cDNA sequence #202.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 221; DB 12; Length 4161;  
Best Local Similarity 83.5%; Pred. No. 1.3e-45;  
RESULT 1242  
ID ADG32780 standard; DNA; 5957 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID104.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Query Match 9.7%; Score 221; DB 10; Length 5957;  
Best Local Similarity 80.2%; Pred. No. 1.5e-45;  
RESULT 1243  
ID ADR24391 standard; DNA; 5957 BP.  
DE Breast cancer prognosis marker #252.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Query Match 9.7%; Score 221; DB 13; Length 5957;  
Best Local Similarity 80.2%; Pred. No. 1.5e-45;  
RESULT 1244  
ID AAK78524 standard; DNA; 8912 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33336.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221; DB 4; Length 8912;  
Best Local Similarity 71.4%; Pred. No. 1.8e-45;  
RESULT 1245  
ID AAK78525 standard; DNA; 9857 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33337.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221; DB 4; Length 9857;  
Best Local Similarity 71.4%; Pred. No. 1.9e-45;  
RESULT 1246  
ID AAL05479 standard; DNA; 9857 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8167.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221; DB 4; Length 9857;  
Best Local Similarity 71.4%; Pred. No. 1.9e-45;  
RESULT 1247  
ID ABL98332 standard; DNA; 9857 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2984.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221; DB 4; Length 9857;  
Best Local Similarity 71.4%; Pred. No. 1.9e-45;  
RESULT 1248  
ID ADB99091 standard; cDNA; 14581 BP.  
DE Human retinal pigment epithelial-derived factor (PEDF) genomic DNA #1.  
PN US2003096750-A1.  
PD 22-MAY-2003.  
PA (TOMB/) TOMBRAN-TINK J.  
PA (STEE/) STEELE F R.  
PA (CHAD/) CHADER G J.

PA (BECE/) BECERRA S P.  
PA (JOHN/) JOHNSON L V.  
PA (RODR/) RODRIGUEZ I R.  
Query Match 9.7%; Score 221; DB 10; Length 14581;  
Best Local Similarity 84.7%; Pred. No. 2.3e-45;  
RESULT 1249  
ID ABS57267 standard; DNA; 14581 BP.  
DE Partial sequence #1 of genomic DNA encoding human PEDF.  
PN US6451763-B1.  
PD 17-SEP-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 9.7%; Score 221; DB 10; Length 14581;  
Best Local Similarity 84.7%; Pred. No. 2.3e-45;  
RESULT 1250  
ID AAS34685 standard; DNA; 19205 BP.  
DE Human DNA for a novel foetal antigen, SEQ ID NO 2109.  
PN WO200155312-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221; DB 5; Length 19205;  
Best Local Similarity 87.0%; Pred. No. 2.6e-45;  
RESULT 1251  
ID AAK90824 standard; DNA; 21393 BP.  
DE Human digestive system antigen genomic sequence SEQ ID NO: 4400.  
PN WO200155314-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 221; DB 4; Length 21393;  
Best Local Similarity 82.4%; Pred. No. 2.7e-45;  
RESULT 1252  
ID AAT11658 standard; DNA; 22481 BP.  
DE PEDF full length sequence and flanking sequences.  
PN WO9533480-A1.  
PD 14-DEC-1995.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 9.7%; Score 221; DB 5; Length 21393;  
Best Local Similarity 82.4%; Pred. No. 2.7e-45;  
RESULT 1253  
ID AAT11658 standard; DNA; 22481 BP.  
DE PEDF full length sequence and flanking sequences.  
PN WO9533480-A1.  
PD 14-DEC-1995.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 9.7%; Score 221; DB 2; Length 22481;  
Best Local Similarity 84.7%; Pred. No. 2.8e-45;  
RESULT 1254  
ID ABA98882 standard; DNA; 22484 BP.  
DE Nucleotide sequence related to the SLED sequence of the invention.  
PN US200202131-A1.  
PD 03-JAN-2002.  
PA (BOUC/) BOUCK N P.  
PA (DAWS/) DAWSON D W.  
PA (GILL/) GILLIS P R.  
Query Match 9.7%; Score 221; DB 6; Length 22484;  
Best Local Similarity 84.7%; Pred. No. 2.8e-45;  
RESULT 1255  
ID ABA05882 standard; DNA; 22484 BP.  
DE Angiogenesis inhibition method related DNA.  
PN US2001049355-A1.  
PD 06-DEC-2001.  
PA (BOUC/) BOUCK N P.  
PA (DAWS/) DAWSON D W.  
PA (GILL/) GILLIS P R.  
Query Match 9.7%; Score 221; DB 6; Length 22484;  
Best Local Similarity 84.7%; Pred. No. 2.8e-45;  
RESULT 1256  
ID ABQ88196 standard; cDNA; 22484 BP.  
DE Human osteoblast differentiation related cDNA SEQ ID NO 103.  
PN WO200250301-A2.  
PD 27-JUN-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (PROC ) PROCTER & GAMBLE CO.  
Query Match 9.7%; Score 221; DB 6; Length 22484;  
Best Local Similarity 84.7%; Pred. No. 2.8e-45;

RESULT 1257  
ID ABN96844 standard; DNA; 22484 BP.  
DE Gene #3342 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 221; DB 6; Length 22484;  
Best Local Similarity 84.7%; Pred. No. 2.8e-45;  
RESULT 1258  
ID ABK14446 standard; DNA; 26201 BP.  
DE Human HMGCL gene, generic sequence.  
PN WO200198315-A2.  
PD 27-DEC-2001.  
PA (GENA-) GENAISANCE PHARM INC.  
Query Match 9.7%; Score 221; DB 6; Length 26201;  
Best Local Similarity 83.5%; Pred. No. 3e-45;  
RESULT 1259  
ID ABK14039 standard; DNA; 26201 BP.  
DE Human 3-hydroxy-3-methylglutaryl coenzyme A lyase (HMGCL) gene sequence.  
PN WO200198315-A2.  
PD 27-DEC-2001.  
PA (GENA-) GENAISANCE PHARM INC.  
Query Match 9.7%; Score 221; DB 6; Length 26201;  
Best Local Similarity 83.5%; Pred. No. 3e-45;  
RESULT 1260  
ID ABS54327 standard; DNA; 32654 BP.  
DE Gene encoding human kinase.  
Query Match 9.7%; Score 221; DB 6; Length 32654;  
Best Local Similarity 85.0%; Pred. No. 3.3e-45;  
RESULT 1261  
ID ABZ09862 standard; DNA; 35962 BP.  
DE Human 5' and/or regulatory region of ABL1 DNA SEQ ID NO:2.  
PN WO20027272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 9.7%; Score 221; DB 8; Length 35962;  
Best Local Similarity 83.5%; Pred. No. 3.4e-45;  
RESULT 1262  
ID ADL13478 standard; DNA; 35962 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #10.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.7%; Score 221; DB 10; Length 35962;  
Best Local Similarity 83.5%; Pred. No. 3.4e-45;  
RESULT 1263  
ID ADR52883 standard; DNA; 35962 BP.  
DE Drug therapy altered expressed gene #234.  
PN WO2004072265-A2.  
PD 26-AUG-2004.  
PA (AMHP ) WYETH.  
PA (BURC/) BURCZYNSKI M.  
PA (TWIN/) TWINE N.  
PA (DORN/) DORNER A J.  
PA (TREP/) TREPICCHIO W L.  
Query Match 9.7%; Score 221; DB 13; Length 35962;  
Best Local Similarity 83.5%; Pred. No. 3.4e-45;  
RESULT 1264  
Query Match 9.7%; Score 221; DB 10; Length 54391;  
Best Local Similarity 82.4%; Pred. No. 4.1e-45;  
RESULT 1265  
Query Match 9.7%; Score 221; DB 14; Length 54396;  
Best Local Similarity 82.4%; Pred. No. 4.1e-45;  
RESULT 1266  
ID ACN44198 standard; DNA; 63313 BP.  
DE Human genomic sequence hCG19397.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221; DB 11; Length 63313;  
Best Local Similarity 86.0%; Pred. No. 4.4e-45;  
RESULT 1267  
ID ACN44362 standard; DNA; 68255 BP.

DE Human genomic sequence hCG39597.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221; DB 11; Length 68255;  
Best Local Similarity 80.3%; Pred. No. 4.6e-45;  
RESULT 1268  
ID ADZ10962 standard; DNA; 74424 BP.  
DE Human STAT3 DNA sequence - SEQ ID 153.  
PN US2005074879-A1.  
PD 07-APR-2005.  
PA (KARR/) KARRAS J G.  
Query Match 9.7%; Score 221; DB 14; Length 74424;  
Best Local Similarity 82.4%; Pred. No. 4.8e-45;  
RESULT 1269  
ID AEK52879 standard; DNA; 74424 BP.  
DE Human chromosome 17 genomic contig DNA SEQ ID: 153.  
PN US2006217339-A1.  
PD 28-SEP-2006.  
PA (KARR/) KARRAS J G.  
Query Match 9.7%; Score 221; DB 15; Length 74424;  
Best Local Similarity 82.4%; Pred. No. 4.8e-45;  
RESULT 1270  
ID AEG05665 standard; DNA; 79950 BP.  
DE Human FLJ14297 genomic DNA SEQ ID NO 2.  
PN WO2006022629-A1.  
PD 02-MAR-2006.  
PA (SEQU-) SEQUENOM INC.  
Query Match 9.7%; Score 221; DB 15; Length 79950;  
Best Local Similarity 63.2%; Pred. No. 4.9e-45;  
RESULT 1271  
ID ABD32673 standard; DNA; 91359 BP.  
DE Human cancer-associated genomic DNA HD13-075.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 221; DB 13; Length 91359;  
Best Local Similarity 81.3%; Pred. No. 5.2e-45;  
RESULT 1272  
Query Match 9.7%; Score 221; DB 4; Length 110000;  
Best Local Similarity 81.6%; Pred. No. 5.7e-45;  
RESULT 1273  
Query Match 9.7%; Score 221; DB 4; Length 110000;  
Best Local Similarity 81.6%; Pred. No. 5.7e-45;  
RESULT 1274  
Query Match 9.7%; Score 221; DB 6; Length 110000;  
Best Local Similarity 81.6%; Pred. No. 5.7e-45;  
RESULT 1275  
Query Match 9.7%; Score 221; DB 6; Length 110000;  
Best Local Similarity 81.6%; Pred. No. 5.7e-45;  
RESULT 1276  
Query Match 9.7%; Score 221; DB 11; Length 110000;  
Best Local Similarity 81.6%; Pred. No. 5.7e-45;  
RESULT 1277  
Query Match 9.7%; Score 221; DB 12; Length 110000;  
Best Local Similarity 81.6%; Pred. No. 5.7e-45;  
RESULT 1278  
ID AEE04879 standard; DNA; 681142 BP.  
DE Cancer-associated gene SEQ ID NO:197.  
PN WO2005107396-A2.  
PD 17-NOV-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 221; DB 14; Length 110000;  
Best Local Similarity 84.7%; Pred. No. 5.7e-45;  
RESULT 1279  
ID ABN95044 standard; DNA; 110096 BP.  
DE Gene #1542 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 221; DB 6; Length 110096;  
Best Local Similarity 83.5%; Pred. No. 5.7e-45;  
RESULT 1280

ID AED18046 standard; DNA; 110096 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 297.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 9.7%; Score 221; DB 14; Length 110096;  
Best Local Similarity 83.5%; Pred. No. 5.7e-45;  
RESULT 1281  
ID AEF74649 standard; DNA; 110096 BP.  
DE Human polynucleotide #163.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.7%; Score 221; DB 15; Length 110096;  
Best Local Similarity 83.5%; Pred. No. 5.7e-45;  
RESULT 1282  
ID AEF74540 standard; DNA; 110096 BP.  
DE Human polynucleotide #54.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.7%; Score 221; DB 15; Length 110096;  
Best Local Similarity 83.5%; Pred. No. 5.7e-45;  
RESULT 1283  
ID AEF74955 standard; DNA; 110096 BP.  
DE Human polynucleotide #469.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Query Match 9.7%; Score 221; DB 15; Length 110096;  
Best Local Similarity 83.5%; Pred. No. 5.7e-45;  
RESULT 1284  
ID ADP84158 standard; DNA; 129017 BP.  
DE Human AST-1 locus DNA representing part of the GPRA gene SeqID 1.  
Query Match 9.7%; Score 221; DB 12; Length 129017;  
Best Local Similarity 81.3%; Pred. No. 6.1e-45;  
RESULT 1285  
ID ADX06911 standard; DNA; 131078 BP.  
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1476.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 9.7%; Score 221; DB 14; Length 131078;  
Best Local Similarity 86.0%; Pred. No. 6.2e-45;  
RESULT 1286  
ID ACF62732 standard; DNA; 177531 BP.  
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:660.  
PN WO2003013534-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 221; DB 8; Length 177531;  
Best Local Similarity 82.4%; Pred. No. 7.1e-45;  
RESULT 1287  
ID ADB20847 standard; DNA; 177531 BP.  
DE MRP1 based cancer related nucleic acid SEQ ID NO:660.  
PN WO2003013533-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 221; DB 8; Length 177531;  
Best Local Similarity 82.4%; Pred. No. 7.1e-45;  
RESULT 1288  
ID ADB87936 standard; DNA; 177531 BP.  
DE Human UGT1A1 gene sequence SEQ ID NO:660.  
PN WO2003013536-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 221; DB 10; Length 177531;  
Best Local Similarity 82.4%; Pred. No. 7.1e-45;  
RESULT 1289  
ID ADB96919 standard; DNA; 177531 BP.

DE Human MDR1 related DNA sequence SEQ ID NO:660.  
PN WO2003013537-A2.  
PA (EPID-) EPIDAUS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 221; DB 10; Length 177531;  
Best Local Similarity 82.4%; Pred. No. 7.1e-45;  
RESULT 1290  
ID ADB92110 standard; DNA; 177531 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:660.  
PN WO2003013535-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAUS BIOTECHNOLOGIE AG.  
Query Match 9.7%; Score 221; DB 10; Length 177531;  
Best Local Similarity 82.4%; Pred. No. 7.1e-45;  
RESULT 1291  
ID ADH74617 standard; DNA; 177531 BP.  
DE Human BAC clone GS1-259H13 CYP3A5 genomic DNA.  
PN US2003143537-A1.  
PD 31-JUL-2003.  
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
Query Match 9.7%; Score 221; DB 10; Length 177531;  
Best Local Similarity 82.4%; Pred. No. 7.1e-45;  
RESULT 1292  
ID ACN44170 standard; DNA; 196686 BP.  
DE Human genomic sequence hCG39530.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221; DB 11; Length 196686;  
Best Local Similarity 80.2%; Pred. No. 7.4e-45;  
RESULT 1293  
ID AEF85801 standard; DNA; 207740 BP.  
DE Human chromosome 20 partial genomic sequence SEQ ID NO:1.  
PN JP2006042735-A.  
PD 16-FEB-2006.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.  
PA (MABU/) MABUCHI A.  
Query Match 9.7%; Score 221; DB 15; Length 207740;  
Best Local Similarity 86.0%; Pred. No. 7.6e-45;  
RESULT 1294  
ID ACN44046 standard; DNA; 260027 BP.  
DE Human genomic sequence hCG1735292.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 221; DB 11; Length 260027;  
Best Local Similarity 86.0%; Pred. No. 8.4e-45;  
RESULT 1295  
ID ADE86352 standard; DNA; 300000 BP.  
DE Human PTPN11 genomic DNA sequence SEQ ID NO:33.  
PN WO2003029422-A2.  
PD 10-APR-2003.  
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.  
Query Match 9.7%; Score 221; DB 10; Length 300000;  
Best Local Similarity 83.5%; Pred. No. 8.9e-45;  
RESULT 1296  
ID ADO14076 standard; DNA; 300001 BP.  
DE Human protein tyrosine phosphatase 11 gene sequence SEQ ID NO:33.  
PN WO2004041216-A2.  
PD 21-MAY-2004.  
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.  
PA (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.  
Query Match 9.7%; Score 221; DB 12; Length 300001;  
Best Local Similarity 83.5%; Pred. No. 8.9e-45;  
RESULT 1297  
ID ABL86091 standard; cDNA; 392 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:9069.  
PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 9.7%; Score 220.8; DB 6; Length 392;  
Best Local Similarity 84.0%; Pred. No. 5.1e-46;  
RESULT 1298

ID ACH74861 standard; DNA; 573 BP.  
DE Human genome derived single exon probe #8056.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 9.7%; Score 220.8; DB 12; Length 573;  
Best Local Similarity 77.0%; Pred. No. 6e-46;  
RESULT 1299  
ID AAL07263 standard; DNA; 1367 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9951.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 4; Length 1367;  
Best Local Similarity 85.4%; Pred. No. 8.9e-46;  
RESULT 1300  
ID ABL98809 standard; DNA; 1367 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3461.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 4; Length 1367;  
Best Local Similarity 85.4%; Pred. No. 8.9e-46;  
RESULT 1301  
ID ADD18515 standard; DNA; 2227 BP.  
DE Human prostate cancer diagnosis related DNA sequence SeqID87.  
PN WO2003012067-A2.  
PD 13-FEB-2003.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 9.7%; Score 220.8; DB 10; Length 2227;  
Best Local Similarity 84.3%; Pred. No. 1.1e-45;  
RESULT 1302  
ID ADR67013 standard; cDNA; 2502 BP.  
DE Human cancer associated gene cDNA sequence SEQ ID NO:59.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 220.8; DB 13; Length 2502;  
Best Local Similarity 84.3%; Pred. No. 1.2e-45;  
RESULT 1303  
ID ADZ12882 standard; cDNA; 2502 BP.  
DE Human cancer-associated cDNA #120.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR) CHIRON CORP.  
Query Match 9.7%; Score 220.8; DB 14; Length 2502;  
Best Local Similarity 84.3%; Pred. No. 1.2e-45;  
RESULT 1304  
ID ADR08039 standard; cDNA; 3071 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1545.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 9.7%; Score 220.8; DB 13; Length 3071;  
Best Local Similarity 83.0%; Pred. No. 1.3e-45;  
RESULT 1305  
ID ACN44535 standard; cDNA; 4779 BP.  
DE Human mRNA sequence hCT29338.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 11; Length 4779;  
Best Local Similarity 84.5%; Pred. No. 1.6e-45;  
RESULT 1306  
ID ABA15436 standard; DNA; 11726 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7767.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 5; Length 11726;  
Best Local Similarity 83.3%; Pred. No. 2.3e-45;



RESULT 1307  
ID ABZ73812 standard; DNA; 11726 BP.  
DE Secreted protein gene 54 genomic fragment HCE1G78, SEQ ID NO:959.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 8; Length 11726;  
Best Local Similarity 83.3%; Pred. No. 2.3e-45;  
RESULT 1308  
ID ADA98478 standard; DNA; 11726 BP.  
DE Human secreted protein-related DNA sequence #71.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 8; Length 11726;  
Best Local Similarity 83.3%; Pred. No. 2.3e-45;  
RESULT 1309  
ID AAS33411 standard; DNA; 18595 BP.  
DE DNA encoding human secreted protein, Seq ID No 694.  
PN WO200155326-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 4; Length 18595;  
Best Local Similarity 76.2%; Pred. No. 2.9e-45;  
RESULT 1310  
ID AAL37007 standard; DNA; 18966 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3372.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 4; Length 18966;  
Best Local Similarity 85.4%; Pred. No. 2.9e-45;  
RESULT 1311  
ID ABA20628 standard; DNA; 18966 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12959.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 5; Length 18966;  
Best Local Similarity 85.4%; Pred. No. 2.9e-45;  
RESULT 1312  
ID ABX59995 standard; cDNA; 18966 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #2339.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.7%; Score 220.8; DB 8; Length 18966;  
Best Local Similarity 85.4%; Pred. No. 2.9e-45;  
RESULT 1313  
ID ADJ30745 standard; DNA; 18966 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3372.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 12; Length 18966;  
Best Local Similarity 85.4%; Pred. No. 2.9e-45;  
RESULT 1314  
ID ACN43982 standard; DNA; 24898 BP.  
DE Human genomic sequence hCG23625.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 11; Length 24898;  
Best Local Similarity 84.3%; Pred. No. 3.3e-45;  
RESULT 1315  
ID AAD47150 standard; DNA; 31814 BP.  
DE Human Ras-like protein encoding gene.  
PN WO200277190-A2.  
PD 03-OCT-2002.  
PA (PEKE ) PE CORP NY.  
Query Match 9.7%; Score 220.8; DB 10; Length 31814;

Best Local Similarity 84.2%; Pred. No. 3.7e-45;  
RESULT 1316  
ID AAS30619 standard; DNA; 31994 BP.  
DE DNA encoding novel lung cancer antigen, Seq ID No 71.  
PN WO200155300-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 4; Length 31994;  
Best Local Similarity 76.7%; Pred. No. 3.7e-45;  
RESULT 1317  
ID AAS28165 standard; DNA; 31994 BP.  
DE Genomic sequence #5 encoding for novel human respiratory antigen.  
PN WO200155448-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 4; Length 31994;  
Best Local Similarity 76.7%; Pred. No. 3.7e-45;  
RESULT 1318  
ID ACA03382 standard; DNA; 31994 BP.  
DE DNA encoding human lung cancer antigen HCLCR09.  
PN US2002173454-A1.  
PD 21-NOV-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.7%; Score 220.8; DB 8; Length 31994;  
Best Local Similarity 76.7%; Pred. No. 3.7e-45;  
RESULT 1319  
ID ADB96730 standard; DNA; 31994 BP.  
DE Novel lung cancer antigen genomic DNA #1.  
PN US2003049703-A1.  
PD 13-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 9; Length 31994;  
Best Local Similarity 76.7%; Pred. No. 3.7e-45;  
RESULT 1320  
ID ADG41361 standard; DNA; 31994 BP.  
DE Human respiratory system associated genomic DNA seq id 599.  
PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 10; Length 31994;  
Best Local Similarity 76.7%; Pred. No. 3.7e-45;  
RESULT 1321  
ID ADI97135 standard; DNA; 31994 BP.  
DE Human respiratory system associated polypeptide-related DNA SeqID599.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 11; Length 31994;  
Best Local Similarity 76.7%; Pred. No. 3.7e-45;  
RESULT 1322  
ID AAS36516 standard; DNA; 32219 BP.  
DE Human cardiovascular system antigen genomic DNA SEQ ID No 2016.  
PN WO200155321-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 4; Length 32219;  
Best Local Similarity 79.1%; Pred. No. 3.7e-45;  
RESULT 1323  
ID ADE47210 standard; DNA; 32219 BP.  
DE Human cardiovascular system related genomic DNA #776.  
PN US2003059908-A1.  
PD 27-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.8; DB 10; Length 32219;  
Best Local Similarity 79.1%; Pred. No. 3.7e-45;  
RESULT 1324  
ID ADJ08628 standard; DNA; 32219 BP.  
DE Human cardiovascular system associated-polypeptide-related DNA SeqID2016.  
PN US2004005575-A1.  
PD 08-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.7%; Score 220.8; DB 13; Length 32219;  
Best Local Similarity 79.1%; Pred. No. 3.7e-45;  
RESULT 1325  
ID ADR67012 standard; DNA; 32229 BP.  
DE Human cancer associated gene genomic sequence SEQ ID NO:58.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 220.8; DB 13; Length 32229;  
Best Local Similarity 84.3%; Pred. No. 3.7e-45;  
RESULT 1326  
ID ADZ12877 standard; DNA; 32229 BP.  
DE Human cancer-associated genomic DNA #34.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 220.8; DB 14; Length 32229;  
Best Local Similarity 84.3%; Pred. No. 3.7e-45;  
RESULT 1327  
ID ACN44534 standard; DNA; 39768 BP.  
DE Human genomic sequence hCG38101.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 11; Length 39768;  
Best Local Similarity 84.5%; Pred. No. 4.1e-45;  
RESULT 1328  
ID ACN44798 standard; DNA; 40491 BP.  
DE Human genomic sequence hCG41911.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 11; Length 40491;  
Best Local Similarity 83.1%; Pred. No. 4.1e-45;  
RESULT 1329  
ID ADA02858 standard; DNA; 53795 BP.  
DE Human LMO2 carcinoma associated gene, SEQ ID NO:1376.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 9; Length 53795;  
Best Local Similarity 83.0%; Pred. No. 4.6e-45;  
RESULT 1330  
ID ADB72596 standard; DNA; 53795 BP.  
DE Human LMO2 gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 10; Length 53795;  
Best Local Similarity 83.0%; Pred. No. 4.6e-45;  
RESULT 1331  
ID ADC85337 standard; DNA; 53795 BP.  
DE Mouse Lmo2 coding sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 10; Length 53795;  
Best Local Similarity 83.0%; Pred. No. 4.6e-45;  
RESULT 1332  
ID ADM74453 standard; DNA; 53795 BP.  
DE Human carcinoma associated (CA) nucleic acid #61.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.7%; Score 220.8; DB 12; Length 53795;  
Best Local Similarity 83.0%; Pred. No. 4.6e-45;  
RESULT 1333  
ID ADC87426 standard; DNA; 59588 BP.  
DE Human GPCR gene SEQ ID NO:1879.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.7%; Score 220.8; DB 10; Length 59588;  
Best Local Similarity 82.1%; Pred. No. 4.9e-45;  
RESULT 1334  
ID ABX13172 standard; DNA; 65464 BP.  
DE Human gene encoding a Noelin-1-like secreted protein.  
PN US2002173459-A1.  
PD 21-NOV-2002.  
PA (PEKE ) PE CORP NY.  
Query Match 9.7%; Score 220.8; DB 8; Length 65464;  
Best Local Similarity 85.7%; Pred. No. 5.1e-45;  
RESULT 1335  
ID ACN44450 standard; DNA; 75252 BP.  
DE Human genomic sequence hCG27772.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 11; Length 75252;  
Best Local Similarity 80.8%; Pred. No. 5.4e-45;  
RESULT 1336  
ID ADC85476 standard; DNA; 96594 BP.  
DE Human Msf genomic sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 10; Length 96594;  
Best Local Similarity 85.4%; Pred. No. 6e-45;  
RESULT 1337  
ID ADE95974 standard; DNA; 96594 BP.  
DE Human SYK gene genomic DNA sequence.  
PN WO2003039484-A2.  
PD 15-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 10; Length 96594;  
Best Local Similarity 85.4%; Pred. No. 6e-45;  
RESULT 1338  
ID ADA02726 standard; DNA; 96595 BP.  
DE Human SYK carcinoma associated gene, SEQ ID NO:1244.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 9; Length 96595;  
Best Local Similarity 85.4%; Pred. No. 6e-45;  
RESULT 1339  
ID ADA02996 standard; DNA; 96595 BP.  
DE Human Msf carcinoma associated gene, SEQ ID NO:1514.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 9; Length 96595;  
Best Local Similarity 85.4%; Pred. No. 6e-45;  
RESULT 1340  
ID ADB72464 standard; DNA; 96595 BP.  
DE Human SYK gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 10; Length 96595;  
Best Local Similarity 85.4%; Pred. No. 6e-45;  
RESULT 1341  
ID ADB72734 standard; DNA; 96595 BP.  
DE Human Msf gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.8; DB 10; Length 96595;  
Best Local Similarity 85.4%; Pred. No. 6e-45;  
RESULT 1342  
ID ADM74591 standard; DNA; 96595 BP.  
DE Human carcinoma associated (CA) nucleic acid #130.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR/) MORRIS D W.

PA (ENGE/) ENGELHARD E K.  
Query Match 9.7%; Score 220.8; DB 12; Length 96595;  
Best Local Similarity 85.4%; Pred. No. 6e-45;  
RESULT 1343  
ID AEK60245 standard; DNA; 96595 BP.  
DE Human SYK genomic sequence, SEQ ID NO: 232.  
PN US2006204982-A1.  
PD 14-SEP-2006.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Query Match 9.7%; Score 220.8; DB 15; Length 96595;  
Best Local Similarity 85.4%; Pred. No. 6e-45;  
RESULT 1344  
ID ABN96931 standard; DNA; 99014 BP.  
DE Gene #3429 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 220.8; DB 6; Length 99014;  
Best Local Similarity 81.9%; Pred. No. 6.1e-45;  
RESULT 1345  
Query Match 9.7%; Score 220.8; DB 4; Length 110000;  
Best Local Similarity 83.7%; Pred. No. 6.4e-45;  
RESULT 1346  
Query Match 9.7%; Score 220.8; DB 4; Length 110000;  
Best Local Similarity 83.7%; Pred. No. 6.4e-45;  
RESULT 1347  
Query Match 9.7%; Score 220.8; DB 6; Length 110000;  
Best Local Similarity 83.7%; Pred. No. 6.4e-45;  
RESULT 1348  
Query Match 9.7%; Score 220.8; DB 6; Length 110000;  
Best Local Similarity 83.7%; Pred. No. 6.4e-45;  
RESULT 1349  
ID ABQ83210 standard; DNA; 397658 BP.  
DE Human transporter protein genomic DNA SEQ ID NO:3.  
Query Match 9.7%; Score 220.8; DB 8; Length 110000;  
Best Local Similarity 83.3%; Pred. No. 6.4e-45;  
RESULT 1350  
Query Match 9.7%; Score 220.8; DB 11; Length 110000;  
Best Local Similarity 83.7%; Pred. No. 6.4e-45;  
RESULT 1351  
Query Match 9.7%; Score 220.8; DB 12; Length 110000;  
Best Local Similarity 83.7%; Pred. No. 6.4e-45;  
RESULT 1352  
ID ABK83567 standard; cDNA; 112460 BP.  
DE Human cDNA differentially expressed in granulocytic cells #138.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.7%; Score 220.8; DB 6; Length 112460;  
Best Local Similarity 80.8%; Pred. No. 6.5e-45;  
RESULT 1353  
ID AEF92731 standard; DNA; 112460 BP.  
DE Human chromosome 22 sequence, contains MGAT3 gene.  
PN WO2006020269-A2.  
PD 23-FEB-2006.  
PA (UYRP ) UNIV ROCHESTER.  
Query Match 9.7%; Score 220.8; DB 15; Length 112460;  
Best Local Similarity 80.8%; Pred. No. 6.5e-45;  
RESULT 1354  
ID ABD32872 standard; DNA; 130244 BP.  
DE Human cancer-associated genomic DNA HD17-083.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.7%; Score 220.8; DB 13; Length 130244;  
Best Local Similarity 86.7%; Pred. No. 6.9e-45;  
RESULT 1355  
ID AAD54538 standard; DNA; 133893 BP.  
DE Human phosphatidylinositol biphosphate (PIB) DNA #1.  
PN WO200299125-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.

Query Match 9.7%; Score 220.8; DB 9; Length 133893;  
Best Local Similarity 83.3%; Pred. No. 7e-45;  
RESULT 1356  
ID AAZ93815 standard; DNA; 144460 BP.  
DE Olfactory receptor operon.  
PN WO200021985-A2.  
PD 20-APR-2000.  
PA (GEST ) GENSET.  
Query Match 9.7%; Score 220.8; DB 3; Length 144460;  
Best Local Similarity 72.5%; Pred. No. 7.2e-45;  
RESULT 1357  
ID ADP65423 standard; DNA; 154068 BP.  
DE Human sequence from clone RP11-363I22 on chromosome 1, complete DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 9.7%; Score 220.8; DB 11; Length 154068;  
Best Local Similarity 83.0%; Pred. No. 7.4e-45;  
RESULT 1358  
ID AED89402 standard; DNA; 155515 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 42.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 220.8; DB 14; Length 155515;  
Best Local Similarity 84.3%; Pred. No. 7.5e-45;  
RESULT 1359  
ID AED89421 standard; DNA; 159497 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 61.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 220.8; DB 14; Length 159497;  
Best Local Similarity 81.9%; Pred. No. 7.6e-45;  
RESULT 1360  
ID AED89403 standard; DNA; 159660 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 43.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 220.8; DB 14; Length 159660;  
Best Local Similarity 84.3%; Pred. No. 7.6e-45;  
RESULT 1361  
ID ADZ13837 standard; DNA; 188267 BP.  
DE Human cancer-associated genomic DNA #115.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.7%; Score 220.8; DB 14; Length 188267;  
Best Local Similarity 86.7%; Pred. No. 8.2e-45;  
RESULT 1362  
ID AED89391 standard; DNA; 207600 BP.  
DE Human breast cancer genetic marker BAC DNA SEQ ID NO 31.  
PN WO2005106044-A1.  
PD 10-NOV-2005.  
PA (EXAG-) EXAGEN DIAGNOSTICS INC.  
Query Match 9.7%; Score 220.8; DB 14; Length 207600;  
Best Local Similarity 85.4%; Pred. No. 8.5e-45;  
RESULT 1363  
ID ADP75187 standard; DNA; 302603 BP.  
DE Human Endophilin 1 gene.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.7%; Score 220.8; DB 11; Length 302603;  
Best Local Similarity 74.6%; Pred. No. 1e-44;  
RESULT 1364  
ID ACF91253 standard; DNA; 459 BP.  
DE Human SIRS/sepsis diagnostic marker DNA fragment 10113.  
PN WO2004087949-A2.  
PD 14-OCT-2004.  
PA (SIRS-) SIRS LAB GMBH.  
Query Match 9.7%; Score 220.6; DB 13; Length 459;

Best Local Similarity 87.5%; Pred. No. 6.1e-46;  
RESULT 1365  
ID AAK70773 standard; DNA; 831 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25585.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 831;  
Best Local Similarity 83.7%; Pred. No. 8e-46;  
RESULT 1366  
ID ADN41750 standard; DNA; 2034 BP.  
DE Novel human secreted protein polynucleotide seqid 872.  
PN US2004044191-A1.  
PD 04-MAR-2004.  
PA (FISC/) FISCHER C L.  
PA (ROSE/) ROSEN C A.  
PA (SOPP/) SOPPET D R.  
PA (RUBE/) RUBEN S M.  
PA (KYAW/) KYAW H.  
PA (LIYY/) LI Y.  
PA (ZENG/) ZENG Z.  
PA (LAFL/) LAFLEUR D W.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (OLSE/) OLSEN H.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match 9.7%; Score 220.6; DB 12; Length 2034;  
Best Local Similarity 83.7%; Pred. No. 1.2e-45;  
RESULT 1367  
ID AAH19188 standard; cDNA; 2912 BP.  
DE Human secreted protein-encoding gene 19 cDNA clone HBMV155, SEQ ID NO:29.  
PN WO200132910-A2.  
PD 10-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 2912;  
Best Local Similarity 84.9%; Pred. No. 1.4e-45;  
RESULT 1368  
ID AAS41970 standard; DNA; 3702 BP.  
DE Genomic sequence #286 encoding novel human enzyme polypeptide.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 3702;  
Best Local Similarity 84.7%; Pred. No. 1.6e-45;  
RESULT 1369  
ID AAS41971 standard; DNA; 3842 BP.  
DE Genomic sequence #287 encoding novel human enzyme polypeptide.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 3842;  
Best Local Similarity 84.7%; Pred. No. 1.6e-45;  
RESULT 1370  
ID ABK92513 standard; DNA; 6096 BP.  
DE Human prostate specific nucleic acid #132.  
PN WO200238810-A2.  
PD 16-MAY-2002.  
PA (DIAD-) DIADEXUS INC.  
Query Match 9.7%; Score 220.6; DB 6; Length 6096;  
Best Local Similarity 87.5%; Pred. No. 2e-45;  
RESULT 1371  
ID ABA20383 standard; DNA; 7074 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12714.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 5; Length 7074;  
Best Local Similarity 86.2%; Pred. No. 2.1e-45;  
RESULT 1372  
ID AAK83072 standard; DNA; 10102 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37884.  
PN WO200157182-A2.

PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 10102;  
Best Local Similarity 70.3%; Pred. No. 2.5e-45;  
RESULT 1373  
ID ABA20382 standard; DNA; 10642 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12713.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 5; Length 10642;  
Best Local Similarity 86.2%; Pred. No. 2.5e-45;  
RESULT 1374  
ID AAI99283 standard; DNA; 15037 BP.  
DE Human excretory related polynucleotide SEQ ID NO 1047.  
PN WO200155313-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 15037;  
Best Local Similarity 81.5%; Pred. No. 2.9e-45;  
RESULT 1375  
ID AAI63633 standard; DNA; 15037 BP.  
DE Human kidney related polynucleotide SEQ ID NO 948.  
PN WO200155323-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 5; Length 15037;  
Best Local Similarity 81.5%; Pred. No. 2.9e-45;  
RESULT 1376  
ID ABK42539 standard; DNA; 16181 BP.  
DE Genomic sequence #438 encoding novel human connective tissue polypeptide.  
PN WO200155343-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 16181;  
Best Local Similarity 82.8%; Pred. No. 3e-45;  
RESULT 1377  
ID AAL04268 standard; DNA; 16181 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 6956.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 16181;  
Best Local Similarity 82.8%; Pred. No. 3e-45;  
RESULT 1378  
ID ADB60695 standard; DNA; 16181 BP.  
DE Connective tissue related genomic DNA #438.  
PN US2003054375-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 9; Length 16181;  
Best Local Similarity 82.8%; Pred. No. 3e-45;  
RESULT 1379  
ID ABZ73855 standard; DNA; 28482 BP.  
DE Secreted protein gene 64 genomic fragment HCEGX05, SEQ ID NO:1002.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 8; Length 28482;  
Best Local Similarity 81.5%; Pred. No. 3.9e-45;  
RESULT 1380  
ID ADA44262 standard; DNA; 28482 BP.  
DE Human secreted protein DNA SEQ ID 455.  
PN WO2003000865-A2.  
PD 03-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 8; Length 28482;  
Best Local Similarity 81.5%; Pred. No. 3.9e-45;  
RESULT 1381  
ID AAS28674 standard; DNA; 32170 BP.  
DE Genomic sequence #514 encoding for novel human respiratory antigen.  
PN WO200155448-A1.  
PD 02-AUG-2001.



PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 32170;  
Best Local Similarity 83.7%; Pred. No. 4.1e-45;  
RESULT 1382  
ID ADG41870 standard; DNA; 32170 BP.  
DE Human respiratory system associated genomic DNA seq id 1108.  
PN US2003215893-A1.  
PD 20-NOV-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 10; Length 32170;  
Best Local Similarity 83.7%; Pred. No. 4.1e-45;  
RESULT 1383  
ID ADI97644 standard; DNA; 32170 BP.  
DE Human respiratory system associated polypeptide-related DNA SeqID1108.  
PN US2003077704-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 11; Length 32170;  
Best Local Similarity 83.7%; Pred. No. 4.1e-45;  
RESULT 1384  
ID ABZ74517 standard; DNA; 32681 BP.  
DE Secreted protein gene 329 genomic fragment HTLBT80, SEQ ID NO:1664.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 8; Length 32681;  
Best Local Similarity 81.5%; Pred. No. 4.2e-45;  
RESULT 1385  
ID ABZ73854 standard; DNA; 32681 BP.  
DE Secreted protein gene 64 genomic fragment HCEGX05, SEQ ID NO:1001.  
PN WO200277013-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 8; Length 32681;  
Best Local Similarity 81.5%; Pred. No. 4.2e-45;  
RESULT 1386  
ID ADA98915 standard; DNA; 32681 BP.  
DE Human secreted protein-related DNA sequence #508.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 8; Length 32681;  
Best Local Similarity 81.5%; Pred. No. 4.2e-45;  
RESULT 1387  
ID ADA44261 standard; DNA; 32681 BP.  
DE Human secreted protein DNA SEQ ID 454.  
PN WO2003000865-A2.  
PD 03-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 8; Length 32681;  
Best Local Similarity 81.5%; Pred. No. 4.2e-45;  
RESULT 1388  
ID ADA44519 standard; DNA; 32681 BP.  
DE Human secreted protein DNA SEQ ID 712.  
PN WO2003000865-A2.  
PD 03-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 8; Length 32681;  
Best Local Similarity 81.5%; Pred. No. 4.2e-45;  
RESULT 1389  
ID ADC20949 standard; DNA; 32681 BP.  
DE Human secreted protein-related DNA sequence #367.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 10; Length 32681;  
Best Local Similarity 81.5%; Pred. No. 4.2e-45;  
RESULT 1390  
ID ABZ68053 standard; DNA; 32681 BP.  
DE Human secreted protein encoding genomic DNA SEQ ID NO 1576.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.7%; Score 220.6; DB 10; Length 32681;  
Best Local Similarity 81.5%; Pred. No. 4.2e-45;  
RESULT 1391  
ID AEH64934 standard; DNA; 35579 BP.  
DE Human 2,4-dienoyl-CoA reductase (DCR-AKL) gene, SEQ ID 27.  
PN JP2005253434-A.  
PD 22-SEP-2005.  
PA (HOKK-) HOKKAIDO TLO KK.  
Query Match 9.7%; Score 220.6; DB 15; Length 35579;  
Best Local Similarity 78.0%; Pred. No. 4.3e-45;  
RESULT 1392  
ID AAK64829 standard; DNA; 36501 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19641.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.7%; Score 220.6; DB 4; Length 36501;  
Best Local Similarity 83.7%; Pred. No. 4.4e-45;  
RESULT 1393  
ID AEA61173 standard; DNA; 37577 BP.  
DE Human IL1R2 gene genomic sequence SEQ ID NO:83.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB ) BAYER CORP.  
Query Match 9.7%; Score 220.6; DB 14; Length 37577;  
Best Local Similarity 81.5%; Pred. No. 4.4e-45;  
RESULT 1394  
ID ADZ70415 standard; cDNA; 43284 BP.  
DE Human cDNA from lung cancer marker, SEQ ID 100.  
PN WO2005032495-A2.  
PD 14-APR-2005.  
PA (FARB ) BAYER PHARM CORP.  
Query Match 9.7%; Score 220.6; DB 14; Length 43284;  
Best Local Similarity 84.9%; Pred. No. 4.7e-45;  
RESULT 1395  
ID ADX98572 standard; DNA; 86950 BP.  
DE Human HT014/LOC148902/LYPLA2/GALE genomic DNA.  
Query Match 9.7%; Score 220.6; DB 14; Length 86950;  
Best Local Similarity 83.2%; Pred. No. 6.5e-45;  
RESULT 1396  
ID ACN44742 standard; DNA; 87731 BP.  
DE Human genomic sequence HCG1738334.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.6; DB 11; Length 87731;  
Best Local Similarity 83.7%; Pred. No. 6.5e-45;  
RESULT 1397  
Query Match 9.7%; Score 220.6; DB 11; Length 110000;  
Best Local Similarity 83.7%; Pred. No. 7.2e-45;  
RESULT 1398  
Query Match 9.7%; Score 220.6; DB 11; Length 110000;  
Best Local Similarity 84.9%; Pred. No. 7.2e-45;  
RESULT 1399  
Query Match 9.7%; Score 220.6; DB 14; Length 110000;  
Best Local Similarity 84.9%; Pred. No. 7.2e-45;  
RESULT 1400  
ID AED18450 standard; DNA; 138839 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 701.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Query Match 9.7%; Score 220.6; DB 14; Length 138839;  
Best Local Similarity 79.8%; Pred. No. 8e-45;  
RESULT 1401  
ID ACN45146 standard; DNA; 226215 BP.  
DE Human genomic sequence HCG1639824.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.7%; Score 220.6; DB 11; Length 226215;  
Best Local Similarity 82.6%; Pred. No. 1e-44;  
RESULT 1402

ID AAL02996 standard; DNA; 1160 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 5684.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.4; DB 4; Length 1160;  
Best Local Similarity 86.9%; Pred. No. 1e-45;  
RESULT 1403  
ID ABL97343 standard; DNA; 1160 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 1995.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.4; DB 4; Length 1160;  
Best Local Similarity 86.9%; Pred. No. 1e-45;  
RESULT 1404  
ID AAK70288 standard; DNA; 1746 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25100.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.4; DB 4; Length 1746;  
Best Local Similarity 84.4%; Pred. No. 1.3e-45;  
RESULT 1405  
ID AAK70289 standard; DNA; 1746 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25101.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.4; DB 4; Length 1746;  
Best Local Similarity 84.4%; Pred. No. 1.3e-45;  
RESULT 1406  
ID AAH14059 standard; cDNA; 2544 BP.  
DE Human cDNA sequence SEQ ID NO:11193.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 9.6%; Score 220.4; DB 4; Length 2544;  
Best Local Similarity 84.5%; Pred. No. 1.5e-45;  
RESULT 1407  
ID AEL63133 standard; DNA; 2576 BP.  
DE Human protooncogene TRG4.  
PN WO2006109942-A1.  
PD 19-OCT-2006.  
PA (KIMH/) KIM H.  
Query Match 9.6%; Score 220.4; DB 15; Length 2576;  
Best Local Similarity 84.5%; Pred. No. 1.5e-45;  
RESULT 1408  
ID AAK65774 standard; DNA; 2635 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20586.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.4; DB 4; Length 2635;  
Best Local Similarity 82.1%; Pred. No. 1.5e-45;  
RESULT 1409  
ID ADF69151 standard; cDNA; 5223 BP.  
DE Human MP53 nucleotide sequence SEQ ID NO:9.  
PN WO2003083047-A2.  
PD 09-OCT-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 9.6%; Score 220.4; DB 10; Length 5223;  
Best Local Similarity 87.0%; Pred. No. 2.1e-45;  
RESULT 1410  
ID AAQ44278 standard; DNA; 17327 BP.  
DE Serglycin - proteoglycan peptide core.  
PN WO9313119-A1.  
PD 08-JUL-1993.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
Query Match 9.6%; Score 220.4; DB 2; Length 17327;  
Best Local Similarity 85.7%; Pred. No. 3.5e-45;  
RESULT 1411  
ID ADR67006 standard; DNA; 22608 BP.

DE Human cancer associated gene genomic sequence SEQ ID NO:52.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.6%; Score 220.4; DB 13; Length 22608;  
Best Local Similarity 81.0%; Pred. No. 4e-45;  
RESULT 1412  
ID ADZ12855 standard; DNA; 22608 BP.  
DE Human cancer-associated genomic DNA #32.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.6%; Score 220.4; DB 14; Length 22608;  
Best Local Similarity 81.0%; Pred. No. 4e-45;  
RESULT 1413  
ID AAK77173 standard; DNA; 23394 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31985.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.4; DB 4; Length 23394;  
Best Local Similarity 82.1%; Pred. No. 4e-45;  
RESULT 1414  
ID ADM57790 standard; DNA; 29485 BP.  
DE Human pres gene.  
PN US2003216564-A1.  
PD 20-NOV-2003.  
PA (DALL/) DALLOS P.  
PA (ZHEN/) ZHENG J.  
PA (MADI/) MADISON L D.  
Query Match 9.6%; Score 220.4; DB 11; Length 29485;  
Best Local Similarity 83.2%; Pred. No. 4.5e-45;  
RESULT 1415  
ID ADE86101 standard; DNA; 29485 BP.  
DE BAC clone containing DNA encoding human prestin protein.  
PN US6602992-B1.  
PD 05-AUG-2003.  
PA (NOUN ) UNIV NORTHWESTERN.  
Query Match 9.6%; Score 220.4; DB 12; Length 29485;  
Best Local Similarity 83.2%; Pred. No. 4.5e-45;  
RESULT 1416  
ID ABK87970 standard; DNA; 29912 BP.  
DE Human prolactin receptor (PRLR) genomic DNA.  
PN WO200250098-A2.  
PD 27-JUN-2002.  
PA (GENA-) GENAISSANCE PHARM INC.  
Query Match 9.6%; Score 220.4; DB 6; Length 29912;  
Best Local Similarity 74.7%; Pred. No. 4.5e-45;  
RESULT 1417  
ID ABA15643 standard; DNA; 30610 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7974.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.4; DB 5; Length 30610;  
Best Local Similarity 82.1%; Pred. No. 4.6e-45;  
RESULT 1418  
ID ABD33628 standard; DNA; 36714 BP.  
DE Human cancer-associated (CA) gene HD07-128.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.6%; Score 220.4; DB 13; Length 36714;  
Best Local Similarity 85.7%; Pred. No. 5e-45;  
RESULT 1419  
ID AEJ13856 standard; DNA; 36714 BP.  
DE Cancer-associated gene sequence - SEQ ID 864.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Query Match 9.6%; Score 220.4; DB 15; Length 36714;  
Best Local Similarity 85.7%; Pred. No. 5e-45;

RESULT 1420  
ID ADZ13602 standard; DNA; 36724 BP.  
DE Human cancer-associated genomic DNA #96.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.6%; Score 220.4; DB 14; Length 36724;  
Best Local Similarity 85.7%; Pred. No. 5e-45;  
RESULT 1421  
ID AAL51353 standard; DNA; 39776 BP.  
DE Human secreted protein genomic DNA sequence.  
PN WO200299072-A2.  
PD 12-DEC-2002.  
PA (PEKE ) PE CORP NY.  
Query Match 9.6%; Score 220.4; DB 10; Length 39776;  
Best Local Similarity 75.5%; Pred. No. 5.1e-45;  
RESULT 1422  
ID AEA61140 standard; DNA; 40085 BP.  
DE Human FMO5 gene genomic sequence SEQ ID NO:50.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB ) BAYER CORP.  
Query Match 9.6%; Score 220.4; DB 14; Length 40085;  
Best Local Similarity 83.2%; Pred. No. 5.2e-45;  
RESULT 1423  
ID ACN44386 standard; DNA; 40136 BP.  
DE Human genomic sequence hCG18551.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.6%; Score 220.4; DB 11; Length 40136;  
Best Local Similarity 85.9%; Pred. No. 5.2e-45;  
RESULT 1424  
ID ABD32754 standard; DNA; 62124 BP.  
DE Human cancer-associated genomic DNA HD16-028.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 9.6%; Score 220.4; DB 13; Length 62124;  
Best Local Similarity 85.7%; Pred. No. 6.3e-45;  
RESULT 1425  
ID ABS52847 standard; DNA; 90541 BP.  
DE Human SR protein-specific kinase 2, SRPK2, genomic DNA.  
PN US2002094560-A1.  
PD 18-JUL-2002.  
PA (ABUT/) ABU-THREIDEH J.  
PA (GONG/) GONG F.  
PA (KETC/) KETCHUM K A.  
PA (DFRA/) DI FRANCESCO V.  
PA (BEAS/) BEASLEY E M.  
Query Match 9.6%; Score 220.4; DB 6; Length 90541;  
Best Local Similarity 83.2%; Pred. No. 7.4e-45;  
RESULT 1426  
ID ADJ37690 standard; DNA; 90541 BP.  
DE Human kinase genomic DNA.  
PN US2003175927-A1.  
PD 18-SEP-2003.  
PA (APPL-) APPLERA CORP.  
Query Match 9.6%; Score 220.4; DB 10; Length 90541;  
Best Local Similarity 83.2%; Pred. No. 7.4e-45;  
RESULT 1427  
ID ADR31219 standard; DNA; 90541 BP.  
DE Human SRPK2 kinase protein alternative splice form genomic DNA.  
PN US2004157297-A1.  
PD 12-AUG-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 9.6%; Score 220.4; DB 13; Length 90541;  
Best Local Similarity 83.2%; Pred. No. 7.4e-45;  
RESULT 1428  
ID AAL54213 standard; DNA; 113033 BP.  
DE SR protein-specific kinase-1 DNA, SEQ ID No 5.  
PN WO200299427-A1.  
PD 12-DEC-2002.

PA (EXEL-) EXELIXIS INC.  
Query Match 9.6%; Score 220.4; DB 8; Length 113033;  
Best Local Similarity 83.2%; Pred. No. 8.2e-45;  
RESULT 1429  
ID ADZ70593 standard; cDNA; 114596 BP.  
DE Human cDNA from lung cancer marker gene B4GALT5.  
PN WO2005032495-A2.  
PD 14-APR-2005.  
PA (FARB ) BAYER PHARM CORP.  
Query Match 9.6%; Score 220.4; DB 14; Length 114596;  
Best Local Similarity 82.1%; Pred. No. 8.3e-45;  
RESULT 1430  
ID AEJ41365 standard; DNA; 119600 BP.  
DE Human c10orf24 gene.  
PN WO2006069592-A2.  
PD 06-JUL-2006.  
PA (VECH-) VER CHRISTELIJK WETENSCHAPPELIJK ONDERW.  
Query Match 9.6%; Score 220.4; DB 15; Length 119600;  
Best Local Similarity 83.2%; Pred. No. 8.4e-45;  
RESULT 1431  
ID AEB45166 standard; DNA; 170001 BP.  
DE Human FAT gene SEQ ID NO 1.  
PN WO2005071104-A1.  
PD 04-AUG-2005.  
PA (GARV-) GARVAN INST MEDICAL RES.  
Query Match 9.6%; Score 220.4; DB 14; Length 170001;  
Best Local Similarity 83.2%; Pred. No. 9.9e-45;  
RESULT 1432  
ID ADV16961 standard; DNA; 290040 BP.  
DE Human protein associated with myc (PAM) genomic DNA.  
PN EP1481685-A1.  
PD 01-DEC-2004.  
PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
Query Match 9.6%; Score 220.4; DB 14; Length 290040;  
Best Local Similarity 85.7%; Pred. No. 1.3e-44;  
RESULT 1433  
ID ADU92049 standard; DNA; 290040 BP.  
DE Human PAM (protein associated with myc) genomic DNA.  
PN EP1481680-A1.  
PD 01-DEC-2004.  
PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
Query Match 9.6%; Score 220.4; DB 14; Length 290040;  
Best Local Similarity 85.7%; Pred. No. 1.3e-44;  
RESULT 1434  
ID ABE33438 standard; DNA; 601 BP.  
DE Human DNA polymorphic region #1018.  
PN US2005147987-A1.  
PD 07-JUL-2005.  
PA (APPL-) APPLERA CORP NY.  
Query Match 9.6%; Score 220.2; DB 14; Length 601;  
Best Local Similarity 84.6%; Pred. No. 8.8e-46;  
RESULT 1435  
ID ADY78516 standard; cDNA; 675 BP.  
DE Human cDNA predominantly expressed in blood cells, PREB-084.  
PN WO2005026314-A2.  
PD 24-MAR-2005.  
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
PA (GENE-) GENEDESIGN INC.  
Query Match 9.6%; Score 220.2; DB 14; Length 675;  
Best Local Similarity 84.0%; Pred. No. 9.3e-46;  
RESULT 1436  
ID ABA15638 standard; DNA; 10489 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 7969.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.2; DB 5; Length 10489;  
Best Local Similarity 79.6%; Pred. No. 3.2e-45;  
RESULT 1437  
ID AAK66569 standard; DNA; 10689 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21381.  
PN WO200157182-A2.  
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.6%; Score 220.2; DB 4; Length 10689;  
 Best Local Similarity 82.8%; Pred. No. 3.2e-45;  
 RESULT 1438  
 ID AAK80647 standard; DNA; 11632 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35459.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.6%; Score 220.2; DB 4; Length 11632;  
 Best Local Similarity 77.6%; Pred. No. 3.3e-45;  
 RESULT 1439  
 ID ABQ88112 standard; cDNA; 18687 BP.  
 DE Human osteoblast differentiation related cDNA SEQ ID NO 19.  
 PN WO200250301-A2.  
 PD 27-JUN-2002.  
 PA (GENE-) GENE LOGIC INC.  
 PA (PROC ) PROCTER & GAMBLE CO.  
 Query Match 9.6%; Score 220.2; DB 6; Length 18687;  
 Best Local Similarity 80.6%; Pred. No. 4.1e-45;  
 RESULT 1440  
 ID ADL15086 standard; DNA; 18687 BP.  
 DE Human C1 inhibitor DNA for cancer treatment.  
 PN WO2003068268-A2.  
 PD 21-AUG-2003.  
 PA (BIOI-) BIOINVENT INT AB.  
 Query Match 9.6%; Score 220.2; DB 10; Length 18687;  
 Best Local Similarity 80.6%; Pred. No. 4.1e-45;  
 RESULT 1441  
 ID ADR52914 standard; DNA; 18687 BP.  
 DE Drug therapy altered expressed gene #265.  
 PN WO2004072265-A2.  
 PD 26-AUG-2004.  
 PA (AMHP ) WYETH.  
 PA (BURC/) BURCZYNSKI M.  
 PA (TWIN/) TWINE N.  
 PA (DORN/) DORNER A J.  
 PA (TREP/) TREPICCHIO W L.  
 Query Match 9.6%; Score 220.2; DB 13; Length 18687;  
 Best Local Similarity 80.6%; Pred. No. 4.1e-45;  
 RESULT 1442  
 ID ADL62089 standard; DNA; 18968 BP.  
 DE Human ovarian cancer DNA marker #20301.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 9.6%; Score 220.2; DB 5; Length 18968;  
 Best Local Similarity 84.2%; Pred. No. 4.1e-45;  
 RESULT 1443  
 ID AAL04782 standard; DNA; 22927 BP.  
 DE Human reproductive system related antigen DNA SEQ ID NO: 7470.  
 PN WO200155320-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.6%; Score 220.2; DB 4; Length 22927;  
 Best Local Similarity 82.8%; Pred. No. 4.5e-45;  
 RESULT 1444  
 ID ABL97677 standard; DNA; 22927 BP.  
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2329.  
 PN WO200155317-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.6%; Score 220.2; DB 4; Length 22927;  
 Best Local Similarity 82.8%; Pred. No. 4.5e-45;  
 RESULT 1445  
 ID AFB31547 standard; DNA; 23353 BP.  
 DE Glutamate-cysteine ligase modulating subunit (GCLM) DNA.  
 PN WO2005068649-A1.  
 PD 28-JUL-2005.  
 PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG.  
 Query Match 9.6%; Score 220.2; DB 14; Length 23353;  
 Best Local Similarity 76.8%; Pred. No. 4.5e-45;  
 RESULT 1446

ID ACN44242 standard; DNA; 26318 BP.  
 DE Human genomic sequence hCG20537.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Query Match 9.6%; Score 220.2; DB 11; Length 26318;  
 Best Local Similarity 83.9%; Pred. No. 4.8e-45;  
 RESULT 1447  
 ID ADZ12935 standard; DNA; 28320 BP.  
 DE Human cancer-associated genomic DNA #39.  
 PN WO2005031001-A2.  
 PD 07-APR-2005.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 9.6%; Score 220.2; DB 14; Length 28320;  
 Best Local Similarity 83.9%; Pred. No. 5e-45;  
 RESULT 1448  
 ID AAL05628 standard; DNA; 32176 BP.  
 DE Human reproductive system related antigen DNA SEQ ID NO: 8316.  
 PN WO200155320-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 9.6%; Score 220.2; DB 4; Length 32176;  
 Best Local Similarity 87.8%; Pred. No. 5.3e-45;  
 RESULT 1449  
 ID ADA02960 standard; DNA; 44325 BP.  
 DE Human DAD1 carcinoma associated gene, SEQ ID NO:1478.  
 PN WO2003057146-A2.  
 PD 17-JUL-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Query Match 9.6%; Score 220.2; DB 9; Length 44325;  
 Best Local Similarity 86.4%; Pred. No. 6.1e-45;  
 RESULT 1450  
 ID ADB72698 standard; DNA; 44325 BP.  
 DE Human DAD1 gene.  
 PN WO2003008583-A2.  
 PD 30-JAN-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Query Match 9.6%; Score 220.2; DB 10; Length 44325;  
 Best Local Similarity 86.4%; Pred. No. 6.1e-45;  
 RESULT 1451  
 ID ADC85440 standard; DNA; 44325 BP.  
 DE Human Dad1 genomic sequence.  
 PN WO2003045230-A2.  
 PD 05-JUN-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Query Match 9.6%; Score 220.2; DB 10; Length 44325;  
 Best Local Similarity 86.4%; Pred. No. 6.1e-45;  
 RESULT 1452  
 ID ADM74555 standard; DNA; 44325 BP.  
 DE Human carcinoma associated (CA) nucleic acid #112.  
 PN US2004072154-A1.  
 PD 15-APR-2004.  
 PA (MORR/) MORRIS D W.  
 PA (ENGE/) ENGELHARD E K.  
 Query Match 9.6%; Score 220.2; DB 12; Length 44325;  
 Best Local Similarity 86.4%; Pred. No. 6.1e-45;  
 RESULT 1453  
 ID ABS57422 standard; DNA; 46718 BP.  
 DE Human protease genomic DNA.  
 PN US2002137180-A1.  
 PD 26-SEP-2002.  
 PA (GANW/) GAN W.  
 PA (YEJJ/) YE J.  
 PA (DFRA/) DI FRANCESCO V.  
 PA (BEAS/) BEASLEY E M.  
 Query Match 9.6%; Score 220.2; DB 8; Length 46718;  
 Best Local Similarity 84.2%; Pred. No. 6.2e-45;  
 RESULT 1454  
 ID ADG62974 standard; DNA; 46718 BP.  
 DE Human protease genomic DNA.  
 PN US2003054489-A1.  
 PD 20-MAR-2003.  
 PA (APPL-) APPLERA CORP.



Query Match 9.6%; Score 220.2; DB 10; Length 46718;  
Best Local Similarity 84.2%; Pred. No. 6.2e-45;  
RESULT 1455  
ID AAK86671 standard; DNA; 53075 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41483.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220.2; DB 4; Length 53075;  
Best Local Similarity 82.0%; Pred. No. 6.6e-45;  
RESULT 1456  
ID ACN43874 standard; DNA; 58845 BP.  
DE Human genomic sequence hCG25637.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 9.6%; Score 220.2; DB 11; Length 58845;  
Best Local Similarity 83.9%; Pred. No. 6.9e-45;  
RESULT 1457  
ID ADH10008 standard; DNA; 85873 BP.  
DE Human chromosome 3p25 DNA fragment.  
PN WO2003093310-A1.  
PD 13-NOV-2003.  
PA (UYBR-) UNIV BREMEN.  
Query Match 9.6%; Score 220.2; DB 10; Length 85873;  
Best Local Similarity 83.9%; Pred. No. 8.2e-45;  
RESULT 1458  
ID AEC82644 standard; cDNA; 90901 BP.  
DE Breast cancer associated cDNA SEQ ID NO 212.  
PN WO2005083429-A2.  
PD 09-SEP-2005.  
PA (VERI-) VERIDEX LLC.  
Query Match 9.6%; Score 220.2; DB 14; Length 90901;  
Best Local Similarity 82.8%; Pred. No. 8.4e-45;  
RESULT 1459  
Query Match 9.6%; Score 220.2; DB 6; Length 110000;  
Best Local Similarity 82.8%; Pred. No. 9.1e-45;  
RESULT 1460  
Query Match 9.6%; Score 220.2; DB 12; Length 110000;  
Best Local Similarity 82.8%; Pred. No. 9.1e-45;  
RESULT 1461  
Query Match 9.6%; Score 220.2; DB 12; Length 110000;  
Best Local Similarity 82.8%; Pred. No. 9.1e-45;  
RESULT 1462  
Query Match 9.6%; Score 220.2; DB 12; Length 110000;  
Best Local Similarity 82.8%; Pred. No. 9.1e-45;  
RESULT 1463  
Query Match 9.6%; Score 220.2; DB 14; Length 110000;  
Best Local Similarity 82.8%; Pred. No. 9.1e-45;  
RESULT 1464  
Query Match 9.6%; Score 220.2; DB 15; Length 110000;  
Best Local Similarity 85.1%; Pred. No. 9.1e-45;  
RESULT 1465  
ID ABK83569 standard; cDNA; 122888 BP.  
DE Human cDNA differentially expressed in granulocytic cells #140.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.6%; Score 220.2; DB 6; Length 122888;  
Best Local Similarity 80.8%; Pred. No. 9.6e-45;  
RESULT 1466  
ID AEF51725 standard; DNA; 126932 BP.  
DE Human ribosomal S6 kinase 4 (RSK4) encoding DNA.  
PN EP1619504-A1.  
PD 25-JAN-2006.  
PA (FRAU-) FRAUNHOFER INST TOXIKOLOGIE & EXPERIMENT.  
Query Match 9.6%; Score 220.2; DB 15; Length 126932;  
Best Local Similarity 85.1%; Pred. No. 9.7e-45;  
RESULT 1467  
ID ADP65634 standard; DNA; 137908 BP.  
DE Human sequence from clone 914P14 on chromosome Xq23 Contains DNA.  
PN WO2003072827-A1.  
PD 04-SEP-2003.

PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 9.6%; Score 220.2; DB 11; Length 137908;  
Best Local Similarity 82.8%; Pred. No. 1e-44;  
RESULT 1468  
ID ABK49586 standard; DNA; 143306 BP.  
DE Human transporter protein gene.  
Query Match 9.6%; Score 220.2; DB 6; Length 143306;  
Best Local Similarity 84.0%; Pred. No. 1e-44;  
RESULT 1469  
ID ADL13739 standard; DNA; 147620 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #271.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 9.6%; Score 220.2; DB 10; Length 147620;  
Best Local Similarity 77.3%; Pred. No. 1e-44;  
RESULT 1470  
ID ADQ19948 standard; DNA; 147620 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2768.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 9.6%; Score 220.2; DB 12; Length 147620;  
Best Local Similarity 77.3%; Pred. No. 1e-44;  
RESULT 1471  
ID ADL08124 standard; DNA; 176080 BP.  
DE Human gene associated with low HDL-C LRPAP1.  
PN US2004043389-A1.  
PD 04-MAR-2004.  
PA (VITI-) VITIVITY INC.  
Query Match 9.6%; Score 220.2; DB 12; Length 176080;  
Best Local Similarity 84.0%; Pred. No. 1.1e-44;  
RESULT 1472  
ID AED18538 standard; DNA; 184666 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 789.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL) UNIV FLORIDA RES FOUND INC.  
Query Match 9.6%; Score 220.2; DB 14; Length 184666;  
Best Local Similarity 84.2%; Pred. No. 1.2e-44;  
RESULT 1473  
ID ABX16034 standard; DNA; 203654 BP.  
DE Human gene encoding calcium channel transporter family member.  
PN US2002142938-A1.  
PD 03-OCT-2002.  
PA (YANC/) YAN C.  
PA (KETC/) KETCHUM K A.  
PA (DFRA/) DI FRANCESCO V.  
PA (BEAS/) BEASLEY E M.  
Query Match 9.6%; Score 220.2; DB 10; Length 203654;  
Best Local Similarity 75.2%; Pred. No. 1.2e-44;  
RESULT 1474  
ID ADP75180 standard; DNA; 304905 BP.  
DE Human Endophilin 2 gene.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.6%; Score 220.2; DB 11; Length 304905;  
Best Local Similarity 82.8%; Pred. No. 1.4e-44;  
RESULT 1475  
ID AAD58431 standard; DNA; 322101 BP.  
DE Human PAOD1 genomic DNA.  
PN WO2003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 9.6%; Score 220.2; DB 10; Length 322101;  
Best Local Similarity 81.7%; Pred. No. 1.5e-44;  
RESULT 1476  
ID ADI35046 standard; DNA; 322101 BP.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) genomic DNA sequence.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO-) DECODE GENETICS EHF.

Query Match 9.6%; Score 220.2; DB 12; Length 322101;  
Best Local Similarity 81.7%; Pred. No. 1.5e-44;  
RESULT 1477  
ID AAL02649 standard; cDNA; 499 BP.  
DE Human reproductive system related antigen cDNA SEQ ID NO: 2650.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 499;  
Best Local Similarity 84.6%; Pred. No. 9.1e-46;  
RESULT 1478  
ID ABA07691 standard; cDNA; 499 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 248.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 499;  
Best Local Similarity 84.6%; Pred. No. 9.1e-46;  
RESULT 1479  
ID ACL59412 standard; cDNA; 546 BP.  
DE Human colon cancer differentially expressed polynucleotide, SEQ ID:5547.  
PN WO200500087-A2.  
PD 06-JAN-2005.  
PA (CHIR ) CHIRON CORP.  
Query Match 9.6%; Score 220; DB 14; Length 546;  
Best Local Similarity 78.2%; Pred. No. 9.5e-46;  
RESULT 1480  
ID ABA16111 standard; DNA; 1314 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 8442.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 5; Length 1314;  
Best Local Similarity 74.9%; Pred. No. 1.4e-45;  
RESULT 1481  
ID ADT61904 standard; cDNA; 3154 BP.  
DE Human PRO92240 cDNA.  
PN US2004198969-A1.  
PD 07-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.6%; Score 220; DB 13; Length 3154;  
Best Local Similarity 78.2%; Pred. No. 2.1e-45;  
RESULT 1482  
ID ADU46702 standard; cDNA; 3154 BP.  
DE DNA340535 encoding human PRO92240.  
PN WO2004096124-A2.  
PD 11-NOV-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 9.6%; Score 220; DB 13; Length 3154;  
Best Local Similarity 78.2%; Pred. No. 2.1e-45;  
RESULT 1483  
ID AAK65080 standard; DNA; 8925 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19892.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 8925;  
Best Local Similarity 82.6%; Pred. No. 3.3e-45;  
RESULT 1484  
ID ADC86204 standard; DNA; 14325 BP.  
DE Human GPCR gene SEQ ID NO:657.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 9.6%; Score 220; DB 10; Length 14325;  
Best Local Similarity 84.6%; Pred. No. 4.1e-45;  
RESULT 1485  
ID AAS41688 standard; DNA; 14332 BP.  
DE Genomic sequence #4 encoding novel human enzyme polypeptide.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 9.6%; Score 220; DB 4; Length 14332;  
Best Local Similarity 82.3%; Pred. No. 4.1e-45;  
RESULT 1486  
ID AAK81810 standard; DNA; 14332 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36622.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 14332;  
Best Local Similarity 82.3%; Pred. No. 4.1e-45;  
RESULT 1487  
ID AAK84386 standard; DNA; 14332 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39198.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 14332;  
Best Local Similarity 82.3%; Pred. No. 4.1e-45;  
RESULT 1488  
ID AAK64803 standard; DNA; 17154 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19615.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 17154;  
Best Local Similarity 85.9%; Pred. No. 4.5e-45;  
RESULT 1489  
ID ABZ20990 standard; DNA; 24801 BP.  
DE Human thyroid tumour associated PKCG genomic sequence SEQ ID NO: 18.  
PN WO200283727-A2.  
PD 24-OCT-2002.  
PA (BULL/) BULLERDIEK J.  
Query Match 9.6%; Score 220; DB 10; Length 24801;  
Best Local Similarity 83.7%; Pred. No. 5.3e-45;  
RESULT 1490  
ID ADO01541 standard; DNA; 25301 BP.  
DE Human protein kinase C gamma (PRKCG) genomic DNA.  
PN US2004106138-A1.  
PD 03-JUN-2004.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 9.6%; Score 220; DB 12; Length 25301;  
Best Local Similarity 83.7%; Pred. No. 5.3e-45;  
RESULT 1491  
ID AAL36313 standard; DNA; 26591 BP.  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2678.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 26591;  
Best Local Similarity 82.3%; Pred. No. 5.4e-45;  
RESULT 1492  
ID ABX59301 standard; cDNA; 26591 BP.  
DE cDNA encoding novel human musculoskeletal system antigen #1645.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 9.6%; Score 220; DB 8; Length 26591;  
Best Local Similarity 82.3%; Pred. No. 5.4e-45;  
RESULT 1493  
ID ADJ30051 standard; DNA; 26591 BP.  
DE Human musculoskeletal system-associated genomic DNA - SEQ ID.2678.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 12; Length 26591;  
Best Local Similarity 82.3%; Pred. No. 5.4e-45;  
RESULT 1494  
ID AEC82969 standard; cDNA; 28247 BP.  
DE Breast cancer associated cDNA SEQ ID NO 537.  
PN WO2005083429-A2.  
PD 09-SEP-2005.

PA (VERI-) VERIDEX LLC.  
Query Match 9.6%; Score 220; DB 14; Length 28247;  
Best Local Similarity 85.9%; Pred. No. 5.6e-45;  
RESULT 1495  
ID ABL68824 standard; DNA; 38374 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:7161.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.6%; Score 220; DB 6; Length 38374;  
Best Local Similarity 81.2%; Pred. No. 6.4e-45;  
RESULT 1496  
ID ABL68363 standard; DNA; 38374 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:6700.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.6%; Score 220; DB 6; Length 38374;  
Best Local Similarity 81.2%; Pred. No. 6.4e-45;  
RESULT 1497  
ID ABL68364 standard; DNA; 38374 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:6701.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 9.6%; Score 220; DB 6; Length 38374;  
Best Local Similarity 81.2%; Pred. No. 6.4e-45;  
RESULT 1498  
ID ABN96966 standard; DNA; 38374 BP.  
DE Gene #3464 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 9.6%; Score 220; DB 6; Length 38374;  
Best Local Similarity 81.2%; Pred. No. 6.4e-45;  
RESULT 1499  
ID AAK78847 standard; DNA; 57296 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33659.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 57296;  
Best Local Similarity 82.3%; Pred. No. 7.7e-45;  
RESULT 1500  
ID AAK78170 standard; DNA; 57296 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32982.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.6%; Score 220; DB 4; Length 57296;  
Best Local Similarity 82.3%; Pred. No. 7.7e-45;

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OM nucleic - nucleic search, using sw model

Run on: September 19, 2007, 20:07:09 ; Search time 872 Seconds  
(without alignments)  
9811.899 Million cell updates/sec

Title: US-09-944-929-82  
Perfect score: 2284  
Sequence: 1 gcggagcatcgctgcggtc.....ataaatctttgttactcaa 2284

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Issued Patents NA:\*  
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10: /EMC\_Celerra\_SIDS2/ptodata/1/ina/RE\_COMB.seq:\*  
11: /EMC\_Celerra\_SIDS2/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2284	100.0	2284	3	US-09-866-028-82	Sequence 82, Appl
2	2284	100.0	2284	3	US-09-944-457-82	Sequence 82, Appl
3	2284	100.0	2284	3	US-09-945-584-82	Sequence 82, Appl
4	2284	100.0	2284	3	US-09-991-181-514	Sequence 514, App
5	2284	100.0	2284	3	US-09-944-944-82	Sequence 82, Appl
6	2284	100.0	2284	3	US-09-990-444-514	Sequence 514, App
7	2284	100.0	2284	3	US-09-945-587-82	Sequence 82, Appl
8	2284	100.0	2284	3	US-09-997-333-514	Sequence 514, App
9	2284	100.0	2284	3	US-09-992-598-514	Sequence 514, App
10	2284	100.0	2284	4	US-09-989-735-514	Sequence 514, App
11	2284	100.0	2284	5	US-09-989-726-514	Sequence 514, App
12	2284	100.0	2284	5	US-09-944-884-82	Sequence 82, Appl
13	2284	100.0	2284	5	US-09-997-514-514	Sequence 514, App
14	2284	100.0	2284	5	US-09-989-728-514	Sequence 514, App
15	2284	100.0	2284	5	US-09-997-349-514	Sequence 514, App
16	2284	100.0	2284	5	US-09-997-653-514	Sequence 514, App
17	2284	100.0	2284	5	US-09-989-293A-514	Sequence 514, App
18	2284	100.0	2284	5	US-09-989-732-514	Sequence 514, App
19	2284	100.0	2284	5	US-09-990-441-514	Sequence 514, App
20	2284	100.0	2284	5	US-09-989-328-514	Sequence 514, App
21	2284	100.0	2284	5	US-09-989-724-514	Sequence 514, App
22	2284	100.0	2284	5	US-09-989-733-514	Sequence 514, App

23	2284	100.0	2284	5	US-09-993-583-514	Sequence 514, App
24	2284	100.0	2284	5	US-09-989-279-514	Sequence 514, App
25	2284	100.0	2284	5	US-09-991-157-514	Sequence 514, App
26	2284	100.0	2284	5	US-09-990-439-514	Sequence 514, App
27	2284	100.0	2284	5	US-09-997-641-514	Sequence 514, App
28	2284	100.0	2284	5	US-09-997-384-514	Sequence 514, App
29	2284	100.0	2284	5	US-09-989-730-514	Sequence 514, App
30	2284	100.0	2284	5	US-09-997-585-514	Sequence 514, App
31	2284	100.0	2284	5	US-09-944-896-82	Sequence 82, Appl
32	2284	100.0	2284	5	US-09-997-601-514	Sequence 514, App
33	2284	100.0	2284	5	US-09-997-666-514	Sequence 474441, App
C 34	342.6	15.0	343	7	US-09-925-065A-474441	Sequence 9897, Ap
35	270.2	11.8	295	3	US-09-513-999C-9897	Sequence 9897, Ap
36	270.2	11.8	295	5	US-10-793-479-9897	Sequence 15326, A
C 37	244	10.7	29930	3	US-09-949-016-15326	Sequence 517320, A
C 38	241.4	10.6	547	7	US-09-925-065A-517320	Sequence 16238, A
39	240.8	10.5	59828	3	US-09-949-016-16238	Sequence 13804, A
40	240.8	10.5	85963	3	US-09-949-016-13804	Sequence 69955, A
C 41	240.4	10.5	601	3	US-09-949-016-69955	Sequence 604542, A
42	238.6	10.4	566	7	US-09-925-065A-604542	Sequence 15676, A
43	237.6	10.4	62873	3	US-09-949-016-15676	Sequence 681005, A
44	237.4	10.4	1937	7	US-09-925-065A-681005	Sequence 681006, A
45	237.4	10.4	1937	7	US-09-925-065A-681006	Sequence 15279, A
46	237.4	10.4	15007	3	US-09-949-016-15279	Sequence 606, App
47	237.4	10.4	74545	3	US-09-949-002-606	Sequence 730, App
48	237.4	10.4	131860	3	US-09-949-002-730	Sequence 604543, A
49	237	10.4	566	7	US-09-925-065A-604543	Sequence 604544, A
50	237	10.4	566	7	US-09-925-065A-604544	Sequence 1635, Ap
C 51	237	10.4	601	3	US-09-949-002-1635	Sequence 5643, Ap
C 52	237	10.4	601	3	US-09-949-002-5643	Sequence 13617, A
C 53	237	10.4	38009	3	US-09-949-016-13617	Sequence 14711, A
C 54	237	10.4	150780	3	US-09-949-016-14711	Sequence 15785, A
C 55	236.8	10.4	10427	3	US-09-949-016-15785	Sequence 11866, A
C 56	236.8	10.4	20901	3	US-09-949-016-11866	Sequence 12511, A
57	236.6	10.4	100463	3	US-09-949-016-12511	Sequence 13725, A
58	236.6	10.4	100468	3	US-09-949-016-13725	Sequence 497272, A
59	236.4	10.4	627	7	US-09-925-065A-497272	Sequence 16089, A
C 60	236.2	10.3	175265	3	US-09-949-016-16089	Sequence 63, Appl
61	236	10.3	168174	3	US-10-071-411A-63	Sequence 2, Appli
62	236	10.3	168273	3	US-10-071-411A-2	Sequence 16386, A
63	235.8	10.3	18888	3	US-09-949-016-16386	Sequence 13296, A
C 64	235.8	10.3	105168	3	US-09-949-016-13296	Sequence 809034, A
C 65	235.6	10.3	611	7	US-09-925-065A-809034	Sequence 809035, A
C 66	235.6	10.3	611	7	US-09-925-065A-809035	Sequence 893913, A
67	235.6	10.3	614	7	US-09-925-065A-893913	Sequence 895353, A
C 68	235.6	10.3	622	7	US-09-925-065A-895353	Sequence 15580, A
69	235.6	10.3	71574	3	US-09-949-016-15580	Sequence 792832, A
C 70	235.4	10.3	578	7	US-09-925-065A-792832	Sequence 14469, A
71	235.4	10.3	58397	3	US-09-949-016-14469	Sequence 15097, A
72	235.4	10.3	59076	3	US-09-949-016-15097	Sequence 12823, A
73	235.2	10.3	62386	3	US-09-949-016-12823	Sequence 94321, A
C 74	235	10.3	601	3	US-09-949-016-94321	Sequence 94322, A
C 75	235	10.3	601	3	US-09-949-016-94322	Sequence 808258, A
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77	234.6	10.3	597	7	US-09-925-065A-823703	Sequence 863172, A
78	234.6	10.3	639	7	US-09-925-065A-863172	Sequence 14050, A
79	234.2	10.3	5819	3	US-09-949-016-14050	Sequence 15697, A
80	234.2	10.3	9822	3	US-09-949-016-15697	Sequence 16722, A
C 81	234.2	10.3	50836	3	US-09-949-016-16722	Sequence 15452, A
82	234	10.2	24299	3	US-09-949-016-15452	Sequence 18060, A
83	233.8	10.2	601	3	US-09-949-016-18060	Sequence 197087, A
84	233.8	10.2	601	3	US-09-949-016-197087	Sequence 11, Appl
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86	233.6	10.2	160552	5	US-10-697-828-11	Sequence 11795, A
C 87	233.4	10.2	27702	3	US-09-949-016-11795	Sequence 14575, A
88	233.4	10.2	32278	3	US-09-949-016-14575	Sequence 9, Appli
89	233.2	10.2	1701	3	US-09-078-294-9	Sequence 9, Appli
90	233.2	10.2	1701	5	US-09-728-552A-9	Sequence 751914, A
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92	233	10.2	597	7	US-09-925-065A-751915	Sequence 45773, A
93	232.8	10.2	601	3	US-09-949-016-45773	Sequence 45774, A
94	232.8	10.2	601	3	US-09-949-016-45774	Sequence 87766, A
95	232.6	10.2	601	3	US-09-949-016-87766	



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97	232.6	10.2	17370	3	US-09-949-016-17331	Sequence 17331, A	Sequence 17331, A	170	229.4	10.0	571	7	US-09-925-065A-327161	Sequence 327161,
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C 106	232.2	10.2	605	7	US-09-925-065A-878037	Sequence 878037,	Sequence 878037,	179	229.4	10.0	72602	3	US-09-949-016-14385	Sequence 14385, A
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C 110	232	10.2	488	7	US-09-925-065A-850388	Sequence 850388,	Sequence 850388,	183	229.4	10.0	112508	3	US-09-949-016-16589	Sequence 16589, A
C 111	232	10.2	489	7	US-09-925-065A-842830	Sequence 842830,	Sequence 842830,	184	229.4	10.0	112508	3	US-09-949-016-16590	Sequence 16590, A
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115	231.8	10.1	18700	3	US-09-949-016-13140	Sequence 13140, A	Sequence 13140, A	188	229.4	10.0	162025	3	US-09-834-700-14	Sequence 14, Appl
116	231.6	10.1	40951	3	US-09-949-016-15846	Sequence 15846, A	Sequence 15846, A	189	229.4	10.0	162025	3	US-09-834-700-17	Sequence 17, Appl
C 117	231.6	10.1	45299	3	US-09-949-016-12465	Sequence 12465, A	Sequence 12465, A	190	229.4	10.0	162025	3	US-09-834-700-18	Sequence 18, Appl
C 118	231.6	10.1	45300	3	US-09-949-016-13045	Sequence 13045, A	Sequence 13045, A	191	229.4	10.0	177797	3	US-09-949-016-14125	Sequence 14125, A
C 119	231.6	10.1	54711	3	US-09-949-016-17489	Sequence 17489, A	Sequence 17489, A	192	229.4	10.0	227979	3	US-09-949-016-11842	Sequence 11842, A
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C 122	231.6	10.1	118923	3	US-09-949-016-13227	Sequence 13227, A	Sequence 13227, A	C 195	229.2	10.0	601	3	US-09-949-016-154402	Sequence 154402,
C 123	231.6	10.1	304533	3	US-09-949-016-15371	Sequence 15371, A	Sequence 15371, A	196	229.2	10.0	656	7	US-09-925-065A-675446	Sequence 675446,
C 124	231.6	10.1	304533	3	US-09-949-016-15372	Sequence 15372, A	Sequence 15372, A	197	229.2	10.0	19377	3	US-09-949-016-15198	Sequence 15198, A
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C 126	231.4	10.1	970	7	US-09-925-065A-727961	Sequence 727961,	Sequence 727961,	C 199	229.2	10.0	193169	3	US-09-949-016-15091	Sequence 15091, A
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C 159	229.8	10.1	489	7	US-09-925-065A-469133	Sequence 469133,	Sequence 469133,	C 233	228.4	10.0	626	7	US-09-925-065A-709437	Sequence 709437,
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307 227.2 9.9 154626 3 US-09-949-016-14000 Sequence 14000, A  
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C 311 227 9.9 601 3 US-09-949-016-128966 Sequence 128966, A  
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C 316 227 9.9 27692 3 US-09-949-002-680 Sequence 680, App  
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C 319 227 9.9 47030 3 US-09-949-016-13038 Sequence 13038, A  
C 320 227 9.9 47030 3 US-09-949-016-15039 Sequence 15039, A  
C 321 227 9.9 47030 3 US-09-949-016-15040 Sequence 15040, A  
C 322 227 9.9 53737 3 US-09-949-016-16197 Sequence 16197, A  
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C 328 226.8 9.9 12951 3 US-09-949-016-14075 Sequence 14075, A  
C 329 226.8 9.9 24841 3 US-09-949-016-14009 Sequence 14009, A  
330 226.8 9.9 110243 3 US-09-949-016-13698 Sequence 13698, A  
331 226.8 9.9 250958 3 US-09-949-016-16061 Sequence 16061, A  
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C 333 226.6 9.9 585 7 US-09-925-065A-257693 Sequence 257693, A  
C 334 226.6 9.9 592 7 US-09-925-065A-785034 Sequence 785034, A  
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339 226.6 9.9 76118 3 US-09-949-016-15593 Sequence 15593, A  
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C 345 226.6 9.9 211528 5 US-10-021-698A-709 Sequence 709, App  
C 346 226.6 9.9 212708 5 US-10-021-698A-708 Sequence 708, App  
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360 226.4 9.9 28843 3 US-09-949-016-17158 Sequence 17158, A  
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366 226.2 9.9 601 3 US-09-949-016-137032 Sequence 137032, A  
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368 226.2 9.9 1485 7 US-09-925-065A-700656 Sequence 700656, A  
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C 373 226.2 9.9 47781 3 US-09-949-016-16494 Sequence 16494, A  
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C 376 226.2 9.9 171065 5 US-10-021-698A-695 Sequence 695, App  
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C 381 226 9.9 601 3 US-09-949-016-193178 Sequence 193178, A  
C 382 226 9.9 601 3 US-09-949-016-193271 Sequence 193271, A  
C 383 226 9.9 601 3 US-09-949-016-193364 Sequence 193364, A  
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390	226	9.9	801	7	US-09-925-065A-88625	Sequence 88625, A	463	225.4	9.9	209274	5	US-09-543-679A-3004	Sequence 3004, Ap
C 391	226	9.9	1008	7	US-09-925-065A-723903	Sequence 723903, A	C 464	225.4	9.9	247299	3	US-09-949-016-17590	Sequence 17590, A
C 392	226	9.9	1008	7	US-09-925-065A-723904	Sequence 723904, A	C 465	225.2	9.9	472	7	US-09-925-065A-45817	Sequence 45817, A
C 393	226	9.9	27916	3	US-09-949-016-15202	Sequence 15202, A	C 466	225.2	9.9	519	7	US-09-925-065A-857427	Sequence 857427, A
C 394	226	9.9	28592	3	US-09-949-002-806	Sequence 806, App	C 467	225.2	9.9	528	7	US-09-925-065A-850425	Sequence 850425, A
395	226	9.9	39960	5	US-09-339-352-7	Sequence 7, Appli	C 468	225.2	9.9	535	7	US-09-925-065A-857432	Sequence 857432, A
396	226	9.9	41612	3	US-09-949-016-12769	Sequence 12769, A	469	225.2	9.9	538	7	US-09-925-065A-834144	Sequence 834144, A
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C 398	226	9.9	264358	3	US-09-949-016-15725	Sequence 15725, A	471	225.2	9.9	601	3	US-09-949-016-140678	Sequence 140678, A
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402	225.8	9.9	576	7	US-09-925-065A-116872	Sequence 116872, A	C 475	225.2	9.9	678	7	US-09-925-065A-864955	Sequence 864955, A
403	225.8	9.9	601	3	US-09-949-016-204425	Sequence 204425, A	C 476	225.2	9.9	2177	5	US-10-294-229A-1	Sequence 1, Appli
404	225.8	9.9	601	3	US-09-949-016-204495	Sequence 204495, A	477	225.2	9.9	8297	3	US-09-949-016-14790	Sequence 14790, A
C 405	225.8	9.9	668	7	US-09-925-065A-91743	Sequence 91743, A	478	225.2	9.9	17086	3	US-09-949-016-13684	Sequence 13684, A
C 406	225.8	9.9	688	7	US-09-925-065A-929103	Sequence 929103, A	C 479	225.2	9.9	19389	3	US-09-949-016-15113	Sequence 15113, A
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C 409	225.8	9.9	25131	3	US-09-949-016-12385	Sequence 12385, A	482	225.2	9.9	78269	3	US-09-949-016-12497	Sequence 12497, A
C 410	225.8	9.9	25131	3	US-09-949-016-13653	Sequence 13653, A	483	225.2	9.9	84839	3	US-09-949-016-15816	Sequence 15816, A
C 411	225.8	9.9	26433	3	US-09-949-016-15401	Sequence 15401, A	C 484	225.2	9.9	109925	3	US-09-949-016-13210	Sequence 13210, A
C 412	225.8	9.9	30456	3	US-09-949-016-14213	Sequence 14213, A	C 485	225.2	9.9	119762	3	US-09-949-016-17313	Sequence 17313, A
413	225.8	9.9	31797	3	US-09-949-016-17188	Sequence 17188, A	C 486	225.2	9.9	135667	3	US-09-949-016-15051	Sequence 15051, A
414	225.8	9.9	33578	3	US-09-949-016-15670	Sequence 15670, A	C 487	225.2	9.9	139257	3	US-09-920-671-11	Sequence 11, Appli
415	225.8	9.9	35465	5	US-10-030-937-56	Sequence 56, Appli	C 488	225.2	9.9	152486	3	US-09-949-016-12869	Sequence 12869, A
416	225.8	9.9	41132	3	US-09-949-016-12021	Sequence 12021, A	C 489	225.2	9.9	264206	3	US-09-949-016-12731	Sequence 12731, A
417	225.8	9.9	41136	3	US-09-949-016-13021	Sequence 13021, A	C 490	225.2	9.9	264304	3	US-09-949-016-13249	Sequence 13249, A
C 418	225.8	9.9	42381	3	US-09-949-016-12012	Sequence 12012, A	491	225.2	9.9	392000	3	US-10-027-983-11	Sequence 11, Appli
C 419	225.8	9.9	44378	3	US-09-949-016-12540	Sequence 12540, A	492	225	9.9	510	7	US-09-925-065A-258233	Sequence 258233, A
C 420	225.8	9.9	74527	3	US-09-949-016-12339	Sequence 12339, A	493	225	9.9	582	7	US-09-925-065A-878470	Sequence 878470, A
C 421	225.8	9.9	74528	3	US-09-949-016-13275	Sequence 13275, A	C 494	225	9.9	601	3	US-09-949-016-81260	Sequence 81260, A
C 422	225.8	9.9	165651	3	US-09-949-016-13032	Sequence 13032, A	C 495	225	9.9	601	3	US-09-949-016-131800	Sequence 131800, A
423	225.6	9.9	541	7	US-09-925-065A-127530	Sequence 127530, A	C 496	225	9.9	603	7	US-09-925-065A-333396	Sequence 333396, A
424	225.6	9.9	601	3	US-09-949-016-32898	Sequence 32898, A	C 497	225	9.9	1968	7	US-09-925-065A-674360	Sequence 674360, A
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C 426	225.6	9.9	624	7	US-09-925-065A-677313	Sequence 677313, A	499	225	9.9	9455	3	US-09-949-016-14650	Sequence 14650, A
C 427	225.6	9.9	627	7	US-09-925-065A-786968	Sequence 786968, A	C 500	225	9.9	22431	3	US-09-949-016-14099	Sequence 14099, A
C 428	225.6	9.9	693	7	US-09-925-065A-719234	Sequence 719234, A	501	225	9.9	24509	3	US-09-949-016-12612	Sequence 12612, A
C 429	225.6	9.9	2946	3	US-10-104-047-794	Sequence 794, App	C 502	225	9.9	24509	3	US-09-949-016-13687	Sequence 13687, A
C 430	225.6	9.9	17590	3	US-09-762-311-1	Sequence 1, Appli	C 503	225	9.9	28109	3	US-09-949-016-14329	Sequence 14329, A
431	225.6	9.9	29889	3	US-09-949-016-13682	Sequence 13682, A	504	225	9.9	54986	3	US-09-949-016-16716	Sequence 16716, A
432	225.6	9.9	43991	5	US-09-984-429-252	Sequence 252, App	505	225	9.9	82612	3	US-09-949-016-16823	Sequence 16823, A
433	225.6	9.9	53562	3	US-09-949-016-16286	Sequence 16286, A	C 506	225	9.9	112114	3	US-09-949-016-17292	Sequence 17292, A
C 434	225.6	9.9	101015	3	US-09-949-016-16981	Sequence 16981, A	507	225	9.9	145928	3	US-09-949-016-15444	Sequence 15444, A
C 435	225.4	9.9	424	7	US-09-925-065A-786430	Sequence 786430, A	C 508	225	9.9	154605	3	US-09-949-016-11894	Sequence 11894, A
C 436	225.4	9.9	601	3	US-09-949-016-80035	Sequence 80035, A	C 509	225	9.9	260286	3	US-09-949-016-17037	Sequence 17037, A
C 437	225.4	9.9	601	3	US-09-949-016-80036	Sequence 80036, A	510	225	9.9	260293	3	US-09-949-016-12106	Sequence 12106, A
438	225.4	9.9	611	7	US-09-925-065A-373334	Sequence 373334, A	511	224.8	9.8	599	7	US-09-925-065A-763319	Sequence 763319, A
439	225.4	9.9	611	7	US-09-925-065A-373335	Sequence 373335, A	512	224.8	9.8	599	7	US-09-925-065A-763320	Sequence 763320, A
440	225.4	9.9	611	7	US-09-925-065A-373336	Sequence 373336, A	C 513	224.8	9.8	600	7	US-09-925-065A-765921	Sequence 765921, A
441	225.4	9.9	1184	7	US-09-925-065A-65816	Sequence 65816, A	C 514	224.8	9.8	600	7	US-09-925-065A-765922	Sequence 765922, A
C 442	225.4	9.9	7481	3	US-09-949-016-14492	Sequence 14492, A	C 515	224.8	9.8	601	3	US-09-949-016-193084	Sequence 193084, A
C 443	225.4	9.9	19650	3	US-09-819-989-3	Sequence 3, Appli	C 516	224.8	9.8	601	3	US-09-949-016-193177	Sequence 193177, A
C 444	225.4	9.9	19650	3	US-10-273-992-3	Sequence 3, Appli	C 517	224.8	9.8	601	3	US-09-949-016-193270	Sequence 193270, A
C 445	225.4	9.9	19650	3	US-10-681-222-3	Sequence 3, Appli	C 518	224.8	9.8	601	3	US-09-949-016-193363	Sequence 193363, A
C 446	225.4	9.9	20598	3	US-09-593-995-10	Sequence 10, Appli	519	224.8	9.8	606	7	US-09-925-065A-520953	Sequence 520953, A
C 447	225.4	9.9	20598	3	US-10-139-667-10	Sequence 10, Appli	C 520	224.8	9.8	608	7	US-09-925-065A-673158	Sequence 673158, A
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C 449	225.4	9.9	32278	3	US-09-949-016-14575	Sequence 14575, A	C 522	224.8	9.8	12708	3	US-09-949-016-13216	Sequence 13216, A
C 450	225.4	9.9	34200	5	US-09-339-352-17	Sequence 17, Appli	C 523	224.8	9.8	19062	3	US-09-949-016-14877	Sequence 14877, A
451	225.4	9.9	72992	3	US-09-949-016-17592	Sequence 17592, A	C 524	224.8	9.8	53442	3	US-09-949-016-11921	Sequence 11921, A
452	225.4	9.9	90541	3	US-09-759-359A-3	Sequence 3, Appli	C 525	224.8	9.8	53453	3	US-09-949-016-13370	Sequence 13370, A
453	225.4	9.9	90541	3	US-10-207-973-3	Sequence 3, Appli	C 526	224.8	9.8	57299	3	US-09-949-016-12141	Sequence 12141, A
454	225.4	9.9	90541	5	US-10-799-676-3	Sequence 3, Appli	C 527	224.8	9.8	67876	3	US-09-949-016-17232	Sequence 17232, A
C 455	225.4	9.9	96845	3	US-09-949-016-13658	Sequence 13658, A	C 528	224.8	9.8	86213	3	US-09-949-016-17240	Sequence 17240, A
456	225.4	9.9	132205	5	US-10-185-047A-25	Sequence 25, Appli	C 529	224.8	9.8	86213	3	US-09-949-016-17241	Sequence 17241, A
457	225.4	9.9	141589	5	US-09-543-679A-2480	Sequence 2480, Ap	C 530	224.8	9.8	86213	3	US-09-949-016-17242	Sequence 17242, A
458	225.4	9.9	141589	5	US-09-543-679A-2694	Sequence 2694, Ap	C 531	224.8	9.8	86213	3	US-09-949-016-17243	Sequence 17243, A
459	225.4	9.9	141589	5	US-09-543-679A-2719	Sequence 2719, Ap	C 532	224.8	9.8	97423	3	US-09-949-016-12742	Sequence 12742, A
460	225.4	9.9	146982	5	US-09-543-679A-3009	Sequence 3009, Ap	C 533	224.8	9.8	97424	3	US-09-949-016-15576	Sequence 15576, A

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536	224.6	9.8	554	7	US-09-925-065A-583715	Sequence 583715,		609	224.2	9.8	2850	4	US-10-094-749-644	Sequence 644, App
C 537	224.6	9.8	562	7	US-09-925-065A-301982	Sequence 301982,		610	224.2	9.8	52874	3	US-09-949-016-14868	Sequence 14868, A
538	224.6	9.8	570	7	US-09-925-065A-561870	Sequence 561870,		C 611	224.2	9.8	63804	3	US-09-949-016-15200	Sequence 15200, A
C 539	224.6	9.8	586	7	US-09-925-065A-409123	Sequence 409123,		612	224.2	9.8	72128	3	US-09-949-016-16018	Sequence 16018, A
C 540	224.6	9.8	17901	3	US-09-949-016-14064	Sequence 14064, A		613	224.2	9.8	86947	3	US-09-949-016-11930	Sequence 11930, A
541	224.6	9.8	26136	3	US-09-949-016-13640	Sequence 13640, A		614	224.2	9.8	96327	3	US-09-949-016-16541	Sequence 16541, A
542	224.6	9.8	61108	3	US-09-949-002-608	Sequence 608, App		615	224.2	9.8	163022	3	US-09-949-016-16515	Sequence 16515, A
C 543	224.6	9.8	84839	3	US-09-949-016-15816	Sequence 15816, A		C 616	224.2	9.8	247781	3	US-09-949-016-14193	Sequence 14193, A
544	224.6	9.8	92387	3	US-09-949-016-14563	Sequence 14563, A		617	224.2	9.8	264358	3	US-09-949-016-15725	Sequence 15725, A
C 545	224.6	9.8	118136	3	US-09-949-016-12439	Sequence 12439, A		C 618	224.2	9.8	285478	3	US-09-949-016-13362	Sequence 13362, A
546	224.6	9.8	151295	3	US-09-949-016-14568	Sequence 14568, A		C 619	224	9.8	551	7	US-09-925-065A-882273	Sequence 882273,
547	224.6	9.8	151295	3	US-09-949-016-14569	Sequence 14569, A		C 620	224	9.8	596	7	US-09-925-065A-938099	Sequence 938099,
548	224.6	9.8	151295	3	US-09-949-016-14570	Sequence 14570, A		C 621	224	9.8	601	3	US-09-949-016-42392	Sequence 42392, A
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550	224.6	9.8	151295	3	US-09-949-016-14572	Sequence 14572, A		C 623	224	9.8	1503	7	US-09-925-065A-680224	Sequence 680224,
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554	224.6	9.8	152822	3	US-09-949-016-17519	Sequence 17519, A		627	224	9.8	22400	3	US-10-143-266-1	Sequence 1, Appli
555	224.6	9.8	234884	3	US-09-949-016-16420	Sequence 16420, A	C	628	224	9.8	41895	3	US-09-949-016-15135	Sequence 15135, A
556	224.6	9.8	393753	3	US-09-949-016-14573	Sequence 14573, A		629	224	9.8	61178	3	US-09-949-016-17369	Sequence 17369, A
557	224.6	9.8	393753	3	US-09-949-016-14574	Sequence 14574, A		630	224	9.8	86945	3	US-09-949-016-13849	Sequence 13849, A
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559	224.6	9.8	818128	3	US-09-949-016-14547	Sequence 14547, A		632	224	9.8	86945	3	US-09-949-016-13851	Sequence 13851, A
560	224.6	9.8	818128	3	US-09-949-016-14548	Sequence 14548, A		633	224	9.8	86945	3	US-09-949-016-13852	Sequence 13852, A
561	224.6	9.8	818128	3	US-09-949-016-14549	Sequence 14549, A		634	224	9.8	86945	3	US-09-949-016-13853	Sequence 13853, A
562	224.6	9.8	818128	3	US-09-949-016-14550	Sequence 14550, A		635	224	9.8	86945	3	US-09-949-016-13854	Sequence 13854, A
563	224.6	9.8	818128	3	US-09-949-016-14551	Sequence 14551, A		636	224	9.8	86945	3	US-09-949-016-13855	Sequence 13855, A
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566	224.6	9.8	818128	3	US-09-949-016-14554	Sequence 14554, A		639	224	9.8	86945	3	US-09-949-016-13858	Sequence 13858, A
567	224.6	9.8	818128	3	US-09-949-016-14555	Sequence 14555, A		640	224	9.8	87523	3	US-09-949-016-12670	Sequence 12670, A
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570	224.6	9.8	818128	3	US-09-949-016-14558	Sequence 14558, A		643	224	9.8	87523	3	US-09-949-016-15049	Sequence 15049, A
571	224.6	9.8	818128	3	US-09-949-016-14559	Sequence 14559, A		644	224	9.8	87869	3	US-09-949-016-11744	Sequence 11744, A
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573	224.6	9.8	818128	3	US-09-949-016-14561	Sequence 14561, A		646	224	9.8	87869	3	US-09-949-016-15045	Sequence 15045, A
574	224.6	9.8	818128	3	US-09-949-016-14562	Sequence 14562, A		647	224	9.8	87869	3	US-09-949-016-15046	Sequence 15046, A
575	224.6	9.8	818128	3	US-09-949-016-14564	Sequence 14564, A		C 648	224	9.8	117391	3	US-09-949-016-13945	Sequence 13945, A
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577	224.6	9.8	818128	3	US-09-949-016-14566	Sequence 14566, A		650	223.8	9.8	601	3	US-09-949-016-55383	Sequence 55383, A
578	224.6	9.8	818128	3	US-09-949-016-14567	Sequence 14567, A		651	223.8	9.8	601	3	US-09-949-016-131718	Sequence 131718,
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C 582	224.4	9.8	548	7	US-09-925-065A-830330	Sequence 830330,		C 655	223.8	9.8	601	3	US-09-949-016-152288	Sequence 152288,
C 583	224.4	9.8	555	7	US-09-925-065A-47368	Sequence 47368, A		C 656	223.8	9.8	601	3	US-09-949-016-159375	





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C 827	222.8	9.8	818128	3	US-09-949-016-14559	Sequence 14559, A	C 900	222.2	9.7	646	7	US-09-925-065A-500330	Sequence 500330,
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C 829	222.8	9.8	818128	3	US-09-949-016-14561	Sequence 14561, A	C 902	222.2	9.7	841	8	PCT-US93-06251-81	Sequence 81, Appl
C 830	222.8	9.8	818128	3	US-09-949-016-14562	Sequence 14562, A	C 903	222.2	9.7	878	7	US-09-925-065A-55287	Sequence 55287, A
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C 846	222.6	9.7	39960	5	US-09-339-352-7	Sequence 7, Appli	919	222	9.7	512	7	US-09-925-065A-155742	Sequence 155742,
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C 850	222.6	9.7	56702	3	US-09-949-016-15423	Sequence 15423, A	C 923	222	9.7	601	3	US-09-949-016-47164	Sequence 47164, A
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852	222.6	9.7	80246	3	US-09-078-294-4	Sequence 4, Appli	C 925	222	9.7	611	7	US-09-925-065A-850137	Sequence 850137,
853	222.6	9.7	80595	3	US-09-078-294-3	Sequence 3, Appli	C 926	222	9.7	613	7	US-09-925-065A-754442	Sequence 754442,
854	222.6	9.7	80595	5	US-09-728-552A-3	Sequence 3, Appli	C 927	222	9.7	621	7	US-09-925-065A-846357	Sequence 846357,
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856	222.6	9.7	128516	3	US-09-949-016-13501	Sequence 13501, A	929	222	9.7	699	7	US-09-925-065A-880171	Sequence 880171,
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C 860	222.6	9.7	156894	3	US-09-949-016-12765	Sequence 12765, A	C 933	222	9.7	17896	3	US-09-949-016-16867	Sequence 16867, A
C 861	222.6	9.7	156894	3	US-09-949-016-12766	Sequence 12766, A	C 934	222	9.7	19237	3	US-09-949-016-13666	Sequence 13666, A
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C 863	222.6	9.7	156895	3	US-09-949-016-16958	Sequence 16958, A	C 936	222	9.7	43086	3	US-09-949-016-13059	Sequence 13059, A
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C 865	222.6	9.7	156895	3	US-09-949-016-13266	Sequence 13266, A	C 938	222	9.7	60376	3	US-09-949-016-12423	Sequence 12423, A
C 866	222.6	9.7	187580	5	US-10-021-698A-697	Sequence 697, App	C 939	222	9.7	70308	3	US-09-949-016-15601	Sequence 15601, A
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C 870	222.4	9.7	601	3	US-09-949-016-139175	Sequence 139175,	C 943	222	9.7	113042	3	US-09-949-016-12343	Sequence 12343, A
871	222.4	9.7	601	3	US-09-949-016-139669	Sequence 139669,	C 944	222	9.7	113042	3	US-09-949-016-15246	Sequence 15246, A
872	222.4	9.7	601	3	US-09-949-016-150942	Sequence 150942,	945	222	9.7	133358	3	US-09-949-016-16964	Sequence 16964, A
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874	222.4	9.7	639	7	US-09-925-065A-92802	Sequence 92802, A	C 947	222	9.7	162025	3	US-09-834-700-13	Sequence 13, Appl
875	222.4	9.7	766	5	US-10-021-698A-428	Sequence 428, App	C 948	222	9.7	162025	3	US-09-834-700-14	Sequence 14, Appl
876	222.4	9.7	11494	3	US-09-949-016-13347	Sequence 13347, A	C 949	222	9.7	162025	3	US-09-834-700-17	Sequence 17, Appl
877	222.4	9.7	18679	3	US-09-949-016-13443	Sequence 13443, A	C 950	222	9.7	162025	3	US-09-834-700-18	Sequence 18, Appl
878	222.4	9.7	26867	3	US-09-949-016-16332	Sequence 16332, A	951	222	9.7	199945	3	US-09-949-016-15436	Sequence 15436, A
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C 885	222.4	9.7	44653	3	US-09-949-016-11944	Sequence 11944, A	C 958	221.8	9.7	601	3	US-09-949-016-63920	Sequence 63920, A
C 886	222.4	9.7	44653	3	US-09-949-016-15690	Sequence 15690, A	C 959	221.8	9.7	601	3	US-09-949-016-65931	Sequence 65931, A
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C 888	222.4	9.7	51773	3	US-09-949-016-16002	Sequence 16002, A	C 961	221.8	9.7	601	3	US-09-949-016-160721	Sequence 160721,
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C 890	222.4	9.7	52865	3	US-09-949-016-15618	Sequence 15618, A	963	221.8	9.7	601	3	US-09-949-016-199161	Sequence 199161,
C 891	222.4	9.7	72602	3	US-09-949-016-14385	Sequence 14385, A	964	221.8	9.7	601	3	US-09-949-002-3495	Sequence 3495, Ap
892	222.4	9.7	190849	5	US-10-021-698A-706	Sequence 706, App	965	221.8	9.7	601	3	US-09-949-002-9467	Sequence 9467, Ap
893	222.4	9.7	264665	3	US-09-949-016-13747	Sequence 13747, A	966	221.8	9.7	603	7	US-09-925-065A-349601	Sequence 349601,
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C 898	222.2	9.7	576	7	US-09-925-065A-431198	Sequence 431198,	971	221.8	9.7	14205	3	US-09-949-016-16196	Sequence 16196, A



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c 976	221.8	9.7	22124	3	US-09-949-016-14666	Sequence 14666, A	1049	221.4	9.7	40546	3	US-09-949-016-12915	Sequence 12915, A
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c 980	221.8	9.7	102520	3	US-09-949-016-17367	Sequence 17367, A	c1053	221.4	9.7	57859	3	US-09-949-016-14658	Sequence 14658, A
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982	221.8	9.7	119594	3	US-09-949-016-12080	Sequence 12080, A	1055	221.4	9.7	83708	3	US-09-949-016-17207	Sequence 17207, A
c 983	221.8	9.7	119601	3	US-09-949-016-15952	Sequence 15952, A	1056	221.4	9.7	133278	3	US-09-949-016-12524	Sequence 12524, A
c 984	221.8	9.7	151088	3	US-09-949-016-16240	Sequence 16240, A	c1057	221.4	9.7	135030	3	US-09-949-016-14896	Sequence 14896, A
c 985	221.6	9.7	469	7	US-09-925-065A-799777	Sequence 799777, A	c1058	221.4	9.7	254964	3	US-09-949-016-12583	Sequence 12583, A
c 986	221.6	9.7	474	7	US-09-925-065A-792523	Sequence 792523, A	c1059	221.4	9.7	254964	3	US-09-949-016-17392	Sequence 17392, A
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988	221.6	9.7	601	3	US-09-949-016-87763	Sequence 87763, A	c1061	221.4	9.7	678533	3	US-09-949-016-14578	Sequence 14578, A
989	221.6	9.7	601	3	US-09-949-016-87764	Sequence 87764, A	c1062	221.2	9.7	501	7	US-09-925-065A-799758	Sequence 799758, A
990	221.6	9.7	601	3	US-09-949-016-135168	Sequence 135168, A	c1063	221.2	9.7	508	7	US-09-925-065A-741605	Sequence 741605, A
c 991	221.6	9.7	629	7	US-09-925-065A-576432	Sequence 576432, A	1064	221.2	9.7	509	7	US-09-925-065A-787319	Sequence 787319, A
c 992	221.6	9.7	1426	7	US-09-620-312D-967	Sequence 967, App	1065	221.2	9.7	561	7	US-09-925-065A-502735	Sequence 502735, A
c 993	221.6	9.7	2092	7	US-09-925-065A-710753	Sequence 710753, A	c1066	221.2	9.7	573	7	US-09-925-065A-833297	Sequence 833297, A
994	221.6	9.7	2345	5	US-10-108-260A-172	Sequence 172, App	1067	221.2	9.7	581	7	US-09-925-065A-318711	Sequence 318711, A
995	221.6	9.7	2405	3	US-10-104-047-1452	Sequence 1452, Ap	c1068	221.2	9.7	601	3	US-09-949-016-182224	Sequence 182224, A
c 996	221.6	9.7	2436	7	US-09-925-065A-670010	Sequence 670010, A	c1069	221.2	9.7	601	3	US-09-949-016-189339	Sequence 189339, A
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c 999	221.6	9.7	2836	7	US-09-925-065A-698795	Sequence 698795, A	c1072	221.2	9.7	688	7	US-09-925-065A-35460	Sequence 35460, A
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c1003	221.6	9.7	13193	3	US-09-949-016-17515	Sequence 17515, A	1075	221.2	9.7	15116	3	US-08-943-731-111	Sequence 3, Appli
c1004	221.6	9.7	14079	3	US-09-949-016-11993	Sequence 11993, A	c1076	221.2	9.7	1867	3	US-09-925-065A-78615	Sequence 78615, A
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c1008	221.6	9.7	22888	3	US-09-949-016-14659	Sequence 14659, A	c1081	221.2	9.7	24183	3	US-08-943-731-111	Sequence 3, Appli
1009	221.6	9.7	25428	3	US-09-949-016-17161	Sequence 17161, A	c1082	221.2	9.7	25951	3	US-09-949-016-16194	Sequence 16194, A
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1012	221.6	9.7	49389	3	US-09-949-016-13630	Sequence 13630, A	c1085	221.2	9.7	50810	3	US-09-949-016-16039	Sequence 16039, A
c1013	221.6	9.7	50518	3	US-09-949-016-12315	Sequence 12315, A	1086	221.2	9.7	54033	3	US-09-949-016-12091	Sequence 12091, A
c1014	221.6	9.7	58162	3	US-09-949-016-16289	Sequence 16289, A	1087	221.2	9.7	54033	3	US-09-949-016-14325	Sequence 14325, A
c1015	221.6	9.7	63982	3	US-09-949-016-16769	Sequence 16769, A	1088	221.2	9.7	57638	3	US-09-949-016-17000	Sequence 17000, A
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1017	221.6	9.7	101951	3	US-09-949-016-15648	Sequence 15648, A	1090	221.2	9.7	60195	3	US-09-949-002-697	Sequence 697, App
1018	221.6	9.7	107980	3	US-09-949-016-14370	Sequence 14370, A	c1091	221.2	9.7	125192	3	US-09-949-016-14120	Sequence 14120, A
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c1020	221.6	9.7	276687	3	US-09-949-016-13840	Sequence 13840, A	c1093	221.2	9.7	278866	3	US-09-949-016-13922	Sequence 13922, A
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c1023	221.4	9.7	598	7	US-09-925-065A-887367	Sequence 887367, A	c1096	221.2	9.7	278866	3	US-09-949-016-13925	Sequence 13925, A
c1024	221.4	9.7	601	3	US-09-949-016-51669	Sequence 51669, A	c1097	221.2	9.7	278866	3	US-09-949-016-13926	Sequence 13926, A
c1025	221.4	9.7	601	3	US-09-949-016-51670	Sequence 51670, A	c1098	221.2	9.7	278866	3	US-09-949-016-14699	Sequence 14699, A
c1026	221.4	9.7	601	3	US-09-949-016-149747	Sequence 149747, A	c1099	221.2	9.7	278866	3	US-09-949-016-14700	Sequence 14700, A
c1027	221.4	9.7	601	3	US-09-949-016-149748	Sequence 149748, A	c1100	221.2	9.7	278866	3	US-09-949-016-14701	Sequence 14701, A
c1028	221.4	9.7	601	3	US-09-949-016-179931	Sequence 179931, A	c1101	221.2	9.7	278866	3	US-09-949-016-14702	Sequence 14702, A
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c1032	221.4	9.7	633	7	US-09-925-065A-723304	Sequence 723304, A	c1105	221	9.7	565	7	US-09-925-065A-414376	Sequence 414376, A
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c1038	221.4	9.7	10751	3	US-09-949-016-12097	Sequence 12097, A	c1111	221	9.7	601	3	US-09-949-016-125476	Sequence 125476, A
c1039	221.4	9.7	10751	3	US-09-949-016-13486	Sequence 13486, A	1112	221	9.7	601	3	US-09-949-016-138588	Sequence 138588, A
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1041	221.4	9.7	12482	3	US-09-512-563C-25	Sequence 25, Appl	1114	221	9.7	605	7	US-09-925-065A-842773	Sequence 842773, A
1042	221.4	9.7	12482	3	US-10-060-607-25	Sequence 25, Appl	c1115	221	9.7	617	7	US-09-925-065A-49035	Sequence 49035, A
1043	221.4	9.7	12482	5	US-10-270-877-25	Sequence 25, Appl	c1116	221	9.7	826	7	US-09-925-065A-722461	Sequence 722461, A
1044	221.4	9.7	12482	5	US-10-270-837-25	Sequence 25, Appl	1117	221	9.7	864	7	US-09-925-065A-82967	Sequence 82967, A

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c1123	221	9.7	1168	7	US-09-925-065A-45033	Sequence 45033, A	1196	220.6	9.7	557	7	US-09-925-065A-177024	Sequence 177024, A
c1124	221	9.7	1421	7	US-09-925-065A-667547	Sequence 667547, A	c1197	220.6	9.7	576	7	US-09-925-065A-431197	Sequence 431197, A
c1125	221	9.7	1421	7	US-09-925-065A-667548	Sequence 667548, A	c1198	220.6	9.7	586	7	US-09-925-065A-175723	Sequence 175723, A
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c1132	221	9.7	2561	3	US-09-270-542-119	Sequence 119, App	c1205	220.6	9.7	601	3	US-09-949-016-91445	Sequence 91445, A
1133	221	9.7	5957	5	US-10-342-887-252	Sequence 252, App	c1206	220.6	9.7	601	3	US-09-949-016-125477	Sequence 125477, A
c1134	221	9.7	11982	3	US-09-949-016-17084	Sequence 17084, A	1207	220.6	9.7	601	3	US-09-949-016-140123	Sequence 140123, A
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1137	221	9.7	18891	3	US-09-949-016-16523	Sequence 16523, A	c1210	220.6	9.7	601	3	US-09-949-002-3305	Sequence 3305, Ap
1138	221	9.7	22480	5	US-09-630-629B-43	Sequence 43, Appl	c1211	220.6	9.7	601	3	US-09-949-002-7764	Sequence 7764, Ap
1139	221	9.7	22481	3	US-08-367-841A-43	Sequence 43, Appl	c1212	220.6	9.7	646	7	US-09-925-065A-500329	Sequence 500329, A
1140	221	9.7	22481	8	PCT-US95-07201-43	Sequence 43, Appl	c1213	220.6	9.7	830	7	US-09-925-065A-10132	Sequence 10132, A
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1144	221	9.7	25260	3	US-09-949-016-11985	Sequence 11985, A	c1217	220.6	9.7	2034	5	US-09-973-278-872	Sequence 872, App
1145	221	9.7	25260	3	US-09-949-016-12907	Sequence 12907, A	c1218	220.6	9.7	2167	7	US-09-925-065A-88279	Sequence 88279, A
c1146	221	9.7	27463	3	US-09-949-016-11876	Sequence 11876, A	c1219	220.6	9.7	2167	7	US-09-925-065A-88281	Sequence 88281, A
c1147	221	9.7	29266	3	US-09-949-002-739	Sequence 739, App	1220	220.6	9.7	23907	3	US-09-949-016-15329	Sequence 15329, A
c1148	221	9.7	29742	3	US-09-949-016-15650	Sequence 15650, A	1221	220.6	9.7	27780	3	US-09-949-016-12013	Sequence 12013, A
c1149	221	9.7	32654	3	US-09-801-191A-3	Sequence 3, Appli	1222	220.6	9.7	27791	3	US-09-949-016-17498	Sequence 17498, A
c1150	221	9.7	32654	3	US-10-345-198-3	Sequence 3, Appli	1223	220.6	9.7	38239	3	US-09-949-016-12348	Sequence 12348, A
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1153	221	9.7	37712	3	US-09-949-016-12692	Sequence 12692, A	1226	220.6	9.7	84132	3	US-09-949-016-16241	Sequence 16241, A
c1154	221	9.7	38944	3	US-09-949-002-615	Sequence 615, App	c1227	220.6	9.7	85854	3	US-09-949-016-12908	Sequence 12908, A
c1155	221	9.7	51905	3	US-09-949-002-667	Sequence 667, App	1228	220.6	9.7	112114	3	US-09-949-016-17292	Sequence 17292, A
c1156	221	9.7	51905	3	US-09-949-002-781	Sequence 781, App	c1229	220.6	9.7	149543	3	US-09-949-016-15947	Sequence 15947, A
c1157	221	9.7	70770	3	US-09-949-016-16938	Sequence 16938, A	1230	220.6	9.7	154605	3	US-09-949-016-11894	Sequence 11894, A
1158	221	9.7	74424	5	US-10-773-678A-153	Sequence 153, App	1231	220.6	9.7	187916	3	US-09-949-016-12980	Sequence 12980, A
c1159	221	9.7	81927	3	US-09-949-016-15623	Sequence 15623, A	1232	220.6	9.7	202111	3	US-09-949-016-13877	Sequence 13877, A
c1160	221	9.7	97195	3	US-09-949-016-12212	Sequence 12212, A	c1233	220.4	9.6	601	3	US-09-949-016-22674	Sequence 22674, A
c1161	221	9.7	97196	3	US-09-949-016-16971	Sequence 16971, A	c1234	220.4	9.6	601	3	US-09-949-016-29409	Sequence 29409, A
1162	221	9.7	110096	4	US-09-880-107-1542	Sequence 1542, Ap	c1235	220.4	9.6	601	3	US-09-949-016-29410	Sequence 29410, A
c1163	221	9.7	143155	3	US-09-949-016-11925	Sequence 11925, A	c1236	220.4	9.6	601	3	US-09-949-016-29411	Sequence 29411, A
c1164	221	9.7	143164	3	US-09-949-016-14368	Sequence 14368, A	1237	220.4	9.6	601	3	US-09-949-016-58609	Sequence 58609, A
c1165	221	9.7	143173	3	US-09-949-016-14513	Sequence 14513, A	c1238	220.4	9.6	601	3	US-09-949-016-89013	Sequence 89013, A
c1166	221	9.7	166698	3	US-09-949-016-16038	Sequence 16038, A	1239	220.4	9.6	601	3	US-09-949-016-143723	Sequence 143723, A
c1167	221	9.7	231129	3	US-09-949-016-16110	Sequence 16110, A	c1240	220.4	9.6	601	3	US-09-949-016-158257	Sequence 158257, A
c1168	221	9.7	255679	3	US-09-949-016-17189	Sequence 17189, A	c1241	220.4	9.6	601	3	US-09-949-016-158258	Sequence 158258, A
c1169	221	9.7	266293	3	US-09-949-016-11934	Sequence 11934, A	c1242	220.4	9.6	601	3	US-09-949-016-158259	Sequence 158259, A
c1170	220.8	9.7	532	7	US-09-925-065A-825849	Sequence 825849, A	c1243	220.4	9.6	601	3	US-09-949-016-172718	Sequence 172718, A
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1174	220.8	9.7	601	3	US-09-949-016-117852	Sequence 117852, A	1247	220.4	9.6	636	7	US-09-925-065A-944020	Sequence 944020, A
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c1190	220.8	9.7	205044	3	US-09-949-016-15853	Sequence 15853, A	c1263	220.4	9.6	32010	3	US-09-949-016-13127	Sequence 13127, A



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c1266	220.4	9.6	36611	3	US-09-949-016-17287	Sequence 17287, A	1339	220	9.6	601	3	US-09-949-016-63315	Sequence 63315, A
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c1269	220.4	9.6	46319	3	US-09-949-016-12526	Sequence 12526, A	c1342	220	9.6	601	3	US-09-949-016-162142	Sequence 162142, A
c1270	220.4	9.6	46323	3	US-09-949-016-13267	Sequence 13267, A	c1343	220	9.6	601	3	US-09-949-016-178888	Sequence 178888, A
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1272	220.4	9.6	85850	3	US-09-949-016-13424	Sequence 13424, A	c1345	220	9.6	644	7	US-09-925-065A-929015	Sequence 929015, A
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1289	220.2	9.6	601	3	US-09-949-016-166861	Sequence 166861, A	c1362	220	9.6	57933	3	US-09-949-002-822	Sequence 822, App
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1301	220.2	9.6	12359	3	US-09-949-016-17004	Sequence 17004, A	1374	220	9.6	144922	3	US-09-949-016-15890	Sequence 15890, A
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1470 219.6 9.6 105168 3 US-09-949-016-13296 Sequence 13296, A  
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1476 219.6 9.6 152740 5 US-09-543-679A-2840 Sequence 2840, Ap  
1477 219.6 9.6 174170 3 US-09-949-016-14810 Sequence 14810, A  
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c1483 219.6 9.6 199261 5 US-10-021-698A-712 Sequence 712, App  
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c1485 219.4 9.6 447 7 US-09-925-065A-46720 Sequence 46720, A  
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ALIGNMENTS

RESULT 1

US-09-866-028-82

; Sequence 82, Application US/098666028

; Patent No. 6642360

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/866,028

; CURRENT FILING DATE: 2001-05-25

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 82

; LENGTH: 2284

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-866-028-82

Query Match 100.0%; Score 2284; DB 3; Length 2284;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 GCCAGAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG 180

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Db 1981 AGTGGGAACCAAATTAGGTAAATTTTGGGTAACTGTCTCTAAATATTAGCTAAAAACAA 2040  
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Db 2101 TATGCAAAGAAACAGGTTAGGACATCTAGGTTCCAAATTCATTCAATTTCTTGTTCCAGA 2160  
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QY 2281 TCAA 2284  
Db 2281 TCAA 2284



US-09-944-457-82  
; Sequence 82, Application US/09944457  
; Patent No. 6734288  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,457  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 82  
; LENGTH: 2284  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-944-457-82  
  
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Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 241 GAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCT 300  
  
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Db 301 AGTCAGATTGCCTCAAAAAGAGTCTAGAGATGTTGTATTGACATCCAGTCTATCTTT 360  
  
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Db 361 TCTAAGGGAATCAGAGGCAATGAGCCCGTATATACCTCAACTCAAGAAGACTGCAATTAAT 420  
  
Qy 421 TCTTGTCTGTTCAACAAAAAATATATCAGGGGACAAAGCATGTAACTTGAATGATCTTCGAC 480  
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Db 421 TCTTGTCTGTTCAACAAAAAATATATCAGGGGACAAAGCATGTAACTTGAATGATCTTCGAC 480  
  
Qy 481 ACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGTCCCAACGAGGAAGCC 540  
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Db 481 ACTCGAAAAACAGCTAGACACCAACTGCTACCTATTTTCTGTCTCCAAACGAGGAAGCC 540

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Qy 1861 GTCTCAAACTCCTGACCTAGTGATCCACCTCCTCGGCCTCCCAAAGTGTGGGATTACA 1920

Db 1861 GTCTCAAACTCCTGACCTAGTGATCCACCTCCTCGGCCTCCCAAAGTGTGGGATTACA 1920

Qy 1921 GGATGAGCCACACAGCTGGCCCCCTTCTGTTTATGTTGGTTTTGAGAGGAATGA 1980

Db 1921 GGATGAGCCACACAGCTGGCCCCCTTCTGTTTATGTTGGTTTTGAGAGGAATGA 1980

Qy 1981 AGTGGGAACCAAAATAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAA 2040

Db 1981 AGTGGGAACCAAAATAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAA 2040

Qy 2041 AGCTCTATGTAAAAGTAAATAAGTATAATTGCCATATAAATTTCAAAATTTCAACTGGCTTT 2100

Db 2041 AGCTCTATGTAAAAGTAAATAAGTATAATTGCCATATAAATTTCAAAATTTCAACTGGCTTT 2100

Qy 2101 TATGCAAAGAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACTTCTGGTCCAGA 2160

Db 2101 TATGCAAAGAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACTTCTGGTCCAGA 2160

Qy 2161 TAAAATCAACTGTTTATATCAATTTCTAAATGGATTTGCTTTTCTTTTATATGGATTCCT 2220

Db 2161 TAAAATCAACTGTTTATATCAATTTCTAAATGGATTTGCTTTTCTTTTATATGGATTCCT 2220

Qy 2221 TTAAAACCTTATTCAGATGTAGTTCCCTTCCAATTAATAATTTGAATAAATCTTTTGTATC 2280

Db 2221 TTAAAACCTTATTCAGATGTAGTTCCCTTCCAATTAATAATTTGAATAAATCTTTTGTATC 2280

Qy 2281 TCAA 2284

Db 2281 TCAA 2284

RESULT 3

US-09-945-584-82

; Sequence 82, Application US/09945584

; Patent No. 6908993

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/945,584  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6908993ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6908993ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 82  
; LENGTH: 2284  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-945-584-82  
  
Query Match 100.0%; Score 2284; DB 3; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GCGGAGCATCCGCTCGGTCCTCGCCGAGACACCCCGCGGATTTCGCCGGTCTTCCCGC 60  
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Db 1 GCGGAGCATCCGCTCGGTCCTCGCCGAGACACCCCGCGGATTTCGCCGGTCTTCCCGC 60  
  
QY 61 GGGCGGACAGAGCTGTCTCGCACCTTGGATGGCAGCAGGGCGCCGGGTCTCTCGAC 120  
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Db 61 GGGCGGACAGAGCTGTCTCGCACCTTGGATGGCAGCAGGGCGCCGGGTCTCTCGAC 120  
  
QY 121 GCCAGAGAGAAATCTCATCTGTGCGACCTTCTTAAAGCAAACTAAGACCAGAGGGAG 180  
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Db 121 GCCAGAGAGAAATCTCATCTGTGCGACCTTCTTAAAGCAAACTAAGACCAGAGGGAG 180  
  
QY 181 GATTATCCTTGACCTTTGAAGACCAAACTAAACTGAAATTTTAAATGTTCTTCGGGGA 240  
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Db 181 GATTATCCTTGACCTTTGAAGACCAAACTAAACTGAAATTTTAAATGTTCTTCGGGGA 240  
  
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Db 241 GAAGGAGCTTGACTTACACTTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCT 300  
  
QY 301 AGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTTCATTGACATCCAGTCATCTCTT 360  
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Db 301 AGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTTCATTGACATCCAGTCATCTCTT 360  
  
QY 361 TCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAT 420  
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Db 361 TCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAT 420  
  
QY 421 TCTTGTCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC 480  
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Db 421 TCTTGTCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC 480  
  
QY 481 ACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGTCCCAACGAGGAAGCC 540  
|||  
Db 481 ACTCGAAAAACAGCTAGACAAACCACTGCTACCTATTTTCTGTCCCAACGAGGAAGCC 540  
  
QY 541 TGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCT 600  
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Db 541 TGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCT 600  
  
QY 601 TTGACCAGAAATTTGCCAAGCCAGAGTTACCCCGAGGAAGATTCTCTTTACATGGCCAA 660  
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Db 601 TTGACCAGAAATTTGCCAAGCCAGAGTTACCCCGAGGAAGATTCTCTTTACATGGCCAA 660  
  
QY 661 TTTTCAAGCAGTCACTCCCCTAGCCCATCATCACAGATTATTCAAAGCCCACCGAT 720  
|||  
Db 661 TTTTCAAGCAGTCACTCCCCTAGCCCATCATCACAGATTATTCAAAGCCCACCGAT 720  
  
QY 721 ATCTCATGGAGAGACACACTTTCTCAGAAAGTTGGATCCTCAGATCACCTGGAGAACTA 780  
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Db 721 ATCTCATGGAGAGACACACTTTCTCAGAAAGTTGGATCCTCAGATCACCTGGAGAACTA 780  
  
QY 781 TTTAAGATGATGAAGCAAGTGCCTGCTTATAAGGAAAAAGGCCATTCTCAG 840  
|||  
Db 781 TTTAAGATGATGAAGCAAGTGCCTGCTTATAAGGAAAAAGGCCATTCTCAG 840

QY 841 AGTTCACAATTTCTCTGTGATCAAGAAATAGCTCATCTGCTGCCTGAAAAATGTGAGTGC 900  
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QY 841 AGTTCACAATTTCTCTGTGATCAAGAAATAGCTCATCTGCTGCCTGAAAAATGTGAGTGC 900  
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QY 901 CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCTACTCCAAAGCCCGCC 960  
Db  
QY 901 CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCTACTCCAAAGCCCGCC 960  
QY 961 ACCCTTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCCAGGCCACAGCTGGCC 1020  
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QY 961 ACCCTTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCCAGGCCACAGCTGGCC 1020  
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QY 1021 ACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCACGACCCCTCATTTCTACA 1080  
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QY 1081 GTTTTTTACACGGCTCGGGCTACACTCCAAGCAATGGCTACAACAGCAGTTCGTACTACC 1140  
QY 1141 ACCTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATACCGTTTACAGAAATC 1200  
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QY 1141 ACCTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATACCGTTTACAGAAATC 1200  
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QY 1321 AGTTCTCTCCAGGGCAGTGTTCAGAGAAATCAGTACGGCCTTCCATTTGAAAAATGGCTT 1380  
QY 1381 CTTATCGGGTCCCTGCTCTTTGGTGTCTTCTGCTGATAGGCCCTCGTCTCCTGGGT 1440  
Db  
QY 1381 CTTATCGGGTCCCTGCTCTTTGGTGTCTTCTGCTGATAGGCCCTCGTCTCCTGGGT 1440  
QY 1441 AGAATCCTTTCCGAATCACTCCGACGGAAGCTTACTCAAGACTGGATTAATGATCAAT 1500  
Db  
QY 1441 AGAATCCTTTCCGAATCACTCCGACGGAAGCTTACTCAAGACTGGATTAATGATCAAT 1500  
QY 1501 GGGATCTATGTGGACATCTAAGGATGGAATCGGTGTCTCTTAATTCATTTAGTAACCAG 1560  
Db  
QY 1501 GGGATCTATGTGGACATCTAAGGATGGAATCGGTGTCTCTTAATTCATTTAGTAACCAG 1560  
QY 1561 AAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTGTATTTTGA 1620  
Db  
QY 1561 AAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTGTATTTTGA 1620  
QY 1621 AGACAGGAAATGCCCCCTTCTGCTTTCTTTTGGAGACAGAGTCTTGCTCTG 1680  
Db  
QY 1621 AGACAGGAAATGCCCCCTTCTGCTTTCTTTTGGAGACAGAGTCTTGCTCTG 1680  
QY 1681 TTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTCCTGG 1740  
Db  
QY 1681 TTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTCCTGG 1740  
QY 1741 GTTCAAGCGATTTCTCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCACC 1800  
Db  
QY 1741 GTTCAAGCGATTTCTCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCACC 1800  
QY 1801 ACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTCCACCATGTGGTCAGGCTG 1860  
Db  
QY 1801 ACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTCCACCATGTGGTCAGGCTG 1860  
QY 1861 GTCTCAAACCTCCTGACCTAGTATCCACCCCTCCTCGGCCCTCCCAAAGTCTGGGATTACA 1920  
Db  
QY 1861 GTCTCAAACCTCCTGACCTAGTATCCACCCCTCCTCGGCCCTCCCAAAGTCTGGGATTACA 1920  
QY 1921 GGCATGAGCCACACAGCTGGCCCCCTTCTGTATTATGTTTGGTTTTTGAAGGAATGA 1980

Db 1921 GGCATGAGCCACACAGCTGGCCCCCTTCTGTATTATGTTTGGTTTTTGAAGGAATGA 1980  
QY 1981 AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAA 2040  
Db  
QY 1981 AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAA 2040  
QY 2041 AGCTCTATGTAAAGTAATAAAGTATAAATTGCCATATAAAATTTCAAAATTCACCTGGCTTT 2100  
Db  
QY 2041 AGCTCTATGTAAAGTAATAAAGTATAAATTGCCATATAAAATTTCAAAATTCACCTGGCTTT 2100  
QY 2101 TATGCAAAAGAAACAGGTTAGGACATCTAGGATTCCTCAATTCATTCACATTCCTTGGTTCCAGA 2160  
Db  
QY 2101 TATGCAAAAGAAACAGGTTAGGACATCTAGGATTCCTCAATTCATTCACATTCCTTGGTTCCAGA 2160  
QY 2161 TAAAATCAACTGTTTATATCAATTTCTAATGGAATTTGCTTTTCTTTTATATGGAATTCCT 2220  
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QY 2161 TAAAATCAACTGTTTATATCAATTTCTAATGGAATTTGCTTTTCTTTTATATGGAATTCCT 2220  
QY 2221 TTAAAACTTATTCAGATGTAGTTCCTTCCAAATTAATTTGAATAAATCTTTTGTGTAC 2280  
Db  
QY 2221 TTAAAACTTATTCAGATGTAGTTCCTTCCAAATTAATTTGAATAAATCTTTTGTGTAC 2280  
QY 2281 TCAA 2284  
Db  
QY 2281 TCAA 2284

RESULT 4  
US-09-991-181-514  
; Sequence 514, Application US/09991181  
; Patent No. 6913919  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C53  
; CURRENT APPLICATION NUMBER: US/09/991,181  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945









Db 1921 GGCATGAGCCACCACAGCTGGCCCCCTTCTGTGTTTATGTTGGTTTTTGAGAAGGAATGA 1980

QY 1981 AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACAA 2040

Db 1981 AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACAA 2040

QY 2041 AGCTCTATGTAAGTAATAAGTATAATTGCCATATAAAATTTCAAAATTCAACTGGCTTT 2100

Db 2041 AGCTCTATGTAAGTAATAAGTATAATTGCCATATAAAATTTCAAAATTCAACTGGCTTT 2100

QY 2101 TATGCAAGAAACAGGTTAGGACATCTAGGTTCCAATTCATTCAATTCCTTGGTTCCAGA 2160

Db 2101 TATGCAAGAAACAGGTTAGGACATCTAGGTTCCAATTCATTCAATTCCTTGGTTCCAGA 2160

QY 2161 TAAAACTAACTGTTTATATCAATTTCTAATGGAATTTGCTTTCTTTTATATGGAATTCCT 2220

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QY 2221 TAAAACTTATCCAGATGTAGTTCCTTCCAATTTAAATATTTGAATAAATCTTTTGTATC 2280

Db 2221 TAAAACTTATCCAGATGTAGTTCCTTCCAATTTAAATATTTGAATAAATCTTTTGTATC 2280

QY 2281 TCAA 2284

Db 2281 TCAA 2284

RESULT 5

US-09-944-944-82

; Sequence 82, Application US/09944944

; Patent No. 6929947

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944,944

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/067,411

; PRIOR FILING DATE: December 3, 1997

; PRIOR APPLICATION NUMBER: 60/069,334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997

; PRIOR APPLICATION NUMBER: 60/069,696

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,702

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,870

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/069,873

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017

; PRIOR FILING DATE: December 18, 1997

; PRIOR APPLICATION NUMBER: 60/070,440

; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/074,092

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/075,945

; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112,850

; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 60/113,296

; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 60/146,222

; PRIOR FILING DATE: July 28, 1999

; PRIOR APPLICATION NUMBER: PCT/US98/19330

; PRIOR FILING DATE: September 16, 1998

; PRIOR APPLICATION NUMBER: PCT/US98/25108

; PRIOR FILING DATE: December 1, 1998

; PRIOR APPLICATION NUMBER: 09/216,021

; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 09/218,517

; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 09/254,311

; PRIOR FILING DATE: March 3, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/12252

; PRIOR FILING DATE: June 22, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: September 15, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/28409

; PRIOR FILING DATE: No. 6929947ember 30, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: No. 6929947ember 30, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/28301

; PRIOR FILING DATE: December 1, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: December 16, 1999

; PRIOR APPLICATION NUMBER: PCT/US00/03565

; PRIOR FILING DATE: February 11, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: February 22, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: March 2, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/08439

; PRIOR FILING DATE: March 30, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/14042

; PRIOR FILING DATE: May 22, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/20710

; PRIOR FILING DATE: July 28, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/32678

; PRIOR FILING DATE: December 1, 2000

; PRIOR APPLICATION NUMBER: PCT/US01/06520

; PRIOR FILING DATE: February 28, 2001

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 82

; LENGTH: 2284

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-944-944-82

Query Match 100.0%; Score 2284; DB 3; Length 2284;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGAGCATCCGCTGCGGTCTCTGCCGAGACCCCGCGGATTGCGCGGTCTTCCGCG 60

Db 1 GCGGAGCATCCGCTGCGGTCTCTGCCGAGACCCCGCGGATTGCGCGGTCTTCCGCG 60

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Db 61 GGGCGGACAGAGCTGTCTCGCACCTGGATGGCAGAGGGGCGCGGGTCTCTCGAC 120

QY 121 GCCAGAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG 180

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QY 181 GATTATCCTTGACCTTTGAAGACCAAAACTAAACTGAAATTTAAAAATGTTCTTCGGGGGA 240

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QY 241 GAAGGAGCTTGACTTACACTTTGGTAAATAATTTGCTTCCCTGACACTAAGGCTGTCTGCT 300

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QY 421 TCTTGCTGTCAACAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGAC 480

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QY 1921 GGCATGAGCCACCAAGCTGGCCCCCTTCTGTTTATAGTTTGTGGTATTTTGAGAAGGAATGA 1980

Db 1921 GGCATGAGCCACCAAGCTGGCCCCCTTCTGTTTATAGTTTGTGGTATTTTGAGAAGGAATGA 1980

QY 1981 AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTTAAATAATTAGCTAAAAACAA 2040

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Db 2101 TATGCAAAGAAACAGGTTAGGACATCTAGGTTCCAAATTCATTCACTTCTTGGTTCAGGA 2160

QY 2161 TAAAACTTATCCAGATGTAGTTCCTTCCAATTAATAATTTGAATAAATCTTTTGTGTAC 2280

Db 2161 TAAAACTTATCCAGATGTAGTTCCTTCCAATTAATAATTTGAATAAATCTTTTGTGTAC 2280

QY 2221 TAAAACTTATCCAGATGTAGTTCCTTCCAATTAATAATTTGAATAAATCTTTTGTGTAC 2280

Db 2221 TAAAACTTATCCAGATGTAGTTCCTTCCAATTAATAATTTGAATAAATCTTTTGTGTAC 2280



Qy 2281 TCAA 2284  
| | | |  
Db 2281 TCAA 2284

RESULT 6  
US-09-990-444-514  
; Sequence 514, Application US/09990444  
; Patent No. 6930170  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C19  
; CURRENT APPLICATION NUMBER: US/09/990,444  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
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; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087827  
; PRIOR FILING DATE: 1998-06-03  
; PRIOR APPLICATION NUMBER: 60/088021  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088025  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088026  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088028  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/088029  
; PRIOR FILING DATE: 1998-06-04  
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; PRIOR FILING DATE: 1998-06-04  
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; PRIOR FILING DATE: 1998-06-04  
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; PRIOR FILING DATE: 1998-06-04  
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; PRIOR APPLICATION NUMBER: 60/088742  
; PRIOR FILING DATE: 1998-06-10  
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; PRIOR FILING DATE: 1998-06-11  
; PRIOR APPLICATION NUMBER: 60/089105  
; PRIOR FILING DATE: 1998-06-12  
; PRIOR APPLICATION NUMBER: 60/089440  
; PRIOR FILING DATE: 1998-06-16  
; PRIOR APPLICATION NUMBER: 60/089512  
; PRIOR FILING DATE: 1998-06-16  
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; PRIOR FILING DATE: 1998-06-17  
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; PRIOR FILING DATE: 1998-06-17  
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; PRIOR FILING DATE: 1998-06-17  
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; PRIOR FILING DATE: 1998-06-18  
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; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/089952  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/090246  
; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 60/090252





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Qy 2221 TTAATAACTTATCCAGATGTAGTTCCTTCCAAATTAATTTGAATAAATCTTTTGTGTAC 2280  
Db 2221 TTAATAACTTATCCAGATGTAGTTCCTTCCAAATTAATTTGAATAAATCTTTTGTGTAC 2280  
Qy 2281 TCAA 2284

Db 2281 TCAA 2284  
RESULT 7  
US-09-945-587-82  
; Sequence 82, Application US/09945587  
; Patent No. 6936254  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548PIC1  
; CURRENT APPLICATION NUMBER: US/09/945,587  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021





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Qy 1561 AAGCCAAATGCAATGAGTTTCTGCTGACTTGCTAGCTTAGCAGGAGGTGTGATTTTGA 1620

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Qy 1861 GTCTCAAACTCCTGACCTAGTATCCACCCTCCTCGGCCCTCCCAAAGTCTGGGATTACA 1920

Db 1861 GTCTCAAACTCCTGACCTAGTATCCACCCTCCTCGGCCCTCCCAAAGTCTGGGATTACA 1920

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Qy 2221 TTAATACTTATCCAGATGTAGTTCCTTCCAATTAATAATTTGAATAAATCTTTTGTAC 2280

Db 2221 TTAATACTTATCCAGATGTAGTTCCTTCCAATTAATAATTTGAATAAATCTTTTGTAC 2280

Qy 2281 TCAA 2284

Db 2281 TCAA 2284

RESULT 8

US-09-997-333-514

; Sequence 514, Application US/09997333

; Patent No. 6953836

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C27

; CURRENT APPLICATION NUMBER: US/09/997,333

; CURRENT FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

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US-09-992-598-514

; Sequence 514, Application US/09992598

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; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

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; APPLICANT: Gerritsen, Mary E.

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; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

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; APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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RESULT 10

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; Patent No. 6972185  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C61  
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; CURRENT FILING DATE: 2001-11-19  
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; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 0;

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QY 1741 GTTCAAGCGATTCTCCTGCTCAGCCTCCTTAAGTATCTGGATTACAGGCATGTGCCACC 1800  
Db 1741 GTTCAAGCGATTCTCCTGCTCAGCCTCCTTAAGTATCTGGATTACAGGCATGTGCCACC 1800  
QY 1801 ACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTCCACCATGTTGGTCAGGCTG 1860  
Db 1801 ACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTCCACCATGTTGGTCAGGCTG 1860  
QY 1861 GTCTCAAACTCCTGACCTAGTGATCCACCTCCTCGGCCCTCCAAAAGTGTGGGATTACA 1920  
Db 1861 GTCTCAAACTCCTGACCTAGTGATCCACCTCCTCGGCCCTCCAAAAGTGTGGGATTACA 1920  
QY 1921 GGATGAGCCACACAGCTGGCCCCCTTCTGTTTATGTTTGTGTTTGTGAGAAATGA 1980  
Db 1921 GGATGAGCCACACAGCTGGCCCCCTTCTGTTTATGTTTGTGTTTGTGAGAAATGA 1980  
QY 1981 AGTGGAAACCAATTAGGTAAATTTTGGGTAACTGTCTCTAAATATTAGCTAAAAACAA 2040  
Db 1981 AGTGGAAACCAATTAGGTAAATTTTGGGTAACTGTCTCTAAATATTAGCTAAAAACAA 2040  
QY 2041 AGCTCTATGTAAAGTAATAAGTATAATTTGCCATATAAATTTCAAAATTTCAACTGGCTTT 2100  
Db 2041 AGCTCTATGTAAAGTAATAAGTATAATTTGCCATATAAATTTCAAAATTTCAACTGGCTTT 2100  
QY 2101 TATGAAAAGAAACAGGTTAGGACATCTAGGTTCCAAATTCATTTCATTCAGATCCAG 2160  
Db 2101 TATGAAAAGAAACAGGTTAGGACATCTAGGTTCCAAATTCATTTCATTCAGATCCAG 2160  
QY 2161 TAAATCAACTGTTTATATCAATTTCTAAAGATTGCTTTTCTTTTATATGGAATCCT 2220  
Db 2161 TAAATCAACTGTTTATATCAATTTCTAAAGATTGCTTTTCTTTTATATGGAATCCT 2220  
QY 2221 TTAAAACTTATTCAGATGTAGTTCCCTTCCAAATTAATAATTTGAATAAATCTTTTGTATC 2280  
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QY 2281 TCAA 2284  
Db 2281 TCAA 2284

RESULT 11  
US-09-989-726-514  
; Sequence 514, Application US/09989726  
; Patent No. 7018811  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C60  
CURRENT APPLICATION NUMBER: US/09/989,726  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
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PRIOR FILING DATE: 1998-06-09  
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; PRIOR APPLICATION NUMBER: 60/091626  
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; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2284; DB 5; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 GCCAGAGAGAAATCTCATCATCTGTCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG 180  
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Qy 181 GATTATCCTTGACCTTTGAAGACCAAAACTAAACTGAAATTTAAATGTTCTCGGGGA 240  
Db 181 GATTATCCTTGACCTTTGAAGACCAAAACTAAACTGAAATTTAAATGTTCTCGGGGA 240  
Qy 241 GAAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCTGCT 300  
Db 241 GAAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCTGCT 300  
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Db 301 AGTCAGAAATGCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCACTCTT 360  
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Db 361 TCTAAGGAAATCAGAGGCAATGAGCCCGTATATCTTCAACTCAAGAAGACTGCATTAAT 420  
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Qy 601 TTGACCAGAAATTTGCCAAGCCAAAGATTACCCAGGAAGATTCTCTTTACATGGCCAA 660  
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Db 1201 TCCAACTTAATTTGAACACAGGGAATGTGTATAACCCCTACTGCACCTTCTATGTCAAAT 1260  
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Db 1261 GTGGAGTCTTCCACTATGAATAAACTGCTTCTTGGGAAGGTAGGGAGGCCAGTCCAGGC 1320  
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Db 1501 GGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGCTCTTAAATTCATTAGTAACAG 1560  
Qy 1561 AAGCCCAATGCAATGAGTTTCTGCTGACTTGTAGTCTTAGCAGGAGGTGTTATTTGA 1620

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Db 1861 GTCTCAAACTCCTGACCTAGTATCCACCTCTCGGCTCCCAAAGTGTGGGATTACA 1920

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QY 2041 AGCTCATGTAAAGTAATAAAGTATAAATGGCATATAAATTTCAAAATTCAACTGGCTTT 2100

Db 2041 AGCTCATGTAAAGTAATAAAGTATAAATGGCATATAAATTTCAAAATTCAACTGGCTTT 2100

QY 2101 TATGCAAGAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATCTTGGTTCCAGA 2160

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QY 2161 TAAATCAACTGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCCCT 2220

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QY 2281 TCAA 2284

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RESULT 12

US-09-944-884-82

; Sequence 82, Application US/09944884

; Patent No. 7018837

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944,884

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 82

; LENGTH: 2284

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-944-884-82

Query Match 100.0%; Score 2284; DB 5; Length 2284;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGAGCATCCGCTGCGGTCTCTGCGGAGACCCCCCGGGGATTTCGCCGGTCTCTCCCGC 60

Db 1 GCGGAGCATCCGCTGCGGTCTCTGCGGAGACCCCCCGGGGATTTCGCCGGTCTCTCCCGC 60

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QY	1021	ACCACAGCTCCACCTGTAACCACCTGTCACTTCTCAGCCTCCCACGACCTCATTTCTACA	1080
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QY	1021	ACCACAGCTCCACCTGTAACCACCTGTCACTTCTCAGCCTCCCACGACCTCATTTCTACA	1080
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QY	1261	GTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGTAGGGAGGCCAGTCCAGGC	1320
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QY	1321	AGTTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCCATTTGAAAAATGGCTT	1380
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QY	1321	AGTTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCCATTTGAAAAATGGCTT	1380
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QY	1381	CTTATCGGGTCCCTGCTCTTTGGTGTCCCTGTTCTGGTGATAGGCCTCGTCTCTGGGT	1440
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QY	1381	CTTATCGGGTCCCTGCTCTTTGGTGTCCCTGTTCTGGTGATAGGCCTCGTCTCTGGGT	1440
Db			
QY	1441	AGAAATCCTTTCCGAATCACTCCGCAGGAAACGTTTACTCAAGACTGGATTATTGATCAAT	1500
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QY	1501	GGGATCTATGTGGACATCTAAGGATGGAATCGGTGTCTCTTAATTCATTAGTAGTAACCAG	1560
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QY	1501	GGGATCTATGTGGACATCTAAGGATGGAATCGGTGTCTCTTAATTCATTAGTAGTAACCAG	1560
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QY	1561	AAGCCCCAAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTGTGATTTGA	1620
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QY	1561	AAGCCCCAAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTGTGATTTGA	1620
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QY	1621	AGACAGGAAAAATGCCCTTCTGCTTTCCCTTTTCTTTTGGAGACAGAGTCTGTCTCTG	1680
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QY	1621	AGACAGGAAAAATGCCCTTCTGCTTTCCCTTTTCTTTTGGAGACAGAGTCTGTCTCTG	1680
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QY	1681	TTGCCCCAGGTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAAACCTCCGTCTCCTGG	1740
Db			
QY	1681	TTGCCCCAGGTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAAACCTCCGTCTCCTGG	1740
Db			
QY	1741	GTTCAAGCGAATCTCTGCTCAGCCTCCTTAAGTACTGGGATTACAGGCAATGTGCCACC	1800
Db			
QY	1741	GTTCAAGCGAATCTCTGCTCAGCCTCCTTAAGTACTGGGATTACAGGCAATGTGCCACC	1800
Db			
QY	1801	ACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTCACCATGTTGGTCAGGCTG	1860
Db			
QY	1801	ACACCTGGGTGATTTTGTATTTTGTAGTAGACGGGGTTTCACCATGTTGGTCAGGCTG	1860
Db			
QY	1861	GTCTCAAACCTCTGACCTAGTGATCCACCCCTCTCGGCCCTCCCAAAGTCTGGATTACA	1920
Db			
QY	1861	GTCTCAAACCTCTGACCTAGTGATCCACCCCTCTCGGCCCTCCCAAAGTCTGGATTACA	1920
Db			
QY	1921	GGCATGAGCCACCAAGCTGGCCCCCTTCTGTTTTATGTTTTGTTTTTGGAAAGGAATGA	1980

Db	1921	GGCATGAGCCACCACAGCTGGCCCCCTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGA	1980
Qy	1981	AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAA	2040
Db	1981	AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAA	2040
Qy	2041	AGCTCTATGTAAAGTAATAAAGTATAATTGCCATATAAAATTTCAAAATTTCAACTGGCTTT	2100
Db	2041	AGCTCTATGTAAAGTAATAAAGTATAATTGCCATATAAAATTTCAAAATTTCAACTGGCTTT	2100
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Db	2101	TATGCAAGAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATTTCTTGGTTCCAGA	2160
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Db	2161	TAAAATCAACTGTTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTT	2220
Qy	2221	TTAAACCTTATCCAGATGTAGTTCCCTTCCAATTAATAATTTGAATAAATCTTTTGTATC	2280
Db	2221	TTAAACCTTATCCAGATGTAGTTCCCTTCCAATTAATAATTTGAATAAATCTTTTGTATC	2280
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RESULT 13

US-09-997-514-514

; Sequence 514, Application US/09997514

; Patent No. 7019116

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C46

; CURRENT APPLICATION NUMBER: US/09/997,514

; CURRENT FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945







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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Db 61 GGGCGGACAGAGCTGTCTCGACCTGGATGGCAGCAGGGCGCGGGTCTCTCTCGAC 120

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Db 121 GCCAGAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCCAGAGGGAG 180

Qy 181 GATTATCCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATTTCTTCGGGGGA 240
Db 181 GATTATCCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATTTCTTCGGGGGA 240

Qy 241 GAAGGGAGCTTGACTTACACTTTGGTAAATAATTTGGTCTTCCTGACACTAAGGCTGTCTGCT 300
Db 241 GAAGGGAGCTTGACTTACACTTTGGTAAATAATTTGGTCTTCCTGACACTAAGGCTGTCTGCT 300

Qy 301 AGTCAGAAATGCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCACTCTT 360
Db 301 AGTCAGAAATGCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCACTCTT 360

Qy 361 TCTAAGGGAAATCAGAGGCAATGAGCCGTATATACCTCAACTCAAGAAAGACTGCAATTAAT 420
Db 361 TCTAAGGGAAATCAGAGGCAATGAGCCGTATATACCTCAACTCAAGAAAGACTGCAATTAAT 420

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Db 421 TCTTGTCTTTCAACAAAAACATATCAGGGGACAAAGCATGTAATTTGATGATCTTCGAC 480

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Db 541 TGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCT 600

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Db 781 TTTAAGATGGATGAAGCAAGTGCCCGAGTCTTGCTTATAAGGAAAGGCGCATTTCTCAG 840

Qy 841 AGTTCACAAATTTCCCTCTGATCAAGAAATAGCTCATCTGCTGCCTGAAAAATGTGAGTGC 900
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Db 961 ACCCTTCTACCCACCAATGCTTCACTGACACCTTCTGGGACTTCCCAGCCACAGCTGGCC 1020

Qy 1021 ACCACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCCACGACCCTCATTTTCTACA 1080
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Qy 1081 GTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACAGCAGTTCTGACTACC 1140
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Qy 1141 ACCTTTCAGGCACCTACCGACTCGAAGAGGAGTCTAGAAAACCATACCGTTTACAGAAATC 1200
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Db 1441 AGAATCCTTTCCGAAATCACTCCGACGAGAAACGTTTACTCAAGACTGGATTATTTGATCAAT 1500

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Db 1501 GGGATCTATGTGACATCTAAGGATGGAACTCGGTGTCTCTTAATTCATTTAGTAACCA 1560

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Qy 1621 AGACAGGAAAAATGCCCTTCTGCTTTTCTGCTTTTCTGAGACAGAGTCTTGCTCTG 1680
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Db 1801 ACACCTGGGTGATTTTGTATTTTTAGTAGAGACGGGTTTACCATTGTTGGTCAGGCTG 1860

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Db 1861 GTCTCAAACTCCTGACCTAGTGTATCCACCCCTCCTCGSCCTCCCAAAGTGTGGGATTACA 1920

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Qy 2281 TCAA 2284  
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RESULT 14

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; Sequence 514, Application US/09989728  
; Patent No. 7029873  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C72  
; CURRENT APPLICATION NUMBER: US/09/989,728  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
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; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
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; PRIOR FILING DATE: 1998-06-02  
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; PRIOR APPLICATION NUMBER: 60/089599  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089600  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089653  
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; PRIOR APPLICATION NUMBER: 60/091978  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2284; DB 5; Length 2284;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 GGGCGGACAGAGCTGTCTCGACCTGGATGGCAGAGGGGCGCGGGTCTCTCGAC 120  
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Db 61 GGGCGGACAGAGCTGTCTCGACCTGGATGGCAGAGGGGCGCGGGTCTCTCGAC 120

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Db 121 GCCAGAGAGAAATCTCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGAG 180

Qy 181 GATTATCCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTCGGGGA 240  
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Db 181 GATTATCCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTCGGGGA 240

Qy 241 GAAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCT 300  
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Db 241 GAAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCT 300

Qy 301 AGTCAGAAATGCCTCAAAAAGAGCTAGAAGATGTTGATGACATCCAGTATCTCT 360  
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Db 421 TCTTGCTGTTCAACAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTCGAC 480

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Db 601 TTGACCAGAAATTTGCCAAGCCAAAGATTACCCAGGAAGATTCTCTTACATGGCCAA 660

Qy 661 TTTTCACAGCAGTCACTCCCTAGCCCATCATCACAGATTATTCAAAGCCCCACCGAT 720  
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Qy 721 ATCTCATGGAGAGACACACTTTCTCAGAAAGTTTGGATCTCTAGATCACCTGGAGAACTA 780  
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Qy 841 AGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCCTGAAATGTAGTGCG 900  
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Db 841 AGTTCACAAATTTTCTCTGTATCAAGAAATAGCTCATCTGCTGCCTGAAAAATGTGAGTGG 900

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Qy 1321 AGTTCTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCATTTGAAAAATGGCTT 1380

Db 1321 AGTTCTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCATTTGAAAAATGGCTT 1380

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Qy 1861 GTCTCAAACTCCTGACCTAGTGATCCACCCTCCTCGGCCCTCCCAAAGTGTGGGATTACA 1920

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Qy 1921 GGCAATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTGGTTTTTTGAGAAGGAATGA 1980

Db 1921 GGCAATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTGGTTTTTTGAGAAGGAATGA 1980

RESULT 15

US-09-997-349-514

; Sequence 514, Application US/09997349

; Patent No. 7034106

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; APPLICANT: Botstein, David

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; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C37

; CURRENT APPLICATION NUMBER: US/09/997,349

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; PRIOR FILING DATE: 1997-11-24

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; PRIOR APPLICATION NUMBER: 60/078910

Qy 1981 AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACAA 2040

Db 1981 AGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACAA 2040

Qy 2041 AGCTCTATGTAAAGTAATAAAGTATAATTGCCATATAAAATTTCAAAATTCAACTGGCTTT 2100

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Db 2101 TATGCAAGAAACAGGTTAGGACATCTAGGTTCCAAATTCATTCAATTCATTGGTCCAGA 2160

Qy 2161 TAAAAATCAACTGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGAATTCCT 2220

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Qy 2281 TCAA 2284

Db 2281 TCAA 2284



[illegible]

; PRIOR FILING DATE: 1998-07-02												
; PRIOR APPLICATION NUMBER: 60/091633												
; PRIOR FILING DATE: 1998-07-02												
; PRIOR APPLICATION NUMBER: 60/091978												
; PRIOR FILING DATE: 1998-07-07												
; PRIOR APPLICATION NUMBER: 60/091982												
; PRIOR FILING DATE: 1998-07-07												
; PRIOR APPLICATION NUMBER: 60/092182												
; PRIOR FILING DATE: 1998-07-09												
Query Match 100.0%; Score 2284; DB 5; Length 2284;												
Best Local Similarity 100.0%; Pred. No. 0;												
Matches 2284; Conservative 0; Mismatches 0; Indels 0; Gaps 0;												
QY	1	GC	GAGCAT	CCGCTG	CGGTCT	CGCTCG	CGGAC	CCCCCG	CGGATT	CGCCGGT	CCCTCCGC	60
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QY	61	GG	CGCGAC	GAGCTG	CTCG	CACCTG	GATGG	CAGCG	CGCGCG	CGGTCT	CTCGAC	120
Db	61	GG	CGCGAC	GAGCTG	CTCG	CACCTG	GATGG	CAGCG	CGCGCG	CGGTCT	CTCGAC	120
QY	121	GC	CAGAGAAA	ATCTCAT	CTGTG	CAGCCT	CTTTAA	GCAAACTA	AGACCAG	AGGGAG		180
Db	121	GC	CAGAGAAA	ATCTCAT	CTGTG	CAGCCT	CTTTAA	GCAAACTA	AGACCAG	AGGGAG		180
QY	181	GA	TATCCT	TGACCT	TGTAAC	TTTGGT	TAATAA	TTTAA	AAATGTT	CTTCGGGG	GA	240
Db	181	GA	TATCCT	TGACCT	TGTAAC	TTTGGT	TAATAA	TTTAA	AAATGTT	CTTCGGGG	GA	240
QY	241	GA	GGGAGCT	TGACCT	TGTAAC	TTTGGT	TAATAA	TTTAA	AAATGTT	CTTCGGGT	GTCTGCT	300
Db	241	GA	GGGAGCT	TGACCT	TGTAAC	TTTGGT	TAATAA	TTTAA	AAATGTT	CTTCGGGT	GTCTGCT	300
QY	301	AG	TGAGAA	TTGCCT	CAAAAAG	AGTCTA	GAAGAT	GTGTG	TCATG	ACATCC	AGTCATCT	360
Db	301	AG	TGAGAA	TTGCCT	CAAAAAG	AGTCTA	GAAGAT	GTGTG	TCATG	ACATCC	AGTCATCT	360
QY	361	TC	TAGGGA	ATCAG	AGGCAAT	GAGCCG	TATATA	CTTCA	ACTCA	AGAAGA	CTGCATTA	420
Db	361	TC	TAGGGA	ATCAG	AGGCAAT	GAGCCG	TATATA	CTTCA	ACTCA	AGAAGA	CTGCATTA	420
QY	421	TC	TGCTGT	TTCAAC	AAAAAC	ATATC	AGGGG	ACAAAG	CAATG	TAACCT	TGATGAT	480
Db	421	TC	TGCTGT	TTCAAC	AAAAAC	ATATC	AGGGG	ACAAAG	CAATG	TAACCT	TGATGAT	480
QY	481	ACT	CGAAAA	ACAGCT	AGCAAC	CCCACT	GCTAC	CTATTT	TCTGT	CTCCCA	CGGAGCC	540
Db	481	ACT	CGAAAA	ACAGCT	AGCAAC	CCCACT	GCTAC	CTATTT	TCTGT	CTCCCA	CGGAGCC	540
QY	541	TG	TCAT	TGAAA	CCAGCA	AAAGG	ACTTAT	GAGTTA	CAGGA	TAATTA	CTTCCATCT	600
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QY	601	TT	GACAGAA	ATTTG	CCAAAG	CCAGAT	TAC	CCCA	GGAAG	ATTCT	CTTACATG	660
Db	601	TT	GACAGAA	ATTTG	CCAAAG	CCAGAT	TAC	CCCA	GGAAG	ATTCT	CTTACATG	660
QY	661	TT	TTCAAG	CAAGCT	CACTCC	CCCTAG	CCCAT	CATC	ACAC	AGATT	TTCAGG	720
Db	661	TT	TTCAAG	CAAGCT	CACTCC	CCCTAG	CCCAT	CATC	ACAC	AGATT	TTCAGG	720
QY	721	AT	CTCATG	GAGAC	ACACT	TTTCT	CAGAA	GTG	TTGAT	CCCTC	AGATCAC	780
Db	721	AT	CTCATG	GAGAC	ACACT	TTTCT	CAGAA	GTG	TTGAT	CCCTC	AGATCAC	780
QY	781	TT	TAGATG	GATGA	AGCAAG	TGCCCC	AGCTCT	TGTTA	TAA	GAAAAA	AGGCCAT	840
Db	781	TT	TAGATG	GATGA	AGCAAG	TGCCCC	AGCTCT	TGTTA	TAA	GAAAAA	AGGCCAT	840
QY	841	AG	TTCAAA	ATTTT	CTCTG	ATCA	AGAAAT	AGCTCA	TCTG	CTGC	CTGAAA	900
Db	841	AG	TTCAAA	ATTTT	CTCTG	ATCA	AGAAAT	AGCTCA	TCTG	CTGC	CTGAAA	900

QY	901	CT	CC	CAGCTAC	GGTGG	CGAGTT	GTCTT	CTCC	CACATAC	CCACCT	CTGGCT	TACTCC	AAAGCC	CGCC	960	
Db	901	CT	CC	CAGCTAC	GGTGG	CGAGTT	GTCTT	CTCC	CACATAC	CCACCT	CTGGCT	TACTCC	AAAGCC	CGCC	960	
QY	961	ACC	TTT	CTACCC	ACCAAT	GC	TTT	CAGT	GACAC	CTT	CTGGG	ACTTCC	CCAGCC	ACAGCT	1020	
Db	961	ACC	TTT	CTACCC	ACCAAT	GC	TTT	CAGT	GACAC	CTT	CTGGG	ACTTCC	CCAGCC	ACAGCT	1020	
QY	1021	ACC	AC	AGCTCC	ACCTGT	AA	CCACTGT	CACTT	CTC	AGCCT	CCC	ACGAC	CCCTCAT	TTTCTACA	1080	
Db	1021	ACC	AC	AGCTCC	ACCTGT	AA	CCACTGT	CACTT	CTC	AGCCT	CCC	ACGAC	CCCTCAT	TTTCTACA	1080	
QY	1081	GT	TTT	TACAC	GGGCTCG	GGCT	TACACT	CCA	AGCAAT	GGCT	TACA	CAAC	AGAGTT	CTGACT	1140	
Db	1081	GT	TTT	TACAC	GGGCTCG	GGCT	TACACT	CCA	AGCAAT	GGCT	TACA	CAAC	AGAGTT	CTGACT	1140	
QY	1141	AC	CTT	TCAGG	CACCTA	CG	ACTCG	AAAGG	CAGCTT	AG	AAACCA	TATAC	CCGTTT	TACAGAAATC	1200	
Db	1141	AC	CTT	TCAGG	CACCTA	CG	ACTCG	AAAGG	CAGCTT	AG	AAACCA	TATAC	CCGTTT	TACAGAAATC	1200	
QY	1201	T	CCAA	CTTAA	CTTT	GAACA	CAGG	GAATGT	GTATA	AACCTA	CTGCA	CTTCT	TATGT	CAAAAT	1260	
Db	1201	T	CCAA	CTTAA	CTTT	GAACA	CAGG	GAATGT	GTATA	AACCTA	CTGCA	CTTCT	TATGT	CAAAAT	1260	
QY	1261	GT	GAGT	CTTCC	ACTAT	GAATA	AAAACT	GTCTT	CT	CTGG	AAAGGT	AGGAGG	CCAGT	CCAGGC	1320	
Db	1261	GT	GAGT	CTTCC	ACTAT	GAATA	AAAACT	GTCTT	CT	CTGG	AAAGGT	AGGAGG	CCAGT	CCAGGC	1320	
QY	1321	AG	TT	CCTCCC	AGGCG	AGTGT	TCC	AGAAAA	ATCAG	TAC	GGCC	TTCC	ATTTG	AAAAAATGGCTT	1380	
Db	1321	AG	TT	CCTCCC	AGGCG	AGTGT	TCC	AGAAAA	ATCAG	TAC	GGCC	TTCC	ATTTG	AAAAAATGGCTT	1380	
QY	1381	CT	TAT	CGGT	CCCT	GTCT	TTT	TGGTGT	CTGT	TCT	GGT	GATAGG	CTCGT	CTCCTGGGT	1440	
Db	1381	CT	TAT	CGGT	CCCT	GTCT	TTT	TGGTGT	CTGT	TCT	GGT	GATAGG	CTCGT	CTCCTGGGT	1440	
QY	1441	AG	AAT	CTTT	TCG	GAATCA	CT	CCG	CAGG	AAACG	TTACT	CAAG	ACTGG	ATTATTTGATCAAT	1500	
Db	1441	AG	AAT	CTTT	TCG	GAATCA	CT	CCG	CAGG	AAACG	TTACT	CAAG	ACTGG	ATTATTTGATCAAT	1500	
QY	1501	GG	AT	CTAT	GTG	GACAT	CTA	AGG	ATG	GAACT	CGGT	GTCT	CTTAA	TTCA	TTAGTAAC	1560
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Db	1561	A	AG	CCCAA	ATG	CAAT	GAGTT	CT	GTCT	GACTT	GTCT	AGTCTT	AG	CAGG	AGTTGTATTTGA	1620
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QY	1861	GT	CT	CAAA	CTC	CT	GAC	CTA	GT	AT	CC	CT	CGG	CT	CCC	1920
Db	1861	GT	CT	CAAA	CTC	CT	GAC	CTA	GT	AT	CC	CT	CGG	CT	CCC	1920
QY	1921	GG	CA	TG	AG	CC	CA	CAG	CTG	G	CC	CT	T	CT	GT	1980
Db	1921	GG	CA	TG	AG	CC	CA	CAG	CTG	G	CC	CT	T	CT	GT	1980

QY	901	CT	CCAGCT	TACG	TGGC	AGTTG	CTTCT	CCAC	ATAC	CACCT	CGGCT	ACTC	CAAAG	CCCCGC	960
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QY	1021	ACC	CAGCT	CCAC	CTGT	AAAC	CACTG	TCA	CTTCT	CAG	CCCTCC	CAC	ACCCT	CA	1080
Db	1021	ACC	CAGCT	CCAC	CTGT	AAAC	CACTG	TCA	CTTCT	CAG	CCCTCC	CAC	ACCCT	CA	1080
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Db	1201	TC	CAACT	TAACT	TTGA	ACAC	AGG	GAAT	GTG	TATA	AA	CCCTA	CTG	CA	1260
QY	1261	GT	GAGT	CTT	CCACT	TATGA	ATA	AA	ACTG	CTT	CTG	GGA	AGGTAG	GG	1320
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QY	1321	AG	TTCT	CTCC	AGG	CAGT	GT	TTCC	AGAAA	ATCAG	TAC	GGCCTT	CCAT	TTG	1380
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Db	1381	CT	TAT	CGGT	CCCTG	CTCT	TTT	GGT	GTCT	GTG	TATAG	CCCTG	CTC	CT	1440
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Db	1501	GG	GAT	CTAT	GTG	GAC	ATCT	A	AGG	ATGGA	ACTCG	GTG	CTCT	TAA	1560
QY	1561	A	AGCC	AAATG	CAAT	GAGT	TTCT	G	CTG	ACTT	GCTAG	TCT	TAG	CAG	1620
Db	1561	A	AGCC	AAATG	CAAT	GAGT	TTCT	G	CTG	ACTT	GCTAG	TCT	TAG	CAG	1620
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QY	1681	TT	GCC	AGCT	GAGT	GAC	GTAG	CAC	AGAT	CTC	GGCT	CTC	AC	CG	1740
Db	1681	TT	GCC	AGCT	GAGT	GAC	GTAG	CAC	AGAT	CTC	GGCT	CTC	AC	CG	1740
QY	1741	GT	TCA	AGC	GAT	TTCT	CTG	CTC	CAG	CCCTC	CTA	AGTAT	CTG	GG	1800
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QY	1861	GT	CT	CAAA	CTC	TGAC	CTAG	TAT	CCAC	CTC	CTC	GGC	CTC	CC	1920
Db	1861	GT	CT	CAAA	CTC	TGAC	CTAG	TAT	CCAC	CTC	CTC	GGC	CTC	CC	1920
QY	1921	GG	CA	TG	AG	CC	CA	CAG	CTG	G	CCCC	CTT	CTG	TTT	1980
Db	1921	GG	CA	TG	AG	CC	CA	CAG	CTG	G	CCCC	CTT	CTG	TTT	1980

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164	241.6	10.6	68123	11	US-10-995-561-13348	Sequence 13348, A
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373	234.8	10.3	187842	26	US-11-443-428A-735341	Sequence 735341,	445	234.2	10.3	128978	22	US-11-378-923-6	Sequence 6, Appli
374	234.8	10.3	187860	26	US-11-443-428A-735291	Sequence 735291,	446	234.2	10.3	232641	16	US-10-990-328-93650	Sequence 93650, A
375	234.8	10.3	187923	26	US-11-443-428A-735303	Sequence 735303,	447	234	10.2	24299	16	US-10-940-774-15452	Sequence 15452, A
376	234.8	10.3	187923	26	US-11-443-428A-735315	Sequence 735315,	448	234	10.2	31871	3	US-09-764-847-1403	Sequence 1403, Ap
377	234.8	10.3	188005	26	US-11-443-428A-735328	Sequence 735328,	449	234	10.2	31871	7	US-10-092-154-1403	Sequence 1403, Ap
378	234.8	10.3	188013	26	US-11-443-428A-735338	Sequence 735338,	450	234	10.2	86361	9	US-10-741-601-5702	Sequence 5702, Ap
379	234.8	10.3	188056	26	US-11-443-428A-735339	Sequence 735339,	451	234	10.2	86361	10	US-10-741-600-17803	Sequence 17803, A
380	234.8	10.3	188086	26	US-11-443-428A-735302	Sequence 735302,	452	234	10.2	86361	11	US-10-995-561-13364	Sequence 13364, A
381	234.8	10.3	188094	26	US-11-443-428A-735312	Sequence 735312,	453	234	10.2	143389	20	US-11-112-908-30	Sequence 30, Appl
382	234.8	10.3	188134	26	US-11-443-428A-735337	Sequence 735337,	454	234	10.2	150314	20	US-11-112-908-24	Sequence 24, Appl
383	234.8	10.3	188137	26	US-11-443-428A-735313	Sequence 735313,	455	234	10.2	150314	20	US-10-775-169-88	Sequence 88, Appl
384	234.8	10.3	188140	26	US-11-443-428A-735333	Sequence 735333,	456	234	10.2	220895	10	US-10-775-169-88	Sequence 88, Appl
385	234.8	10.3	188158	26	US-11-443-428A-735340	Sequence 735340,	457	234	10.2	220895	11	US-10-775-169-88	Sequence 88, Appl
386	234.8	10.3	188176	26	US-11-443-428A-735325	Sequence 735325,	c 458	234	10.2	312453	23	US-11-033-056A-36041	Sequence 36041, A
387	234.8	10.3	188177	26	US-11-443-428A-735336	Sequence 735336,	459	233.8	10.2	601	16	US-10-940-774-18060	Sequence 18060, A
388	234.8	10.3	188183	26	US-11-443-428A-735334	Sequence 735334,	460	233.8	10.2	601	16	US-10-940-774-197087	Sequence 197087,
389	234.8	10.3	188215	26	US-11-443-428A-735311	Sequence 735311,	461	233.8	10.2	2300	27	US-11-636-385-29032	Sequence 29032, A
390	234.8	10.3	188219	26	US-11-443-428A-735326	Sequence 735326,	462	233.8	10.2	7001	9	US-10-304-116-15	Sequence 15, Appl
							463	233.8	10.2	25284	16	US-10-990-328-93630	Sequence 93630, A



C 464	233.8	10.2	103665	12	US-10-330-773-680	Sequence 680, App
C 465	233.8	10.2	103665	14	US-10-540-898-680	Sequence 680, App
466	233.8	10.2	104073	23	US-11-033-056A-37679	Sequence 37679, A
467	233.8	10.2	104073	23	US-11-033-056A-37958	Sequence 37958, A
468	233.8	10.2	824376	25	US-11-066-316A-9906	Sequence 9906, Ap
469	233.6	10.2	34260	16	US-10-990-328-93427	Sequence 93427, A
470	233.6	10.2	68445	15	US-10-796-280-12493	Sequence 12493, A
C 471	233.6	10.2	76573	15	US-10-767-471-10718	Sequence 10718, A
472	233.6	10.2	81709	16	US-10-990-328-97674	Sequence 97674, A
473	233.6	10.2	160552	10	US-10-697-828-11	Sequence 11, Appl
C 474	233.6	10.2	168516	20	US-11-121-086-3	Sequence 3, Appli
C 475	233.4	10.2	832	13	US-10-301-480-545764	Sequence 545764, A
C 476	233.4	10.2	832	13	US-10-301-480-1159173	Sequence 1159173, A
477	233.4	10.2	2300	27	US-11-636-385-23069	Sequence 23069, A
478	233.4	10.2	19739	16	US-10-990-328-97775	Sequence 97775, A
C 479	233.4	10.2	27702	16	US-10-940-774-11795	Sequence 11795, A
480	233.4	10.2	32278	16	US-10-940-774-14575	Sequence 14575, A
481	233.4	10.2	215281	15	US-10-767-471-10745	Sequence 10745, A
482	233.4	10.2	232234	16	US-10-990-328-93684	Sequence 93684, A
C 483	233.4	10.2	2132949	23	US-11-033-056A-38500	Sequence 38500, A
484	233.2	10.2	1701	3	US-09-728-552-9	Sequence 9, Appli
485	233.2	10.2	1701	27	US-11-641-626-9	Sequence 9, Appli
C 486	233.2	10.2	2300	27	US-11-636-385-10226	Sequence 10226, A
487	233.2	10.2	2300	27	US-11-636-385-25182	Sequence 25182, A
C 488	233.2	10.2	173602	20	US-11-121-086-25	Sequence 25, Appl
C 489	233.2	10.2	176001	9	US-10-210-556-27	Sequence 27, Appl
C 490	233.2	10.2	180531	21	US-11-114-798-57	Sequence 57, Appl
491	233.2	10.2	185035	10	US-10-723-860-3104	Sequence 3104, Ap
492	233.2	10.2	185035	11	US-10-756-149-2896	Sequence 2896, Ap
493	233.2	10.2	185035	14	US-10-470-050-281	Sequence 281, App
494	233.2	10.2	185035	21	US-11-266-748A-59932	Sequence 59932, A
C 495	233.2	10.2	186739	9	US-10-210-556-19	Sequence 19, Appl
496	233	10.2	597	4	US-09-925-065A-751914	Sequence 751914, A
497	233	10.2	597	4	US-09-925-065A-751915	Sequence 751915, A
498	233	10.2	597	5	US-09-925-065A-751914	Sequence 751914, A
499	233	10.2	597	5	US-09-925-065A-751915	Sequence 751915, A
C 500	233	10.2	1329	26	US-11-443-428A-665898	Sequence 665898, A
C 501	233	10.2	5633	15	US-10-105-299-13373	Sequence 13373, A
C 502	233	10.2	5633	16	US-10-868-184-11222	Sequence 11222, A
503	233	10.2	68610	15	US-10-796-280-12467	Sequence 12467, A
504	233	10.2	68610	16	US-10-796-307-8843	Sequence 8843, Ap
505	233	10.2	256493	7	US-10-087-192-1000	Sequence 1000, Ap
C 506	233	10.2	1184710	15	US-10-796-280-12394	Sequence 12394, A
507	232.8	10.2	601	16	US-10-940-774-45773	Sequence 45773, A
508	232.8	10.2	601	16	US-10-940-774-45774	Sequence 45774, A
509	232.8	10.2	797	7	US-10-027-632-127789	Sequence 127789, A
510	232.8	10.2	797	8	US-10-027-632-127789	Sequence 127789, A
C 511	232.8	10.2	78568	16	US-10-990-328-96022	Sequence 96022, A
C 512	232.8	10.2	109472	16	US-10-990-328-98005	Sequence 98005, A
513	232.8	10.2	121160	12	US-10-330-773-847	Sequence 847, App
514	232.8	10.2	121160	14	US-10-540-898-847	Sequence 847, App
515	232.8	10.2	136017	16	US-10-990-328-93377	Sequence 93377, A
516	232.8	10.2	138627	12	US-10-330-773-159	Sequence 159, App
C 517	232.8	10.2	138627	14	US-10-540-898-159	Sequence 159, App
C 518	232.8	10.2	211148	16	US-10-990-328-94673	Sequence 94673, A
519	232.8	10.2	430700	23	US-11-033-056A-37994	Sequence 37994, A
C 520	232.6	10.2	461	10	US-10-357-930-49228	Sequence 49228, A
521	232.6	10.2	601	16	US-10-940-774-87766	Sequence 87766, A
C 522	232.6	10.2	624	7	US-10-027-632-78403	Sequence 78403, A
C 523	232.6	10.2	624	7	US-10-027-632-78404	Sequence 78404, A
C 524	232.6	10.2	624	7	US-10-027-632-78405	Sequence 78405, A
C 525	232.6	10.2	624	7	US-10-027-632-78406	Sequence 78406, A
C 526	232.6	10.2	624	7	US-10-027-632-78407	Sequence 78407, A
C 527	232.6	10.2	624	7	US-10-027-632-78408	Sequence 78408, A
C 528	232.6	10.2	624	8	US-10-027-632-78403	Sequence 78403, A
C 529	232.6	10.2	624	8	US-10-027-632-78404	Sequence 78404, A
C 530	232.6	10.2	624	8	US-10-027-632-78405	Sequence 78405, A
C 531	232.6	10.2	624	8	US-10-027-632-78406	Sequence 78406, A
C 532	232.6	10.2	624	8	US-10-027-632-78407	Sequence 78407, A
C 533	232.6	10.2	624	8	US-10-027-632-78408	Sequence 78408, A
534	232.6	10.2	765	7	US-10-027-632-173966	Sequence 173966, A
535	232.6	10.2	765	8	US-10-027-632-173966	Sequence 173966, A
C 536	232.6	10.2	816	13	US-10-301-480-559035	Sequence 559035, A
13	816	10.2	103665	13	US-10-301-480-1172444	Sequence 1172444, A
16	16573	10.2	16573	16	US-10-940-774-11764	Sequence 11764, A
16	17370	10.2	17370	16	US-10-940-774-17331	Sequence 17331, A
16	35336	10.2	35336	16	US-10-990-328-98148	Sequence 98148, A
11	36360	10.2	36360	11	US-10-995-561-13498	Sequence 13498, A
15	36360	10.2	36360	15	US-10-796-280-12589	Sequence 12589, A
16	36360	10.2	36360	16	US-10-990-328-95949	Sequence 95949, A
16	43537	10.2	43537	16	US-10-990-328-98109	Sequence 98109, A
16	74881	10.2	74881	16	US-10-940-774-15545	Sequence 15545, A
16	74914	10.2	74914	16	US-10-940-774-12286	Sequence 12286, A
9	100301	10.2	100301	9	US-10-450-826-83	Sequence 83, Appl
10	100301	10.2	100301	10	US-10-723-860-3574	Sequence 3574, Ap
23	238526	10.2	238526	23	US-11-033-056A-37739	Sequence 37739, A
23	238526	10.2	238526	23	US-11-033-056A-37740	Sequence 37740, A
23	238526	10.2	238526	23	US-11-033-056A-38776	Sequence 38776, A
23	238579	10.2	238579	23	US-11-033-056A-35686	Sequence 35686, A
23	238579	10.2	238579	23	US-11-033-056A-35687	Sequence 35687, A
23	238579	10.2	238579	23	US-11-033-056A-38766	Sequence 38766, A
16	246230	10.2	246230	16	US-10-940-774-17019	Sequence 17019, A
16	246230	10.2	246230	16	US-10-940-774-17020	Sequence 17020, A
16	246230	10.2	246230	16	US-10-940-774-17021	Sequence 17021, A
16	246230	10.2	246230	16	US-10-940-774-17022	Sequence 17022, A
23	281370	10.2	281370	23	US-11-033-056A-36547	Sequence 36547, A
26	472	10.2	472	26	US-11-443-428A-628165	Sequence 628165, A
15	28475	10.2	28475	15	US-10-767-471-10766	Sequence 10766, A
16	31385	10.2	31385	16	US-10-940-774-13310	Sequence 13310, A
16	73788	10.2	73788	16	US-10-940-774-12358	Sequence 12358, A
16	74853	10.2	74853	16	US-10-990-328-98074	Sequence 98074, A
16	90380	10.2	90380	16	US-10-990-328-97546	Sequence 97546, A
23	100525	10.2	100525	23	US-11-033-056A-35916	Sequence 35916, A
23	150248	10.2	150248	23	US-11-033-056A-36438	Sequence 36438, A
20	171427	10.2	171427	20	US-11-112-908-60	Sequence 60, Appl
21	184666	10.2	184666	21	US-11-266-748A-23088	Sequence 23088, A
16	217214	10.2	217214	16	US-10-990-328-94062	Sequence 94062, A
16	293046	10.2	293046	16	US-10-990-328-94327	Sequence 94327, A
16	295525	10.2	295525	16	US-10-990-328-97181	Sequence 97181, A
11	389627	10.2	389627	11	US-10-504-689-3	Sequence 3, Appli
3	402850	10.2	402850	3	US-09-844-653-5	Sequence 5, Appli
14	405660	10.2	405660	14	US-10-322-696-82	Sequence 82, Appl
9	408438	10.2	408438	9	US-10-669-920-1277	Sequence 1277, Ap
14	4647455	10.2	4647455	14	US-10-641-321-205	Sequence 205, App
4	605	10.2	605	4	US-09-925-065A-878037	Sequence 878037, A
5	605	10.2	605	5	US-09-925-065A-878037	Sequence 878037, A
607	4	10.2	607	4	US-09-925-065A-873360	Sequence 873360, A
607	5	10.2	607	5	US-09-925-065A-873360	Sequence 873360, A
614	4	10.2	614	4	US-09-925-065A-878367	Sequence 878367, A
614	5	10.2	614	5	US-09-925-065A-878367	Sequence 878367, A
2300	27	10.2	2300	27	US-11-636-385-17771	Sequence 17771, A
12878	16	10.2	12878	16	US-10-990-328-97194	Sequence 97194, A
12960	23	10.2	12960	23	US-11-033-056A-38495	Sequence 38495, A
18008	16	10.2	18008	16	US-10-940-774-13291	Sequence 13291, A
26878	16	10.2	26878	16	US-10-990-328-97667	Sequence 97667, A
31451	16	10.2	31451	16	US-10-990-328-97757	Sequence 97757, A
60463	16	10.2	60463	16	US-10-719-993-6783	Sequence 6783, Ap
60463	16	10.2	60463	16	US-10-990-328-94067	Sequence 94067, A
68004	16	10.2	68004	16	US-10-990-328-95083	Sequence 95083, A
78568	15	10.2	78568	15	US-10-767-471-10897	Sequence 10897, A
488	4	10.2	488	4	US-09-925-065A-850388	Sequence 850388, A
488	5	10.2	488	5	US-09-925-065A-850388	Sequence 850388, A
489	4	10.2	489	4	US-09-925-065A-842830	Sequence 842830, A
489	5	10.2	489	5	US-09-925-065A-842830	Sequence 842830, A
984	13	10.2	984	13	US-10-301-480-537929	Sequence 537929, A
984	13	10.2	984	13	US-10-301-480-1151338	Sequence 1151338, A
994	13	10.2	994	13	US-10-301-480-586474	Sequence 586474, A
994	13	10.2	994	13	US-10-301-480-1199883	Sequence 1199883, A
15366	3	10.2	15366	3	US-09-764-860-1057	Sequence 1057, Ap
15366	7	10.2	15366	7	US-10-074-095-1057	Sequence 1057, Ap
15366	8	10.2	15366	8	US-10-212-872-1057	Sequence 1057, Ap
23410	23	10.2	23410	23	US-11-033-056A-37244	Sequence 37244, A
53046	23	10.2	53046	23	US-11-033-056A-38464	Sequence 38464, A
63885	16	10.2	63885	16	US-10-990-328-96682	Sequence 96682, A
126552	20	10.2	126552	20	US-11-121-086-1	Sequence 1, Appli
162510	16	10.2	162510	16	US-10-990-328-97157	Sequence 97157, A

C 610	232	10.2	170245	9	US-10-717-597-322	Sequence 322, App	683	231.4	10.1	1463	4	US-09-925-065A-678834	Sequence 678834,
611	232	10.2	191684	20	US-11-121-086-2	Sequence 2, Appli	684	231.4	10.1	1463	5	US-09-925-065A-678834	Sequence 678834,
612	232	10.2	194275	23	US-11-033-056A-37687	Sequence 37687, A	685	231.4	10.1	18218	23	US-11-033-056A-36208	Sequence 36208, A
613	232	10.2	194275	23	US-11-033-056A-37689	Sequence 37689, A	C 686	231.4	10.1	18700	16	US-10-940-774-13140	Sequence 13140, A
614	232	10.2	260209	8	US-10-265-071-23	Sequence 23, Appl	687	231.4	10.1	28054	16	US-10-990-328-97317	Sequence 97317, A
615	232	10.2	260209	8	US-10-025-966A-23	Sequence 23, Appl	C 688	231.4	10.1	31489	16	US-10-990-328-95215	Sequence 95215, A
616	232	10.2	260209	11	US-10-933-025-23	Sequence 23, Appl	689	231.4	10.1	32124	16	US-10-990-328-93448	Sequence 93448, A
617	232	10.2	260209	21	US-11-219-360-23	Sequence 23, Appl	C 690	231.4	10.1	39451	9	US-10-322-281-554	Sequence 554, App
C 618	232	10.2	300351	16	US-10-990-328-96853	Sequence 96853, A	C 691	231.4	10.1	39451	14	US-10-539-228-554	Sequence 554, App
C 619	232	10.2	385460	23	US-11-033-056A-36444	Sequence 36444, A	692	231.4	10.1	44244	16	US-10-940-774-11743	Sequence 11743, A
620	232	10.2	482767	23	US-11-033-056A-38391	Sequence 38391, A	693	231.4	10.1	44245	16	US-10-940-774-13579	Sequence 13579, A
621	232	10.2	486468	23	US-11-033-056A-35962	Sequence 35962, A	694	231.4	10.1	48490	16	US-10-990-328-94910	Sequence 94910, A
C 622	231.8	10.1	596	13	US-10-301-480-14081	Sequence 14081, A	695	231.4	10.1	52410	16	US-10-990-328-97453	Sequence 97453, A
C 623	231.8	10.1	596	13	US-10-301-480-627490	Sequence 627490, A	C 696	231.4	10.1	58014	16	US-10-940-774-17448	Sequence 17448, A
624	231.8	10.1	601	23	US-11-033-545-6961	Sequence 6961, Ap	C 697	231.4	10.1	66641	16	US-10-990-328-94333	Sequence 94333, A
C 625	231.8	10.1	970	4	US-09-925-065A-727962	Sequence 727962,	698	231.4	10.1	87648	16	US-10-940-774-13655	Sequence 13655, A
C 626	231.8	10.1	970	5	US-09-925-065A-727962	Sequence 727962,	C 699	231.4	10.1	104245	8	US-10-160-807-4	Sequence 4, Appli
C 627	231.8	10.1	998	13	US-10-301-480-587769	Sequence 587769,	C 700	231.4	10.1	104245	9	US-10-655-847-4	Sequence 4, Appli
C 628	231.8	10.1	998	13	US-10-301-480-1201178	Sequence 1201178,	C 701	231.4	10.1	114693	10	US-10-473-392-3	Sequence 3, Appli
C 629	231.8	10.1	10000	22	US-11-375-359-258	Sequence 258, App	702	231.4	10.1	147300	11	US-10-723-681-3	Sequence 3, Appli
630	231.8	10.1	18396	23	US-11-033-545-763	Sequence 763, App	703	231.4	10.1	147700	11	US-10-857-780-3	Sequence 3, Appli
631	231.8	10.1	18700	16	US-10-940-774-13140	Sequence 13140, A	C 704	231.4	10.1	154091	17	US-10-674-575-785	Sequence 785, App
C 632	231.8	10.1	57038	11	US-10-287-436A-646	Sequence 646, App	705	231.4	10.1	170245	9	US-10-717-597-322	Sequence 322, App
C 633	231.8	10.1	83016	23	US-11-033-056A-35589	Sequence 35589, A	706	231.4	10.1	171162	20	US-11-112-908-38	Sequence 38, Appl
C 634	231.8	10.1	83016	23	US-11-033-056A-36123	Sequence 36123, A	707	231.4	10.1	201144	21	US-11-266-748A-23494	Sequence 23494, A
C 635	231.8	10.1	83016	23	US-11-033-056A-37409	Sequence 37409, A	708	231.4	10.1	202814	25	US-11-066-316A-9947	Sequence 9947, Ap
C 636	231.8	10.1	83016	23	US-11-033-056A-37463	Sequence 37463, A	C 709	231.4	10.1	262518	16	US-10-990-328-97221	Sequence 97221, A
C 637	231.8	10.1	92794	11	US-10-287-436A-708	Sequence 708, App	710	231.4	10.1	290518	23	US-11-033-056A-37634	Sequence 37634, A
C 638	231.8	10.1	207433	8	US-10-277-216-5	Sequence 5, Appli	711	231.4	10.1	290518	23	US-11-033-056A-37637	Sequence 37637, A
C 639	231.8	10.1	207433	9	US-10-126-022-5	Sequence 5, Appli	712	231.4	10.1	403035	9	US-10-741-601-5729	Sequence 5729, Ap
640	231.8	10.1	219909	23	US-11-405-322-1	Sequence 1, Appli	713	231.4	10.1	403035	16	US-10-990-328-94144	Sequence 94144, A
641	231.8	10.1	256164	21	US-11-266-748A-60910	Sequence 60910, A	714	231.4	10.1	403278	11	US-10-995-561-13421	Sequence 13421, A
642	231.8	10.1	394191	13	US-10-506-549-3	Sequence 3, Appli	715	231.4	10.1	670689	16	US-10-940-774-12505	Sequence 12505, A
C 643	231.6	10.1	461	10	US-10-357-930-19427	Sequence 19427, A	716	231.4	10.1	670690	16	US-10-940-774-14207	Sequence 14207, A
644	231.6	10.1	737	13	US-10-301-480-580734	Sequence 580734,	717	231.4	10.1	687411	12	US-10-330-773-26	Sequence 26, Appl
645	231.6	10.1	737	13	US-10-301-480-1194143	Sequence 1194143,	718	231.4	10.1	687411	14	US-10-540-898-26	Sequence 26, Appl
C 646	231.6	10.1	2271	26	US-11-443-428A-299112	Sequence 299112,	719	231.2	10.1	630	7	US-10-027-632-8952	Sequence 8952, Ap
C 647	231.6	10.1	2300	27	US-11-636-385-42069	Sequence 42069, A	720	231.2	10.1	630	8	US-10-027-632-8952	Sequence 8952, Ap
C 648	231.6	10.1	3158	26	US-11-443-428A-299111	Sequence 299111,	C 721	231.2	10.1	2300	27	US-11-636-385-4876	Sequence 4876, Ap
C 649	231.6	10.1	3158	26	US-11-443-428A-299105	Sequence 299105,	722	231.2	10.1	2300	27	US-11-636-385-22577	Sequence 22577, A
C 650	231.6	10.1	3230	26	US-11-443-428A-299110	Sequence 299110,	723	231.2	10.1	14084	16	US-10-940-774-13889	Sequence 13889, A
C 651	231.6	10.1	3301	26	US-11-443-428A-299107	Sequence 299107,	724	231.2	10.1	19640	7	US-10-087-192-1084	Sequence 1084, Ap
C 652	231.6	10.1	3310	26	US-11-443-428A-299108	Sequence 299108,	725	231.2	10.1	44019	16	US-10-940-774-14902	Sequence 14902, A
C 653	231.6	10.1	3364	26	US-11-443-428A-299104	Sequence 299104,	C 726	231.2	10.1	152759	9	US-10-322-281-10	Sequence 10, Appl
C 654	231.6	10.1	3408	26	US-11-443-428A-299109	Sequence 299109,	C 727	231.2	10.1	152759	14	US-10-539-228-10	Sequence 10, Appl
C 655	231.6	10.1	3464	26	US-11-443-428A-299106	Sequence 299106,	728	231	10.1	292	3	US-09-764-891-6009	Sequence 6009, Ap
656	231.6	10.1	17932	16	US-10-990-328-97852	Sequence 97852, A	729	231	10.1	601	16	US-10-940-774-87765	Sequence 87765, A
657	231.6	10.1	23748	3	US-09-764-891-7917	Sequence 7917, Ap	C 730	231	10.1	678	7	US-10-027-632-136097	Sequence 136097,
C 658	231.6	10.1	25376	16	US-10-990-328-96948	Sequence 96948, A	C 731	231	10.1	678	8	US-10-027-632-136097	Sequence 136097,
C 659	231.6	10.1	39140	16	US-10-990-328-95630	Sequence 95630, A	732	231	10.1	791	26	US-11-443-428A-261885	Sequence 261885,
660	231.6	10.1	40951	16	US-10-940-774-15846	Sequence 15846, A	C 733	231	10.1	1830	7	US-10-027-632-262063	Sequence 262063,
C 661	231.6	10.1	45299	16	US-10-940-774-12465	Sequence 12465, A	C 734	231	10.1	1830	8	US-10-027-632-262063	Sequence 262063,
C 662	231.6	10.1	45300	16	US-10-940-774-13045	Sequence 13045, A	C 735	231	10.1	1830	13	US-10-301-480-96881	Sequence 96881, A
C 663	231.6	10.1	48185	23	US-11-033-056A-36768	Sequence 36768, A	C 736	231	10.1	1830	13	US-10-301-480-96881	Sequence 96881, A
C 664	231.6	10.1	54711	16	US-10-940-774-17489	Sequence 17489, A	737	231	10.1	1833	4	US-09-925-065A-68653	Sequence 710290,
C 665	231.6	10.1	58289	16	US-10-990-328-94348	Sequence 94348, A	738	231	10.1	1833	5	US-09-925-065A-68653	Sequence 68653, A
666	231.6	10.1	68615	23	US-11-033-056A-36425	Sequence 36425, A	739	231	10.1	1833	13	US-10-301-480-169892	Sequence 169892,
667	231.6	10.1	75159	15	US-10-796-280-12543	Sequence 12543, A	740	231	10.1	1833	13	US-10-301-480-783301	Sequence 783301,
668	231.6	10.1	75159	16	US-10-990-328-97698	Sequence 97698, A	C 741	231	10.1	3165	4	US-09-925-065A-688877	Sequence 688877,
669	231.6	10.1	105045	23	US-11-033-545-663	Sequence 663, App	C 742	231	10.1	3165	4	US-09-925-065A-688878	Sequence 688878,
670	231.6	10.1	107045	23	US-11-033-545-772	Sequence 772, App	C 743	231	10.1	3165	5	US-09-925-065A-688877	Sequence 688877,
C 671	231.6	10.1	118923	16	US-10-940-774-13227	Sequence 13227, A	C 744	231	10.1	25825	16	US-09-925-065A-688878	Sequence 688878,
672	231.6	10.1	148037	25	US-11-066-316A-9911	Sequence 9911, Ap	C 745	231	10.1	25825	16	US-10-990-328-95272	Sequence 95272, A
C 673	231.6	10.1	164702	10	US-10-484-577-658	Sequence 658, App	C 746	231	10.1	32865	7	US-10-087-192-964	Sequence 964, App
674	231.6	10.1	210748	23	US-11-033-056A-36345	Sequence 36345, A	747	231	10.1	36472	23	US-11-033-056A-36769	Sequence 36769, A
675	231.6	10.1	239879	16	US-10-990-328-93921	Sequence 93921, A	748	231	10.1	40168	16	US-10-940-774-13225	Sequence 13225, A
C 676	231.6	10.1	304533	16	US-10-940-774-15371	Sequence 15371, A	749	231	10.1	52299	15	US-10-767-471-10687	Sequence 10687, A
C 677	231.6	10.1	304533	16	US-10-940-774-15372	Sequence 15372, A	750	231	10.1	52299	16	US-10-990-328-95102	Sequence 95102, A
678	231.4	10.1	601	23	US-11-033-545-6962	Sequence 6962, Ap	751	231	10.1	52710	9	US-10-322-281-572	Sequence 572, App
C 679	231.4	10.1	970	4	US-09-925-065A-727961	Sequence 727961,	752	231	10.1	52710	14	US-10-539-228-572	Sequence 572, App
C 680	231.4	10.1	970	5	US-09-925-065A-727961	Sequence 727961,	753	231	10.1	58181	16	US-10-990-328-97833	Sequence 97833, A
681	231.4	10.1	996	13	US-10-301-480-594154	Sequence 594154,	C 754	231	10.1	102148	16	US-10-990-328-96742	Sequence 96742, A
682	231.4	10.1	996	13	US-10-301-480-1207563	Sequence 1207563,	755	231	10.1	106274	16	US-10-990-328-95126	Sequence 95126, A



c 756	231	10.1	116644	16	US-10-990-328-96120	Sequence 96120, A	c 829	230.2	10.1	1000	21	US-11-266-748A-344371	Sequence 344371,
c 757	231	10.1	126001	8	US-10-175-492-13	Sequence 13, Appl	c 830	230.2	10.1	1427	4	US-09-925-065A-726021	Sequence 726021,
c 758	231	10.1	176503	20	US-11-121-086-53	Sequence 53, Appl	c 831	230.2	10.1	1427	5	US-09-925-065A-726021	Sequence 726021,
759	231	10.1	197645	16	US-10-990-328-96919	Sequence 96919, A	c 832	230.2	10.1	1721	7	US-10-027-632-97145	Sequence 97145, A
760	231	10.1	224235	16	US-10-990-328-97252	Sequence 97252, A	c 833	230.2	10.1	1721	8	US-10-027-632-97145	Sequence 97145, A
761	231	10.1	261381	23	US-11-033-056A-37874	Sequence 37874, A	834	230.2	10.1	2291	21	US-11-266-748A-31369	Sequence 31369, A
c 762	230.8	10.1	679	4	US-09-925-065A-532787	Sequence 532787, A	835	230.2	10.1	2291	23	US-11-371-354-11097	Sequence 11097, A
c 763	230.8	10.1	679	5	US-09-925-065A-532787	Sequence 532787, A	836	230.2	10.1	2300	27	US-11-636-385-12508	Sequence 12508, A
c 764	230.8	10.1	875	7	US-10-027-632-169472	Sequence 169472, A	837	230.2	10.1	2300	27	US-11-636-385-17035	Sequence 17035, A
765	230.8	10.1	875	8	US-10-027-632-169472	Sequence 169472, A	838	230.2	10.1	6777	8	US-10-376-566-10	Sequence 10, Appl
766	230.8	10.1	2300	27	US-11-636-385-35266	Sequence 35266, A	839	230.2	10.1	10281	16	US-10-940-774-15812	Sequence 15812, A
c 767	230.8	10.1	17628	16	US-10-940-774-16718	Sequence 16718, A	c 840	230.2	10.1	10465	16	US-10-940-774-13136	Sequence 13136, A
768	230.8	10.1	22135	16	US-10-990-328-96594	Sequence 96594, A	841	230.2	10.1	13286	13	US-10-517-441-113	Sequence 113, App
c 769	230.8	10.1	40859	16	US-10-990-328-95269	Sequence 95269, A	c 842	230.2	10.1	14670	10	US-10-741-600-17749	Sequence 17749, A
770	230.8	10.1	45091	16	US-10-990-328-95100	Sequence 95100, A	c 843	230.2	10.1	17901	16	US-10-990-328-97628	Sequence 97628, A
771	230.8	10.1	71879	16	US-10-940-774-17465	Sequence 17465, A	c 844	230.2	10.1	18097	10	US-10-741-600-17981	Sequence 17981, A
772	230.8	10.1	87878	9	US-10-052-482-82	Sequence 82, Appl	845	230.2	10.1	18895	10	US-10-741-600-17750	Sequence 17750, A
773	230.8	10.1	87878	15	US-10-035-832-1094	Sequence 1094, Ap	c 846	230.2	10.1	22131	16	US-10-990-328-94882	Sequence 94882, A
774	230.8	10.1	87878	22	US-11-330-726-82	Sequence 82, Appl	c 847	230.2	10.1	26059	15	US-10-105-299-10406	Sequence 10406, A
775	230.8	10.1	127369	16	US-10-990-328-93789	Sequence 93789, A	c 848	230.2	10.1	26059	16	US-10-868-184-8255	Sequence 8255, Ap
776	230.8	10.1	285669	23	US-11-033-056A-38757	Sequence 38757, A	c 849	230.2	10.1	26665	22	US-11-073-360-1599	Sequence 1599, Ap
777	230.8	10.1	418196	23	US-11-033-056A-37368	Sequence 37368, A	850	230.2	10.1	66916	9	US-10-741-601-5708	Sequence 5708, Ap
778	230.8	10.1	418196	23	US-11-033-056A-37414	Sequence 37414, A	851	230.2	10.1	66916	10	US-10-741-600-17810	Sequence 17810, A
c 779	230.8	10.1	479168	16	US-10-990-328-97660	Sequence 97660, A	852	230.2	10.1	66916	11	US-10-995-561-13374	Sequence 13374, A
c 780	230.6	10.1	601	16	US-10-940-774-68606	Sequence 68606, A	853	230.2	10.1	66916	16	US-10-990-328-93218	Sequence 93218, A
c 781	230.6	10.1	616	4	US-09-925-065A-931112	Sequence 931112, A	854	230.2	10.1	68452	16	US-10-940-774-13305	Sequence 13305, A
c 782	230.6	10.1	616	5	US-09-925-065A-931112	Sequence 931112, A	855	230.2	10.1	86168	16	US-10-990-328-95490	Sequence 95490, A
c 783	230.6	10.1	806	13	US-10-301-480-560813	Sequence 560813, A	856	230.2	10.1	102541	16	US-10-990-328-96643	Sequence 96643, A
c 784	230.6	10.1	806	13	US-10-301-480-1174222	Sequence 1174222, A	857	230.2	10.1	113000	8	US-10-376-566-16	Sequence 16, Appl
c 785	230.6	10.1	2300	27	US-11-636-385-316	Sequence 316, App	858	230.2	10.1	114503	16	US-10-990-328-94201	Sequence 94201, A
786	230.6	10.1	2300	27	US-11-636-385-10727	Sequence 10727, A	c 859	230.2	10.1	188056	21	US-11-120-925-1	Sequence 1, Appl
c 787	230.6	10.1	2300	27	US-11-636-385-19804	Sequence 19804, A	c 860	230.2	10.1	189252	20	US-11-121-086-54	Sequence 54, Appl
c 788	230.6	10.1	2300	27	US-11-636-385-35371	Sequence 35371, A	861	230.2	10.1	202814	10	US-10-719-993-6812	Sequence 6812, Ap
789	230.6	10.1	14863	23	US-11-033-056A-37210	Sequence 37210, A	862	230.2	10.1	202814	16	US-10-990-328-97440	Sequence 97440, A
790	230.6	10.1	17498	3	US-09-764-860-798	Sequence 798, App	863	230.2	10.1	246826	23	US-11-033-056A-37194	Sequence 37194, A
791	230.6	10.1	17498	7	US-10-074-095-798	Sequence 798, App	864	230.2	10.1	246826	23	US-11-033-056A-37195	Sequence 37195, A
792	230.6	10.1	17498	8	US-10-212-872-798	Sequence 798, App	865	230.2	10.1	246826	23	US-11-033-056A-38778	Sequence 38778, A
793	230.6	10.1	20090	23	US-11-033-056A-37933	Sequence 37933, A	866	230.2	10.1	290040	10	US-10-850-591-3	Sequence 3, Appl
794	230.6	10.1	24005	16	US-10-940-774-13758	Sequence 13758, A	867	230.2	10.1	290040	10	US-10-850-586-3	Sequence 1, Appl
795	230.6	10.1	25659	16	US-10-940-774-15052	Sequence 15052, A	868	230.2	10.1	325791	4	US-09-768-185A-1	Sequence 36747, A
c 796	230.6	10.1	26509	16	US-10-990-328-94126	Sequence 94126, A	c 869	230.2	10.1	332704	23	US-11-033-056A-36747	Sequence 36747, A
797	230.6	10.1	29490	16	US-10-990-328-97394	Sequence 97394, A	c 870	230.2	10.1	332704	23	US-11-033-056A-37600	Sequence 37600, A
798	230.6	10.1	30381	16	US-10-990-328-95595	Sequence 95595, A	c 871	230.2	10.1	405740	16	US-10-796-307-8716	Sequence 8716, Ap
c 799	230.6	10.1	69920	15	US-10-767-471-10739	Sequence 10739, A	c 872	230.2	10.1	408997	23	US-11-033-056A-36439	Sequence 36439, A
c 800	230.6	10.1	69920	16	US-10-990-328-95794	Sequence 95794, A	c 873	230.2	10.1	524169	23	US-11-033-056A-36660	Sequence 36660, A
c 801	230.6	10.1	86141	15	US-10-796-280-12292	Sequence 12292, A	874	230	10.1	955	7	US-10-037-270-228	Sequence 228, App
802	230.6	10.1	87001	10	US-10-741-600-17792	Sequence 17792, A	875	230	10.1	955	8	US-10-117-722-228	Sequence 228, App
c 803	230.6	10.1	89171	16	US-10-990-328-96720	Sequence 96720, A	876	230	10.1	955	11	US-10-122-851-228	Sequence 228, App
804	230.6	10.1	95597	16	US-10-990-328-95297	Sequence 95297, A	877	230	10.1	2300	27	US-11-636-385-27569	Sequence 27569, A
805	230.6	10.1	102993	23	US-11-033-056A-37458	Sequence 37458, A	c 878	230	10.1	2300	27	US-11-636-385-43081	Sequence 43081, A
806	230.6	10.1	130877	9	US-10-322-281-54	Sequence 54, Appl	c 879	230	10.1	17146	3	US-09-764-877-3850	Sequence 3850, Ap
807	230.6	10.1	130877	14	US-10-539-228-54	Sequence 54, Appl	c 880	230	10.1	17146	8	US-10-242-515-3850	Sequence 3850, Ap
c 808	230.6	10.1	177531	10	US-10-484-577-660	Sequence 660, App	881	230	10.1	25708	16	US-10-990-328-94068	Sequence 94068, A
c 809	230.6	10.1	215595	16	US-10-990-328-94061	Sequence 94061, A	c 882	230	10.1	30568	3	US-09-764-877-3851	Sequence 3851, Ap
810	230.6	10.1	295669	23	US-11-033-056A-38457	Sequence 38457, A	c 883	230	10.1	30568	8	US-10-242-515-3851	Sequence 3851, Ap
811	230.4	10.1	601	16	US-10-940-774-120457	Sequence 120457, A	884	230	10.1	40512	16	US-10-940-774-16612	Sequence 16612, A
812	230.4	10.1	601	16	US-10-940-774-120458	Sequence 120458, A	c 885	230	10.1	45720	16	US-10-990-328-94980	Sequence 94980, A
813	230.4	10.1	631	4	US-09-925-065A-499794	Sequence 499794, A	c 886	230	10.1	88645	23	US-11-417-450-38	Sequence 38, Appl
814	230.4	10.1	631	5	US-09-925-065A-499794	Sequence 499794, A	c 887	230	10.1	165213	23	US-11-417-450-37	Sequence 37, Appl
815	230.4	10.1	1000	21	US-11-266-748A-202568	Sequence 202568, A	888	230	10.1	183704	23	US-11-033-056A-37169	Sequence 37169, A
816	230.4	10.1	2300	27	US-11-636-385-4145	Sequence 4145, Ap	889	230	10.1	183704	23	US-11-033-056A-37170	Sequence 37170, A
817	230.4	10.1	12993	16	US-10-990-328-93372	Sequence 93372, A	c 890	230	10.1	193636	23	US-11-417-450-36	Sequence 36, Appl
818	230.4	10.1	24268	16	US-10-100-683-13305	Sequence 13305, A	c 891	230	10.1	249293	16	US-10-990-328-96176	Sequence 96176, A
819	230.4	10.1	24268	23	US-11-001-793-13305	Sequence 13305, A	c 892	229.8	10.1	489	4	US-09-925-065A-469133	Sequence 469133, A
c 820	230.4	10.1	334385	16	US-10-990-328-96323	Sequence 96323, A	c 893	229.8	10.1	489	5	US-09-925-065A-469133	Sequence 469133, A
821	230.2	10.1	574	13	US-10-301-480-49061	Sequence 49061, A	c 894	229.8	10.1	578	7	US-10-027-632-289745	Sequence 289745, A
822	230.2	10.1	574	13	US-10-301-480-662470	Sequence 662470, A	c 895	229.8	10.1	578	8	US-10-027-632-289745	Sequence 289745, A
c 823	230.2	10.1	628	13	US-10-301-480-545191	Sequence 545191, A	896	229.8	10.1	591	4	US-09-925-065A-526304	Sequence 526304, A
c 824	230.2	10.1	628	13	US-10-301-480-1158600	Sequence 1158600, A	897	229.8	10.1	591	5	US-09-925-065A-526304	Sequence 526304, A
c 825	230.2	10.1	986	13	US-10-301-480-593168	Sequence 593168, A	c 898	229.8	10.1	619	4	US-09-925-065A-536042	Sequence 536042, A
c 826	230.2	10.1	986	13	US-10-301-480-1206577	Sequence 1206577, A	c 899	229.8	10.1	619	5	US-09-925-065A-536042	Sequence 536042, A
827	230.2	10.1	1000	21	US-11-266-748A-224259	Sequence 224259, A	c 900	229.8	10.1	2300	27	US-11-636-385-20755	Sequence 20755, A
828	230.2	10.1	1000	21	US-11-266-748A-292942	Sequence 292942, A	c 901	229.8	10.1	14670	11	US-10-995-561-13328	Sequence 13328, A

c 902	229.8	10.1	18097	11	US-10-995-561-13486	Sequence 13486, A	975	229.4	10.0	576	13	US-10-301-480-1014615	Sequence 1014615,
903	229.8	10.1	18895	11	US-10-995-561-13329	Sequence 13329, A	976	229.4	10.0	576	13	US-10-301-480-1014616	Sequence 1014616,
904	229.8	10.1	24590	16	US-10-990-328-96793	Sequence 96793, A	c 977	229.4	10.0	578	7	US-10-027-632-289743	Sequence 289743,
c 905	229.8	10.1	31737	14	US-10-219-051B-13986	Sequence 13986, A	c 978	229.4	10.0	578	7	US-10-027-632-289744	Sequence 289744,
c 906	229.8	10.1	31737	14	US-10-219-051B-14699	Sequence 14699, A	c 979	229.4	10.0	578	8	US-10-027-632-289743	Sequence 289743,
907	229.8	10.1	38206	16	US-10-940-774-15527	Sequence 15527, A	c 980	229.4	10.0	578	8	US-10-027-632-289744	Sequence 289744,
908	229.8	10.1	46215	10	US-10-741-600-17973	Sequence 17973, A	c 981	229.4	10.0	619	4	US-09-925-065A-536043	Sequence 536043,
909	229.8	10.1	46215	11	US-10-995-561-13483	Sequence 13483, A	c 982	229.4	10.0	619	5	US-09-925-065A-536043	Sequence 536043,
910	229.8	10.1	46215	15	US-10-796-280-12563	Sequence 12563, A	c 983	229.4	10.0	713	4	US-09-925-065A-93712	Sequence 93712, A
911	229.8	10.1	66972	7	US-10-087-192-556	Sequence 556, App	c 984	229.4	10.0	713	5	US-09-925-065A-93712	Sequence 93712, A
912	229.8	10.1	75007	9	US-10-741-601-5612	Sequence 5612, Ap	c 985	229.4	10.0	713	13	US-10-301-480-194954	Sequence 194954,
913	229.8	10.1	75007	10	US-10-741-600-17556	Sequence 17556, A	c 986	229.4	10.0	713	13	US-10-301-480-808363	Sequence 808363,
914	229.8	10.1	75007	11	US-10-995-561-13194	Sequence 13194, A	c 987	229.4	10.0	998	7	US-10-027-632-31285	Sequence 31285, A
915	229.8	10.1	75007	16	US-10-990-328-93232	Sequence 93232, A	c 988	229.4	10.0	998	8	US-10-027-632-31285	Sequence 31285, A
916	229.8	10.1	149133	16	US-10-990-328-94291	Sequence 94291, A	c 989	229.4	10.0	1000	21	US-11-266-748A-205592	Sequence 205592,
c 917	229.8	10.1	152335	20	US-11-121-086-73	Sequence 73, Appl	c 990	229.4	10.0	1412	4	US-09-925-065A-63600	Sequence 63600, A
918	229.8	10.1	179666	20	US-11-121-086-67	Sequence 67, Appl	c 991	229.4	10.0	1412	4	US-09-925-065A-63601	Sequence 63601, A
919	229.8	10.1	318999	16	US-10-990-328-94160	Sequence 94160, A	c 992	229.4	10.0	1412	4	US-09-925-065A-63602	Sequence 63602, A
c 920	229.8	10.1	368716	23	US-11-033-056A-38696	Sequence 38696, A	c 993	229.4	10.0	1412	4	US-09-925-065A-63603	Sequence 63603, A
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922	229.8	10.1	816609	22	US-11-073-360-1606	Sequence 1606, Ap	c 995	229.4	10.0	1412	5	US-09-925-065A-63601	Sequence 63601, A
c 923	229.8	10.1	1080000	11	US-10-928-446A-1	Sequence 1, Appli	c 996	229.4	10.0	1412	5	US-09-925-065A-63602	Sequence 63602, A
c 924	229.8	10.1	1080000	11	US-10-928-446A-181	Sequence 181, App	c 997	229.4	10.0	1412	5	US-09-925-065A-63603	Sequence 63603, A
c 925	229.8	10.1	1080000	11	US-10-928-446A-183	Sequence 183, App	c 998	229.4	10.0	1412	13	US-10-301-480-164838	Sequence 164838,
c 926	229.8	10.1	1080000	11	US-10-928-446A-185	Sequence 185, App	c 999	229.4	10.0	1412	13	US-10-301-480-164839	Sequence 164839,
c 927	229.8	10.1	1080000	11	US-10-928-446A-187	Sequence 187, App	c1000	229.4	10.0	1412	13	US-10-301-480-164840	Sequence 164840,
c 928	229.8	10.1	1080000	11	US-10-928-446A-189	Sequence 189, App	c1001	229.4	10.0	1412	13	US-10-301-480-164841	Sequence 164841,
c 929	229.8	10.1	1080000	11	US-10-928-446A-191	Sequence 191, App	c1002	229.4	10.0	1412	13	US-10-301-480-778247	Sequence 778247,
c 930	229.8	10.1	1080000	11	US-10-928-446A-193	Sequence 193, App	c1003	229.4	10.0	1412	13	US-10-301-480-778248	Sequence 778248,
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c 932	229.8	10.1	1080000	11	US-10-928-446A-197	Sequence 197, App	c1005	229.4	10.0	1412	13	US-10-301-480-778250	Sequence 778250,
c 933	229.8	10.1	1080000	11	US-10-928-446A-199	Sequence 199, App	1006	229.4	10.0	2300	27	US-11-636-385-35742	Sequence 35742, A
c 934	229.8	10.1	1080000	11	US-10-928-446A-201	Sequence 201, App	1007	229.4	10.0	27499	9	US-10-367-094-111	Sequence 111, App
c 935	229.8	10.1	1656406	23	US-11-033-056A-37967	Sequence 37967, A	1008	229.4	10.0	28693	11	US-10-995-561-13341	Sequence 13341, A
c 936	229.6	10.1	1645	16	US-10-917-503-13851	Sequence 13851, A	1009	229.4	10.0	37976	16	US-10-940-774-13441	Sequence 13441, A
c 937	229.6	10.1	1645	26	US-11-443-428A-237126	Sequence 237126,	1010	229.4	10.0	42790	21	US-11-266-748A-23980	Sequence 23980, A
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c 939	229.6	10.1	12945	16	US-10-990-328-97961	Sequence 97961, A	1012	229.4	10.0	72602	16	US-10-940-774-14385	Sequence 14385, A
c 940	229.6	10.1	14050	16	US-10-990-328-97961	Sequence 93390, A	1013	229.4	10.0	79417	16	US-10-990-328-93614	Sequence 93614, A
941	229.6	10.1	15696	15	US-10-105-299-73386	Sequence 7386, Ap	c1014	229.4	10.0	95597	16	US-10-990-328-95297	Sequence 95297, A
942	229.6	10.1	15696	16	US-10-868-184-5235	Sequence 5235, Ap	c1015	229.4	10.0	98302	16	US-10-940-774-16847	Sequence 16847, A
943	229.6	10.1	20840	16	US-10-940-774-14115	Sequence 14115, A	1016	229.4	10.0	112507	16	US-10-940-774-12420	Sequence 12420, A
c 944	229.6	10.1	21850	12	US-10-330-773-474	Sequence 474, App	1017	229.4	10.0	112507	16	US-10-940-774-12794	Sequence 12794, A
c 945	229.6	10.1	21850	14	US-10-540-898-474	Sequence 474, App	1018	229.4	10.0	112508	16	US-10-940-774-16589	Sequence 16589, A
946	229.6	10.1	32248	3	US-09-764-860-802	Sequence 802, App	1019	229.4	10.0	112508	16	US-10-940-774-16590	Sequence 16590, A
947	229.6	10.1	32248	7	US-10-074-095-802	Sequence 802, App	1020	229.4	10.0	113042	16	US-10-940-774-12343	Sequence 12343, A
948	229.6	10.1	32248	8	US-10-212-872-802	Sequence 802, App	1021	229.4	10.0	113042	16	US-10-940-774-15246	Sequence 15246, A
c 949	229.6	10.1	36731	16	US-10-940-774-13770	Sequence 13770, A	1022	229.4	10.0	119472	10	US-10-741-600-17865	Sequence 17865, A
c 950	229.6	10.1	40441	16	US-10-990-328-96946	Sequence 96946, A	1023	229.4	10.0	121053	16	US-10-990-328-95324	Sequence 95324, A
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c 952	229.6	10.1	79977	11	US-10-737-082-58	Sequence 58, Appl	1025	229.4	10.0	128668	7	US-10-087-192-340	Sequence 340, App
c 953	229.6	10.1	79977	11	US-10-765-790-58	Sequence 58, Appl	1026	229.4	10.0	129042	7	US-10-087-192-1240	Sequence 1240, Ap
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957	229.6	10.1	121033	17	US-10-674-575-1159	Sequence 1159, Ap	1030	229.4	10.0	162025	3	US-09-834-700-18	Sequence 18, Appl
c 958	229.6	10.1	133632	7	US-10-087-192-1810	Sequence 1810, Ap	1031	229.4	10.0	162025	8	US-10-272-665-35	Sequence 35, Appl
c 959	229.6	10.1	133642	14	US-10-669-920-805	Sequence 805, App	1032	229.4	10.0	162025	8	US-10-272-665-36	Sequence 36, Appl
960	229.6	10.1	144362	16	US-10-940-774-16066	Sequence 16066, A	1033	229.4	10.0	162025	8	US-10-273-321-35	Sequence 35, Appl
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962	229.6	10.1	193689	16	US-10-990-328-93508	Sequence 93508, A	1035	229.4	10.0	162025	8	US-10-272-756-35	Sequence 35, Appl
963	229.6	10.1	198522	7	US-10-087-192-244	Sequence 244, App	1036	229.4	10.0	162025	8	US-10-272-756-36	Sequence 36, Appl
964	229.6	10.1	304905	9	US-10-271-416-1	Sequence 1, Appli	1037	229.4	10.0	162025	8	US-10-273-228-35	Sequence 35, Appl
965	229.6	10.1	332350	23	US-11-033-056A-38154	Sequence 38154, A	1038	229.4	10.0	162025	8	US-10-273-228-36	Sequence 36, Appl
966	229.6	10.1	567564	10	US-10-699-156-3	Sequence 3, Appli	1039	229.4	10.0	162025	17	US-10-548-336A-13	Sequence 13, Appl
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c 968	229.6	10.1	766455	16	US-10-990-328-98054	Sequence 98054, A	1041	229.4	10.0	162025	17	US-10-548-336A-17	Sequence 17, Appl
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971	229.4	10.0	571	5	US-09-925-065A-327160	Sequence 327160,	c1044	229.4	10.0	179012	16	US-10-990-328-94764	Sequence 94764, A
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973	229.4	10.0	576	13	US-10-301-480-401206	Sequence 401206,	c1046	229.4	10.0	186391	7	US-10-087-192-136	Sequence 136, App
974	229.4	10.0	576	13	US-10-301-480-401207	Sequence 401207,	1047	229.4	10.0	225587	12	US-10-330-773-374	Sequence 374, App



1048	229.4	10.0	225587	14	US-10-540-898-374	Sequence 374, App	1121	229	10.0	2246	26	US-11-443-428A-362345	Sequence 362345,
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c1056	229.4	10.0	505854	16	US-10-990-328-94315	Sequence 94315, A	1129	229	10.0	2495	8	US-10-059-579-104	Sequence 104, App
c1057	229.2	10.0	454	10	US-10-357-930-50096	Sequence 50096, A	1130	229	10.0	2495	11	US-10-872-229-104	Sequence 104, App
c1058	229.2	10.0	601	16	US-10-940-774-141088	Sequence 141088,	1131	229	10.0	2539	26	US-11-443-428A-362360	Sequence 362360,
c1059	229.2	10.0	601	16	US-10-940-774-154401	Sequence 154401,	c1132	229	10.0	3961	3	US-09-764-891-6205	Sequence 6205, Ap
c1060	229.2	10.0	601	16	US-10-940-774-154402	Sequence 154402,	c1133	229	10.0	3961	3	US-09-764-891-6206	Sequence 6206, Ap
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1062	229.2	10.0	656	5	US-09-925-065A-675446	Sequence 675446,	1135	229	10.0	10758	3	US-09-764-869-1647	Sequence 1647, Ap
1063	229.2	10.0	759	7	US-10-027-632-147208	Sequence 147208,	1136	229	10.0	10758	3	US-09-764-869-1650	Sequence 1650, Ap
1064	229.2	10.0	759	7	US-10-027-632-147209	Sequence 147209,	1137	229	10.0	10758	7	US-10-091-504-1647	Sequence 1647, Ap
1065	229.2	10.0	759	8	US-10-027-632-147208	Sequence 147208,	1138	229	10.0	10758	7	US-10-091-504-1650	Sequence 1650, Ap
1066	229.2	10.0	759	8	US-10-027-632-147209	Sequence 147209,	1139	229	10.0	10758	8	US-10-227-577-1647	Sequence 1647, Ap
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c1068	229.2	10.0	2300	27	US-11-636-385-18004	Sequence 18004, A	1141	229	10.0	10759	3	US-09-764-869-1649	Sequence 1649, Ap
c1069	229.2	10.0	2300	27	US-11-636-385-19010	Sequence 19010, A	1142	229	10.0	10759	7	US-10-091-504-1649	Sequence 1649, Ap
c1070	229.2	10.0	2300	27	US-11-636-385-31359	Sequence 31359, A	1143	229	10.0	10759	8	US-10-227-577-1649	Sequence 1649, Ap
1071	229.2	10.0	19377	16	US-10-940-774-15198	Sequence 15198, A	c1144	229	10.0	12585	16	US-10-990-328-97219	Sequence 97219, A
1072	229.2	10.0	20534	23	US-11-033-056A-35697	Sequence 35697, A	c1145	229	10.0	18328	16	US-10-990-328-93923	Sequence 93923, A
1073	229.2	10.0	28874	16	US-10-990-328-93465	Sequence 93465, A	1146	229	10.0	25899	9	US-10-322-696-10	Sequence 10, Appl
c1074	229.2	10.0	31670	8	US-10-004-113-22	Sequence 22, Appl	1147	229	10.0	33870	16	US-10-990-328-97220	Sequence 97220, A
c1075	229.2	10.0	31670	15	US-10-035-832-974	Sequence 974, App	1148	229	10.0	36578	10	US-10-741-600-17600	Sequence 17600, A
c1076	229.2	10.0	31670	22	US-11-330-648-22	Sequence 22, Appl	1149	229	10.0	36578	16	US-10-990-328-93825	Sequence 93825, A
c1077	229.2	10.0	31704	14	US-10-669-920-4	Sequence 4, Appli	c1150	229	10.0	57336	16	US-10-990-328-97065	Sequence 97065, A
c1078	229.2	10.0	32111	23	US-11-033-056A-35657	Sequence 35657, A	1151	229	10.0	61666	23	US-11-033-056A-36501	Sequence 36501, A
c1079	229.2	10.0	32111	23	US-11-033-056A-35658	Sequence 35658, A	c1152	229	10.0	63506	16	US-10-990-328-96064	Sequence 96064, A
c1080	229.2	10.0	32111	23	US-11-033-056A-35659	Sequence 35659, A	1153	229	10.0	65744	16	US-10-940-774-12591	Sequence 12591, A
c1081	229.2	10.0	32111	23	US-11-033-056A-38047	Sequence 38047, A	1154	229	10.0	65745	16	US-10-940-774-15871	Sequence 15871, A
1082	229.2	10.0	42808	23	US-11-033-056A-36928	Sequence 36928, A	c1155	229	10.0	65813	23	US-11-033-056A-36364	Sequence 36364, A
1083	229.2	10.0	50694	23	US-11-033-056A-36122	Sequence 36122, A	c1156	229	10.0	65813	23	US-11-033-056A-36365	Sequence 36365, A
1084	229.2	10.0	52317	16	US-10-990-328-94375	Sequence 94375, A	1157	229	10.0	74562	23	US-11-033-056A-38685	Sequence 38685, A
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c1088	229.2	10.0	129554	23	US-11-033-545-765	Sequence 765, App	1161	229	10.0	421987	21	US-11-266-748A-28210	Sequence 28210, A
c1089	229.2	10.0	143418	23	US-11-033-056A-36118	Sequence 36118, A	1162	229	10.0	452163	23	US-11-033-056A-37365	Sequence 37365, A
c1090	229.2	10.0	146656	20	US-11-121-086-68	Sequence 68, Appl	1163	228.8	10.0	560	4	US-09-925-065A-589226	Sequence 589226,
c1091	229.2	10.0	193169	16	US-10-940-774-15091	Sequence 15091, A	1164	228.8	10.0	560	5	US-09-925-065A-589226	Sequence 589226,
c1092	229.2	10.0	203249	23	US-11-033-056A-36674	Sequence 36674, A	1165	228.8	10.0	601	16	US-10-940-774-120456	Sequence 120456,
1093	229	10.0	601	4	US-09-925-065A-811520	Sequence 811520,	c1166	228.8	10.0	839	26	US-11-443-428A-250605	Sequence 250605,
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1096	229	10.0	601	5	US-09-925-065A-812401	Sequence 812401,	c1169	228.8	10.0	2300	27	US-11-636-385-26897	Sequence 26897, A
c1097	229	10.0	601	16	US-10-940-774-51144	Sequence 51144, A	c1170	228.8	10.0	11995	8	US-10-017-161-1865	Sequence 1865, Ap
c1098	229	10.0	601	16	US-10-940-774-109427	Sequence 109427,	c1171	228.8	10.0	11995	8	US-10-292-798-1521	Sequence 1521, Ap
1099	229	10.0	609	4	US-09-925-065A-809539	Sequence 809539,	c1172	228.8	10.0	11995	23	US-11-214-063A-1521	Sequence 1521, Ap
1100	229	10.0	609	5	US-09-925-065A-809539	Sequence 809539,	c1173	228.8	10.0	14191	16	US-10-990-328-97570	Sequence 97570, A
1101	229	10.0	653	4	US-09-925-065A-698440	Sequence 698440,	c1174	228.8	10.0	16489	3	US-09-764-868-1483	Sequence 1483, Ap
1102	229	10.0	653	5	US-09-925-065A-698440	Sequence 698440,	c1175	228.8	10.0	25760	23	US-11-033-056A-37176	Sequence 37176, A
c1103	229	10.0	713	4	US-09-925-065A-93711	Sequence 93711, A	1176	228.8	10.0	36618	16	US-10-940-774-15723	Sequence 15723, A
c1104	229	10.0	713	5	US-09-925-065A-93711	Sequence 93711, A	1177	228.8	10.0	61642	23	US-11-033-056A-37383	Sequence 37383, A
c1105	229	10.0	713	13	US-10-301-480-194953	Sequence 194953,	1178	228.8	10.0	65990	16	US-10-940-774-11830	Sequence 11830, A
c1106	229	10.0	713	13	US-10-301-480-808362	Sequence 808362,	1179	228.8	10.0	68571	8	US-10-401-194-1	Sequence 1, Appli
1107	229	10.0	722	4	US-09-925-065A-31275	Sequence 31275, A	1180	228.8	10.0	73482	16	US-10-990-328-94912	Sequence 94912, A
1108	229	10.0	722	5	US-09-925-065A-31275	Sequence 31275, A	1181	228.8	10.0	81968	9	US-10-322-696-142	Sequence 142, App
1109	229	10.0	722	13	US-10-301-480-132513	Sequence 132513,	1182	228.8	10.0	84105	14	US-10-669-920-1403	Sequence 1403, Ap
1110	229	10.0	722	13	US-10-301-480-745922	Sequence 745922,	c1183	228.8	10.0	107365	16	US-10-990-328-95871	Sequence 95871, A
1111	229	10.0	841	26	US-11-443-428A-362350	Sequence 362350,	1184	228.8	10.0	116368	27	US-11-606-619A-25	Sequence 25, Appl
c1112	229	10.0	988	13	US-10-301-480-578759	Sequence 578759,	1185	228.8	10.0	152589	16	US-10-990-328-95688	Sequence 95688, A
c1113	229	10.0	988	13	US-10-301-480-578760	Sequence 578760,	c1186	228.8	10.0	175077	7	US-10-087-192-1168	Sequence 1168, Ap
c1114	229	10.0	988	13	US-10-301-480-1192168	Sequence 1192168,	c1187	228.6	10.0	519	26	US-11-443-428A-336473	Sequence 336473,
c1115	229	10.0	988	13	US-10-301-480-1192169	Sequence 1192169,	1188	228.6	10.0	601	16	US-10-940-774-19500	Sequence 19500, A
1116	229	10.0	1910	26	US-11-443-428A-362363	Sequence 362363,	1189	228.6	10.0	601	16	US-10-940-774-205300	Sequence 205300,
1117	229	10.0	2012	26	US-11-443-428A-362344	Sequence 362344,	c1190	228.6	10.0	601	23	US-11-033-545-2639	Sequence 2639, Ap
1118	229	10.0	2056	26	US-11-443-428A-362362	Sequence 362362,	c1191	228.6	10.0	601	23	US-11-033-545-2640	Sequence 2640, Ap
1119	229	10.0	2095	26	US-11-443-428A-362361	Sequence 362361,	c1192	228.6	10.0	601	23	US-11-033-545-9909	Sequence 9909, Ap
1120	229	10.0	2166	26	US-11-443-428A-362343	Sequence 362343,	c1193	228.6	10.0	601	23	US-11-033-545-9910	Sequence 9910, Ap

1194	228.6	10.0	788	26	US-11-443-428A-213712	Sequence 213712,	1267	228.4	10.0	524169	23	US-11-033-056A-36660	Sequence 36660, A
1195	228.6	10.0	2300	27	US-11-636-385-1795	Sequence 1795, Ap	1268	228.4	10.0	894593	23	US-11-033-056A-36625	Sequence 36625, A
1196	228.6	10.0	2300	27	US-11-636-385-17956	Sequence 17956, A	1269	228.4	10.0	894593	23	US-11-033-056A-37490	Sequence 37490, A
c1197	228.6	10.0	10093	3	US-09-764-869-1390	Sequence 1390, Ap	1270	228.2	10.0	407	3	US-09-803-719-1531	Sequence 1531, Ap
c1198	228.6	10.0	10093	7	US-10-091-504-1390	Sequence 1390, Ap	1271	228.2	10.0	407	11	US-10-779-543-14801	Sequence 14801, A
c1199	228.6	10.0	10093	8	US-10-227-577-1390	Sequence 1390, Ap	1272	228.2	10.0	546	4	US-09-925-065A-799095	Sequence 799095, A
c1200	228.6	10.0	10093	16	US-10-100-683-11550	Sequence 11550, A	1273	228.2	10.0	546	5	US-09-925-065A-799095	Sequence 799095, A
c1201	228.6	10.0	10093	23	US-11-001-793-11550	Sequence 11550, A	c1274	228.2	10.0	601	16	US-10-940-774-64990	Sequence 64990, A
1202	228.6	10.0	13203	16	US-10-940-774-17544	Sequence 17544, A	c1275	228.2	10.0	601	16	US-10-940-774-172794	Sequence 172794, A
1203	228.6	10.0	16273	16	US-10-940-774-11826	Sequence 11826, A	1276	228.2	10.0	601	23	US-11-033-545-3497	Sequence 3497, Ap
1204	228.6	10.0	26631	16	US-10-990-328-96937	Sequence 96937, A	1277	228.2	10.0	601	23	US-11-033-545-9469	Sequence 9469, Ap
1205	228.6	10.0	28693	10	US-10-741-600-17761	Sequence 17761, A	1278	228.2	10.0	604	4	US-09-925-065A-799096	Sequence 799096, A
c1206	228.6	10.0	34110	16	US-10-990-328-93738	Sequence 93738, A	1279	228.2	10.0	604	5	US-09-925-065A-799096	Sequence 799096, A
1207	228.6	10.0	39480	16	US-10-940-774-13634	Sequence 13634, A	c1280	228.2	10.0	635	4	US-09-925-065A-856307	Sequence 856307, A
c1208	228.6	10.0	46725	16	US-10-940-774-15680	Sequence 15680, A	c1281	228.2	10.0	635	5	US-09-925-065A-856307	Sequence 856307, A
1209	228.6	10.0	48420	16	US-10-990-328-98029	Sequence 98029, A	1282	228.2	10.0	1437	4	US-09-925-065A-694852	Sequence 694852, A
1210	228.6	10.0	48453	23	US-11-033-056A-35921	Sequence 35921, A	1283	228.2	10.0	1437	5	US-09-925-065A-694852	Sequence 694852, A
c1211	228.6	10.0	54022	16	US-10-990-328-95497	Sequence 95497, A	c1284	228.2	10.0	3208	21	US-11-091-883-367	Sequence 367, App
1212	228.6	10.0	98828	16	US-10-940-774-16630	Sequence 16630, A	c1285	228.2	10.0	3208	25	US-11-437-797-367	Sequence 367, App
1213	228.6	10.0	112141	16	US-10-990-328-93217	Sequence 93217, A	1286	228.2	10.0	11850	8	US-10-017-161-669	Sequence 669, App
1214	228.6	10.0	161323	16	US-10-990-328-94088	Sequence 94088, A	1287	228.2	10.0	24486	16	US-10-990-328-94423	Sequence 94423, A
1215	228.6	10.0	164875	8	US-10-085-117-322	Sequence 322, App	1288	228.2	10.0	32726	16	US-10-990-328-95087	Sequence 95087, A
1216	228.6	10.0	166004	23	US-11-417-450-26	Sequence 26, Appl	c1289	228.2	10.0	34547	15	US-10-105-299-7482	Sequence 7482, Ap
c1217	228.6	10.0	166111	20	US-11-112-908-47	Sequence 47, Appl	c1290	228.2	10.0	34547	16	US-10-868-184-5331	Sequence 5331, Ap
c1218	228.6	10.0	168298	17	US-10-674-575-90	Sequence 90, Appl	c1291	228.2	10.0	35574	16	US-10-990-328-94436	Sequence 94436, A
1219	228.6	10.0	188409	23	US-11-417-450-27	Sequence 27, Appl	c1292	228.2	10.0	58181	16	US-10-990-328-97833	Sequence 97833, A
c1220	228.6	10.0	223051	16	US-10-990-328-94106	Sequence 94106, A	1293	228.2	10.0	60593	16	US-10-940-774-13779	Sequence 13779, A
1221	228.6	10.0	235452	16	US-10-940-774-13675	Sequence 13675, A	1294	228.2	10.0	60607	16	US-10-990-328-95118	Sequence 95118, A
1222	228.6	10.0	257744	16	US-10-990-328-94040	Sequence 94040, A	1295	228.2	10.0	61985	23	US-11-033-056A-36230	Sequence 36230, A
1223	228.6	10.0	294836	16	US-10-940-774-15974	Sequence 15974, A	1296	228.2	10.0	61985	23	US-11-033-056A-36231	Sequence 36231, A
c1224	228.6	10.0	312470	16	US-10-940-774-14043	Sequence 14043, A	c1297	228.2	10.0	63588	7	US-10-243-735-3	Sequence 3, Appli
1225	228.6	10.0	330973	7	US-10-087-192-1498	Sequence 1498, Ap	c1298	228.2	10.0	63588	9	US-10-730-010-3	Sequence 3, Appli
c1226	228.6	10.0	336024	16	US-10-940-774-12373	Sequence 12373, A	c1299	228.2	10.0	73909	23	US-11-033-056A-38645	Sequence 38645, A
1227	228.6	10.0	505854	16	US-10-990-328-94315	Sequence 94315, A	c1300	228.2	10.0	84171	16	US-10-940-774-16356	Sequence 16356, A
1228	228.4	10.0	599	4	US-09-925-065A-557593	Sequence 557593, A	1301	228.2	10.0	87417	17	US-10-674-575-155	Sequence 155, App
1229	228.4	10.0	599	5	US-09-925-065A-557593	Sequence 557593, A	1302	228.2	10.0	156321	13	US-10-960-414-483	Sequence 483, App
c1230	228.4	10.0	626	4	US-09-925-065A-709437	Sequence 709437, A	1303	228.2	10.0	163487	23	US-11-033-056A-36408	Sequence 36408, A
c1231	228.4	10.0	626	5	US-09-925-065A-709437	Sequence 709437, A	c1304	228.2	10.0	171660	23	US-11-033-056A-38706	Sequence 38706, A
1232	228.4	10.0	874	13	US-10-301-480-571170	Sequence 571170, A	c1305	228.2	10.0	173787	16	US-10-940-774-12542	Sequence 12542, A
1233	228.4	10.0	874	13	US-10-301-480-1184579	Sequence 1184579, A	c1306	228.2	10.0	173791	16	US-10-940-774-17302	Sequence 17302, A
c1234	228.4	10.0	1000	21	US-11-266-748A-196274	Sequence 196274, A	c1307	228.2	10.0	193702	16	US-10-796-307-8804	Sequence 8804, Ap
c1235	228.4	10.0	2300	27	US-11-636-385-2368	Sequence 2368, Ap	1308	228.2	10.0	254025	23	US-11-033-056A-36184	Sequence 36184, A
1236	228.4	10.0	2300	27	US-11-636-385-25642	Sequence 25642, A	c1309	228.2	10.0	285020	7	US-10-087-192-1666	Sequence 1666, Ap
c1237	228.4	10.0	12458	16	US-10-100-683-12638	Sequence 12638, A	c1310	228.2	10.0	430700	23	US-11-033-056A-37994	Sequence 37994, A
c1238	228.4	10.0	12458	23	US-11-001-793-12638	Sequence 12638, A	c1311	228.2	10.0	757875	23	US-11-033-056A-38439	Sequence 38439, A
c1239	228.4	10.0	15849	3	US-09-880-107-2362	Sequence 2362, Ap	1312	228	10.0	601	16	US-10-940-774-66391	Sequence 66391, A
1240	228.4	10.0	17052	23	US-11-033-056A-36263	Sequence 36263, A	1313	228	10.0	766	4	US-09-925-065A-957017	Sequence 957017, A
1241	228.4	10.0	17052	23	US-11-033-056A-38167	Sequence 38167, A	1314	228	10.0	766	5	US-09-925-065A-957017	Sequence 957017, A
1242	228.4	10.0	22872	23	US-11-033-056A-37904	Sequence 37904, A	c1315	228	10.0	887	13	US-10-301-480-577334	Sequence 577334, A
1243	228.4	10.0	23901	16	US-10-940-774-16773	Sequence 16773, A	c1316	228	10.0	887	13	US-10-301-480-1190743	Sequence 1190743, A
1244	228.4	10.0	28749	16	US-10-990-328-98120	Sequence 98120, A	c1317	228	10.0	2300	27	US-11-636-385-278	Sequence 278, App
1245	228.4	10.0	34096	7	US-10-087-192-952	Sequence 952, App	c1318	228	10.0	2300	27	US-11-636-385-21096	Sequence 21096, A
1246	228.4	10.0	53687	17	US-10-674-575-927	Sequence 927, App	c1319	228	10.0	2300	27	US-11-636-385-25452	Sequence 25452, A
c1247	228.4	10.0	57631	16	US-10-990-328-94455	Sequence 94455, A	c1320	228	10.0	2300	27	US-11-636-385-42542	Sequence 42542, A
1248	228.4	10.0	67810	7	US-10-087-192-1738	Sequence 1738, Ap	1321	228	10.0	2323	26	US-11-443-428A-99113	Sequence 99113, A
1249	228.4	10.0	69062	16	US-10-990-328-95895	Sequence 95895, A	1322	228	10.0	2616	26	US-11-443-428A-99114	Sequence 99114, A
c1250	228.4	10.0	102541	16	US-10-990-328-96643	Sequence 96643, A	1323	228	10.0	2732	26	US-11-443-428A-99116	Sequence 99116, A
1251	228.4	10.0	112955	16	US-10-990-307-8930	Sequence 8930, Ap	1324	228	10.0	2941	16	US-10-777-288A-1238	Sequence 1238, Ap
1252	228.4	10.0	112955	16	US-10-990-328-98231	Sequence 98231, A	1325	228	10.0	6040	15	US-10-105-299-9856	Sequence 9856, Ap
c1253	228.4	10.0	127602	11	US-10-737-082-65	Sequence 65, Appl	1326	228	10.0	6040	16	US-10-868-184-7705	Sequence 7705, Ap
c1254	228.4	10.0	127602	11	US-10-765-790-65	Sequence 65, Appl	c1327	228	10.0	13526	3	US-09-764-887-645	Sequence 645, App
c1255	228.4	10.0	139035	16	US-10-990-328-95994	Sequence 95994, A	c1328	228	10.0	13526	7	US-10-073-961-645	Sequence 645, App
1256	228.4	10.0	146428	16	US-10-940-774-12620	Sequence 12620, A	c1329	228	10.0	14337	3	US-09-764-887-644	Sequence 644, App
1257	228.4	10.0	146438	16	US-10-940-774-12081	Sequence 12081, A	c1330	228	10.0	14337	7	US-10-073-961-644	Sequence 644, App
1258	228.4	10.0	150275	11	US-10-981-277-55	Sequence 55, Appl	1331	228	10.0	16933	9	US-10-741-601-5642	Sequence 5642, Ap
c1259	228.4	10.0	150833	16	US-10-940-774-14859	Sequence 14859, A	1332	228	10.0	16933	10	US-10-741-600-17647	Sequence 17647, A
c1260	228.4	10.0	159963	16	US-10-940-774-14858	Sequence 14858, A	1333	228	10.0	16933	11	US-10-995-561-13257	Sequence 13257, A
c1261	228.4	10.0	171130	16	US-10-940-774-14861	Sequence 14861, A	1334	228	10.0	16933	16	US-10-990-328-94534	Sequence 94534, A
1262	228.4	10.0	190381	16	US-10-990-328-95378	Sequence 95378, A	1335	228	10.0	25367	16	US-10-990-328-97777	Sequence 97777, A
1263	228.4	10.0	196200	20	US-11-121-086-9	Sequence 9, Appli	c1336	228	10.0	27544	16	US-10-990-328-94580	Sequence 94580, A
c1264	228.4	10.0	201529	16	US-10-940-774-12740	Sequence 12740, A	1337	228	10.0	31318	16	US-10-940-774-12495	Sequence 12495, A
c1265	228.4	10.0	201859	16	US-10-990-328-94369	Sequence 94369, A	1338	228	10.0	31319	16	US-10-940-774-15963	Sequence 15963, A
c1266	228.4	10.0	318488	21	US-11-114-798-58	Sequence 58, Appl	c1339	228	10.0	31320	11	US-10-995-561-13309	Sequence 13309, A



c1340	228	10.0	31364	9	US-10-741-601-5672	Sequence 5672, Ap	c1413	227.6	10.0	3487	26	US-11-443-428A-251825	Sequence 251825,
c1341	228	10.0	31364	10	US-10-741-600-17711	Sequence 17711, A	1414	227.6	10.0	3958	26	US-11-443-428A-289607	Sequence 289607,
c1342	228	10.0	31364	16	US-10-796-307-8908	Sequence 8908, Ap	1415	227.6	10.0	4214	26	US-11-443-428A-289606	Sequence 289606,
c1343	228	10.0	31364	16	US-10-990-328-95240	Sequence 95240, A	1416	227.6	10.0	4273	26	US-11-443-428A-289605	Sequence 289605,
c1344	228	10.0	32194	3	US-09-764-891-7028	Sequence 7028, Ap	1417	227.6	10.0	4335	26	US-11-443-428A-289601	Sequence 289601,
c1345	228	10.0	32607	7	US-10-087-192-106	Sequence 106, App	1418	227.6	10.0	5115	9	US-10-322-281-683	Sequence 683, App
c1346	228	10.0	36907	16	US-10-940-774-12633	Sequence 12633, A	1419	227.6	10.0	5115	14	US-10-539-228-683	Sequence 683, App
c1347	228	10.0	36913	16	US-10-940-774-15585	Sequence 15585, A	c1420	227.6	10.0	14305	16	US-10-990-328-93747	Sequence 93747, A
c1348	228	10.0	40334	16	US-10-990-328-95494	Sequence 95494, A	1421	227.6	10.0	14803	16	US-10-990-328-96770	Sequence 96770, A
c1349	228	10.0	42127	16	US-10-990-328-95164	Sequence 95164, A	c1422	227.6	10.0	17045	16	US-10-940-774-13681	Sequence 13681, A
c1350	228	10.0	51917	10	US-10-741-600-17758	Sequence 17758, A	c1423	227.6	10.0	17335	16	US-10-990-328-97776	Sequence 97776, A
c1351	228	10.0	51917	11	US-10-995-561-13338	Sequence 13338, A	1424	227.6	10.0	24923	10	US-10-719-993-7043	Sequence 7043, Ap
c1352	228	10.0	51917	25	US-11-066-316A-10017	Sequence 10017, A	c1425	227.6	10.0	27671	16	US-10-990-328-95077	Sequence 95077, A
c1353	228	10.0	62124	10	US-10-417-375-82	Sequence 82, Appl	1426	227.6	10.0	34325	23	US-11-033-056A-38720	Sequence 38720, A
c1354	228	10.0	68993	16	US-10-990-328-97124	Sequence 97124, A	1427	227.6	10.0	36871	9	US-10-322-281-682	Sequence 682, App
c1355	228	10.0	71406	23	US-11-033-056A-37772	Sequence 37772, A	1428	227.6	10.0	36871	14	US-10-539-228-682	Sequence 682, App
c1356	228	10.0	71406	23	US-11-033-056A-38033	Sequence 38033, A	1429	227.6	10.0	40829	16	US-10-990-328-94843	Sequence 94843, A
c1357	228	10.0	73441	23	US-11-033-056A-36302	Sequence 36302, A	1430	227.6	10.0	45687	16	US-10-990-328-95103	Sequence 95103, A
c1358	228	10.0	78011	16	US-10-990-328-96650	Sequence 96650, A	1431	227.6	10.0	47448	16	US-10-990-328-94689	Sequence 94689, A
c1359	228	10.0	84761	16	US-10-940-774-11919	Sequence 11919, A	1432	227.6	10.0	51030	16	US-10-990-328-94681	Sequence 94681, A
c1360	228	10.0	84763	16	US-10-940-774-13914	Sequence 13914, A	1433	227.6	10.0	53345	16	US-10-990-328-97466	Sequence 97466, A
c1361	228	10.0	85571	10	US-10-719-993-6778	Sequence 6778, Ap	c1434	227.6	10.0	77280	16	US-10-990-328-95328	Sequence 95328, A
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c1363	228	10.0	100822	14	US-10-669-920-1419	Sequence 1419, Ap	1436	227.6	10.0	99014	3	US-09-880-107-3428	Sequence 3428, Ap
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C 94	197.6	8.7 5857	1	US-10-533-069-1003	Sequence 1003, Ap
C 95	197.6	8.7 45944	8	US-11-257-477-38	Sequence 38, Appl
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c 105	195.8	8.6	42450	8	US-11-730-664-3	Sequence 3, Appli	c 178	182.6	8.0	1255	1	US-10-533-069-1121	Sequence 1121, Ap
c 106	195.2	8.5	49175	8	US-11-257-477-4	Sequence 4, Appli	c 179	182.6	8.0	1692	1	US-10-533-069-119	Sequence 119, App
c 107	195	8.5	1015	8	US-11-632-012-49	Sequence 49, Appl	c 180	182.6	8.0	2604	1	US-10-533-069-499	Sequence 499, App
c 108	195	8.5	2308	1	US-10-533-069-600	Sequence 600, App	c 181	181.8	8.0	2176	1	US-10-533-069-2322	Sequence 2322, Ap
c 109	195	8.5	5338	1	US-10-533-069-1036	Sequence 1036, Ap	c 182	181.8	8.0	4068	1	US-10-533-069-1739	Sequence 1739, Ap
c 110	194.8	8.5	149062	8	US-11-257-477-93	Sequence 93, Appl	c 183	181.6	8.0	9229	1	US-10-594-969-3	Sequence 3, Appli
c 111	194.6	8.5	2439	8	US-11-112-327-32	Sequence 32, Appl	c 184	181.4	7.9	12169	8	US-11-656-316-16	Sequence 16, Appl
c 112	194.6	8.5	2448	8	US-11-112-327-24	Sequence 24, Appl	c 185	181.2	7.9	2547	1	US-10-533-069-1969	Sequence 3, Appli
c 113	194.6	8.5	4592	8	US-11-498-489-26	Sequence 26, Appl	c 186	180.2	7.9	5232	8	US-11-509-784-3	Sequence 42, Appl
c 114	194.6	8.5	4592	8	US-11-498-489-28	Sequence 28, Appl	c 187	179.4	7.9	735	8	US-11-632-012-42	Sequence 17, Appl
c 115	194.6	8.5	17788	8	US-11-498-489-38	Sequence 38, Appl	c 188	179.4	7.9	1557	8	US-11-680-414-17	Sequence 211, App
c 116	194.4	8.5	4098	8	US-11-365-630-5	Sequence 5, Appli	c 189	178.8	7.8	1177	8	US-11-552-437-211	Sequence 1731, Ap
c 117	194.2	8.5	24810	8	US-11-257-477-145	Sequence 145, App	c 190	178.6	7.8	2688	1	US-10-533-069-1731	Sequence 1586, Ap
c 118	193.6	8.5	9229	1	US-10-594-969-3	Sequence 3, Appli	c 191	177.8	7.8	1683	1	US-10-533-069-1586	Sequence 2389, Ap
c 119	193	8.5	21478	8	US-11-257-477-201	Sequence 201, App	c 192	177.8	7.8	2040	1	US-10-533-069-2389	Sequence 181, App
c 120	192.8	8.4	3105	8	US-11-551-744-156	Sequence 156, App	c 193	177.8	7.8	2294	8	US-11-552-437-181	Sequence 1911, Ap
c 121	192.8	8.4	9803	1	US-10-565-626-73	Sequence 73, Appl	c 194	177.4	7.8	2446	1	US-10-533-069-1911	Sequence 71, Appl
c 122	192.8	8.4	9803	1	US-10-565-626-74	Sequence 74, Appl	c 195	177	7.7	1976	8	US-11-234-694-71	Sequence 1126, Ap
c 123	192.6	8.4	5207	1	US-10-533-069-2055	Sequence 2055, Ap	c 196	176.4	7.7	2507	1	US-10-533-069-1126	Sequence 202, App
c 124	192.6	8.4	10380	8	US-11-657-766-3	Sequence 3, Appli	c 197	176.2	7.7	2307	1	US-10-533-069-202	Sequence 133, App
c 125	192.4	8.4	5990	8	US-11-407-888-3	Sequence 3, Appli	c 198	176.2	7.7	32677	8	US-11-257-477-133	Sequence 2401, Ap
c 126	192	8.4	5985	1	US-10-565-626-76	Sequence 76, Appl	c 199	175.8	7.7	2698	1	US-10-533-069-2401	Sequence 7, Appli
c 127	192	8.4	7136	1	US-10-533-069-2395	Sequence 2395, Ap	c 200	175.4	7.7	2377	1	US-10-562-377-7	Sequence 2271, Ap
c 128	192	8.4	26815	8	US-11-257-477-26	Sequence 26, Appl	c 201	175.2	7.7	2619	1	US-10-533-069-2271	Sequence 75, Appl
c 129	192	8.4	142976	8	US-11-257-477-99	Sequence 99, Appl	c 202	175	7.7	2280	1	US-10-565-626-75	Sequence 76, Appl
c 130	191.8	8.4	10380	8	US-11-657-766-3	Sequence 3, Appli	c 203	175	7.7	5985	1	US-10-565-626-76	Sequence 73, Appl
c 131	191.6	8.4	163382	8	US-11-257-477-179	Sequence 179, App	c 204	175	7.7	9803	1	US-10-565-626-73	Sequence 74, Appl
c 132	191.2	8.4	37961	8	US-11-257-477-16	Sequence 16, Appl	c 205	175	7.7	9803	1	US-10-565-626-74	Sequence 12, Appl
c 133	190.8	8.4	10616	8	US-11-600-739-3	Sequence 3, Appli	c 206	175	7.7	18524	8	US-11-650-478-12	Sequence 12, Appl
c 134	190.2	8.3	170001	1	US-10-586-772A-1	Sequence 1, Appli	c 207	175	7.7	18524	8	US-11-650-479-12	Sequence 63, Appl
c 135	190	8.3	23965	8	US-11-257-477-139	Sequence 139, App	c 208	174.8	7.7	1410	8	US-11-632-012-63	Sequence 1, Appli
c 136	189.6	8.3	50927	8	US-11-257-477-56	Sequence 56, Appl	c 209	174.8	7.7	2475	1	US-10-562-377-1	Sequence 1, Appli
c 137	189.4	8.3	15418	8	US-11-710-864-1	Sequence 1, Appli	c 210	174.8	7.7	2475	1	US-10-562-377-3	Sequence 3, Appli
c 138	189.2	8.3	3941	1	US-10-533-069-1287	Sequence 1287, Ap	c 211	174.2	7.6	3178	1	US-10-533-069-541	Sequence 541, App
c 139	189.2	8.3	21725	8	US-11-700-462-1	Sequence 1, Appli	c 212	174.2	7.6	9963	1	US-10-369-909-14	Sequence 14, Appl
c 140	189	8.3	22685	8	US-11-629-808-8	Sequence 8, Appli	c 213	174	7.6	3381	1	US-10-533-069-311	Sequence 311, App
c 141	188.8	8.3	3999	8	US-11-712-222-5	Sequence 5, Appli	c 214	173.8	7.6	1169	1	US-10-533-069-676	Sequence 676, App
c 142	188.6	8.3	1660	8	US-11-713-306-5	Sequence 5, Appli	c 215	173.4	7.6	12354	8	US-11-596-506-1	Sequence 1, Appli
c 143	188.4	8.2	2368	1	US-10-562-377-21	Sequence 21, Appl	c 216	173	7.6	2990	1	US-10-533-069-2318	Sequence 4, Appli
c 144	188.2	8.2	2651	1	US-10-533-069-1947	Sequence 1947, Ap	c 217	172.8	7.6	2345	1	US-10-562-377-4	Sequence 55, Appl
c 145	188.2	8.2	5036	8	US-11-365-630-10	Sequence 10, Appl	c 218	172.8	7.6	4429	8	US-11-407-888-55	Sequence 2354, Ap
c 146	188	8.2	2818	1	US-10-562-377-20	Sequence 20, Appl	c 219	172.2	7.5	3916	1	US-10-533-069-2175	Sequence 2175, Ap
c 147	188	8.2	3073	8	US-11-234-694-77	Sequence 77, Appl	c 220	170.8	7.5	1180	8	US-11-738-671-21	Sequence 644, App
c 148	187.6	8.2	1405	8	US-11-738-671-40	Sequence 40, Appl	c 221	170.8	7.5	3452	1	US-10-533-069-644	Sequence 830, App
c 149	187.2	8.2	1766	8	US-11-234-694-47	Sequence 47, Appl	c 222	170.8	7.5	3452	1	US-10-533-069-830	Sequence 3, Appli
c 150	186.8	8.2	5659	8	US-11-585-666-44	Sequence 44, Appl	c 223	170.4	7.5	4261	1	US-10-573-215-3	Sequence 6, Appli
c 151	186.8	8.2	12354	8	US-11-596-506-1	Sequence 1, Appli	c 224	170.4	7.5	16781	1	US-10-586-772A-6	Sequence 1, Appli
c 152	186.8	8.2	13602	8	US-11-650-478-1	Sequence 1, Appli	c 225	170.2	7.5	2259	1	US-10-553-459-1	Sequence 1, Appli
c 153	186.8	8.2	13602	8	US-11-650-479-1	Sequence 1, Appli	c 226	169.6	7.4	1295	8	US-11-725-076-8	Sequence 8, Appli
c 154	186.8	8.2	17534	8	US-11-650-478-7	Sequence 7, Appli	c 227	169	7.4	2239	1	US-10-596-627-7	Sequence 7, Appli
c 155	186.8	8.2	17534	8	US-11-650-479-7	Sequence 7, Appli	c 228	168.6	7.4	2420	8	US-11-600-739-4	Sequence 4, Appli
c 156	186.8	8.2	30756	8	US-11-650-478-16	Sequence 16, Appl	c 229	168.4	7.4	5350	1	US-10-533-069-2297	Sequence 2297, Ap
c 157	186.8	8.2	30756	8	US-11-650-479-16	Sequence 16, Appl	c 230	167.8	7.3	2420	8	US-11-600-739-4	Sequence 4, Appli
c 158	186.2	8.2	2910	1	US-10-533-069-531	Sequence 531, App	c 231	167.8	7.3	4685	1	US-10-533-069-2175	Sequence 2175, Ap
c 159	186.2	8.2	3322	1	US-10-533-069-136	Sequence 136, App	c 232	167.4	7.3	3430	1	US-10-533-069-764	Sequence 764, App
c 160	186.2	8.2	21725	8	US-11-700-462-1	Sequence 1, Appli	c 233	166.6	7.3	1349	1	US-10-533-069-1235	Sequence 1235, Ap
c 161	186.2	8.2	21725	8	US-11-257-477-38	Sequence 38, Appl	c 234	165.6	7.3	1741	1	US-10-533-069-2097	Sequence 2097, Ap
c 162	186	8.1	2956	1	US-10-533-069-1241	Sequence 1241, Ap	c 235	164.2	7.2	6406	1	US-10-533-069-656	Sequence 656, App
c 163	186	8.1	4513	8	US-11-257-477-11	Sequence 11, Appl	c 236	164.2	7.2	40782	1	US-10-592-435-11	Sequence 11, Appl
c 164	185.2	8.1	1185	1	US-10-533-069-1319	Sequence 1319, Ap	c 237	164	7.2	6834	1	US-10-533-069-389	Sequence 389, App
c 165	184.8	8.1	1914	8	US-11-257-477-21	Sequence 21, Appl	c 238	163.6	7.2	2396	1	US-10-562-377-27	Sequence 27, Appl
c 166	184.6	8.1	65423	8	US-11-257-477-32	Sequence 32, Appl	c 239	162.8	7.1	14248	1	US-10-533-069-1584	Sequence 1584, Ap
c 167	184.4	8.1	2291	1	US-10-562-377-5	Sequence 5, Appli	c 240	162.4	7.1	3118	1	US-10-533-069-1446	Sequence 1446, Ap
c 168	183.8	8.0	2346	1	US-10-562-377-36	Sequence 36, Appl	c 241	161.6	7.1	2088	8	US-11-625-795-18	Sequence 18, Appl
c 169	183.6	8.0	7967	1	US-10-568-695-1	Sequence 1, Appli	c 242	161.4	7.1	2507	1	US-10-533-069-1126	Sequence 1126, Ap
c 170	183.6	8.0	9821	1	US-10-568-695-2	Sequence 2, Appli	c 243	161.4	7.1	2751	1	US-10-533-069-1782	Sequence 1782, Ap
c 171	183.4	8.0	2116	1	US-10-533-069-2107	Sequence 2107, Ap	c 244	160	7.0	2331	8	US-11-632-012-39	Sequence 39, Appl

C 245	159.4	7.0	3915	8	US-11-699-930-8	Sequence 8, Appli	C 318	116.8	5.1	3925	1	US-10-533-069-939	Sequence 939, App
C 246	159.4	7.0	5915	8	US-11-699-930-11	Sequence 11, Appl	319	116.8	5.1	7044	8	US-11-551-744-95	Sequence 95, Appl
C 247	159.4	7.0	5915	8	US-11-699-930-12	Sequence 12, Appl	C 320	116.4	5.1	619	8	US-11-744-695-17	Sequence 17, Appl
C 248	159.4	7.0	5915	8	US-11-699-930-13	Sequence 13, Appl	C 321	115.6	5.1	2508	1	US-10-562-377-184	Sequence 184, App
C 249	159.4	7.0	5915	8	US-11-699-930-14	Sequence 14, Appl	C 322	115	5.0	2346	1	US-10-562-377-110	Sequence 110, App
C 250	159.4	7.0	5915	8	US-11-699-930-15	Sequence 15, Appl	C 323	113.2	5.0	2673	1	US-10-562-377-104	Sequence 104, App
C 251	159.4	7.0	5915	8	US-11-699-930-16	Sequence 16, Appl	C 324	113.2	5.0	2673	1	US-10-562-377-182	Sequence 182, App
C 252	159.4	7.0	18524	8	US-11-650-478-12	Sequence 12, Appl	325	113	4.9	2591	8	US-11-112-327-21	Sequence 21, Appl
C 253	159.4	7.0	18524	8	US-11-650-479-12	Sequence 12, Appl	326	113	4.9	2591	8	US-11-112-327-28	Sequence 28, Appl
C 254	159.2	7.0	2894	1	US-10-533-069-2198	Sequence 2198, Ap	327	111.6	4.9	2333	1	US-10-533-069-2387	Sequence 2387, Ap
C 255	158.2	6.9	1135	8	US-11-632-012-41	Sequence 41, Appl	C 328	111.6	4.9	2368	1	US-10-562-377-80	Sequence 80, Appl
C 256	158	6.9	4316	8	US-11-510-314-3	Sequence 3, Appli	329	111.6	4.9	2652	8	US-11-738-671-23	Sequence 23, Appl
C 257	157.8	6.9	1914	1	US-10-533-069-1508	Sequence 1508, Ap	330	111.2	4.9	1774	8	US-11-680-414-20	Sequence 20, Appl
C 258	157	6.9	3200	1	US-10-533-069-301	Sequence 301, App	C 331	110.2	4.8	2346	1	US-10-562-377-188	Sequence 188, App
C 259	156.2	6.8	4152	1	US-10-533-069-2295	Sequence 2295, Ap	C 332	110	4.8	2475	1	US-10-562-377-40	Sequence 40, Appl
C 260	155.4	6.8	3487	1	US-10-533-069-917	Sequence 917, App	C 333	110	4.8	2475	1	US-10-562-377-44	Sequence 44, Appl
C 261	155	6.8	8158	8	US-11-496-050-30	Sequence 30, Appl	334	109.8	4.8	2002	1	US-10-533-069-961	Sequence 961, App
C 262	154.4	6.8	1520	8	US-11-632-012-27	Sequence 27, Appl	C 335	109.6	4.8	2818	1	US-10-562-377-78	Sequence 78, Appl
C 263	154.2	6.8	907	8	US-11-552-437-97	Sequence 97, Appl	336	108.8	4.8	3882	8	US-11-407-888-5	Sequence 5, Appli
C 264	153.8	6.7	9886	1	US-10-533-069-905	Sequence 905, App	337	108.2	4.7	5000	1	US-10-533-069-2049	Sequence 2049, Ap
C 265	153	6.7	2101	8	US-11-632-012-7	Sequence 7, Appli	C 338	106.2	4.6	2291	1	US-10-562-377-127	Sequence 127, App
C 266	151	6.6	939	8	US-11-632-012-24	Sequence 24, Appl	C 339	106	4.6	2291	1	US-10-562-377-49	Sequence 49, Appl
C 267	151	6.6	2122	1	US-10-533-069-240	Sequence 240, App	C 340	106	4.6	2475	1	US-10-562-377-118	Sequence 118, App
C 268	150.4	6.6	5237	8	US-11-407-888-59	Sequence 59, Appl	C 341	106	4.6	2475	1	US-10-562-377-122	Sequence 122, App
C 269	149.8	6.6	1774	8	US-11-680-414-20	Sequence 20, Appl	C 342	105.2	4.6	1976	8	US-11-552-437-33	Sequence 33, Appl
C 270	149.2	6.5	32677	8	US-11-257-477-133	Sequence 133, App	C 343	105	4.6	2308	1	US-10-562-377-152	Sequence 152, App
C 271	148.6	6.5	3846	8	US-11-234-694-55	Sequence 55, Appl	C 344	104.6	4.6	2368	1	US-10-562-377-158	Sequence 158, App
C 272	147.8	6.5	1697	1	US-10-533-069-1201	Sequence 1201, Ap	C 345	103.8	4.5	2818	1	US-10-562-377-156	Sequence 156, App
C 273	147.8	6.5	2243	1	US-10-533-069-852	Sequence 852, App	346	103.6	4.5	5932	1	US-10-533-069-1145	Sequence 1145, Ap
C 274	147.8	6.5	2518	1	US-10-533-069-1693	Sequence 1693, Ap	C 347	103.4	4.5	2308	1	US-10-562-377-74	Sequence 74, Appl
C 275	147.4	6.5	2049	1	US-10-533-069-808	Sequence 808, App	348	102.8	4.5	2368	1	US-10-562-377-81	Sequence 81, Appl
C 276	147	6.4	1709	1	US-10-596-627-6	Sequence 6, Appli	349	102.8	4.5	2764	1	US-10-533-069-2311	Sequence 2311, Ap
C 277	145.4	6.4	4828	8	US-11-365-630-6	Sequence 6, Appli	350	102	4.5	2673	1	US-10-562-377-104	Sequence 104, App
C 278	144.4	6.3	2308	1	US-10-533-069-588	Sequence 588, App	351	101	4.4	2508	1	US-10-562-377-107	Sequence 107, App
C 279	143	6.3	1840	8	US-11-632-012-19	Sequence 19, Appl	C 352	100.6	4.4	2377	1	US-10-562-377-52	Sequence 52, Appl
C 280	142.2	6.2	2196	8	US-11-534-850-1	Sequence 1, Appli	353	100.6	4.4	3328	1	US-10-533-069-2285	Sequence 2285, Ap
C 281	142.2	6.2	3583	1	US-10-533-069-2003	Sequence 2003, Ap	C 354	100	4.4	2345	1	US-10-562-377-124	Sequence 124, App
C 282	141.6	6.2	2974	1	US-10-565-068-103	Sequence 103, App	355	99.8	4.4	2044	1	US-10-533-069-13	Sequence 13, Appl
C 283	140.8	6.2	1167	8	US-11-632-012-10	Sequence 10, Appl	C 356	99.4	4.4	2345	1	US-10-562-377-46	Sequence 46, Appl
C 284	140.2	6.1	29018	8	US-11-257-477-105	Sequence 105, App	357	98	4.3	2673	1	US-10-562-377-105	Sequence 105, App
C 285	140	6.1	2338	1	US-10-533-069-1464	Sequence 1464, Ap	C 358	97.6	4.3	2396	1	US-10-562-377-93	Sequence 93, Appl
C 286	139.6	6.1	4604	1	US-10-533-069-467	Sequence 467, App	359	96.6	4.2	5496	1	US-10-533-069-2005	Sequence 2005, Ap
C 287	138.6	6.1	1859	8	US-11-632-012-46	Sequence 46, Appl	C 360	96	4.2	2396	1	US-10-562-377-171	Sequence 171, App
C 288	136.4	6.0	1556	1	US-10-533-069-2338	Sequence 2338, Ap	C 361	95.8	4.2	2377	1	US-10-562-377-130	Sequence 130, App
C 289	136	6.0	2597	8	US-11-544-070-1	Sequence 1, Appli	362	95.4	4.2	5065	1	US-10-533-069-479	Sequence 479, App
C 290	134	5.9	1024	8	US-11-599-517-44	Sequence 44, Appl	363	94.4	4.1	2430	1	US-10-533-069-867	Sequence 867, App
C 291	134	5.9	1024	8	US-11-599-517-102	Sequence 102, App	C 364	93.2	4.1	2871	1	US-10-533-069-2263	Sequence 2263, Ap
C 292	133.8	5.9	1167	8	US-11-632-012-10	Sequence 10, Appl	365	93	4.1	2508	1	US-10-562-377-185	Sequence 185, App
C 293	133.6	5.8	2714	1	US-10-533-069-347	Sequence 347, App	366	92.2	4.0	2368	1	US-10-562-377-159	Sequence 159, App
C 294	133.6	5.8	5207	1	US-10-533-069-2055	Sequence 2055, Ap	367	89.8	3.9	2291	1	US-10-562-377-48	Sequence 48, Appl
C 295	133.2	5.8	2426	1	US-10-533-069-1315	Sequence 1315, Ap	368	89.4	3.9	1836	1	US-10-533-069-2315	Sequence 2315, Ap
C 296	132.6	5.8	2120	1	US-10-567-074-1	Sequence 1, Appli	369	88.4	3.9	2673	1	US-10-562-377-182	Sequence 182, App
C 297	132.4	5.8	289	1	US-10-596-627-1	Sequence 1, Appli	C 370	88	3.9	5726	1	US-10-533-069-977	Sequence 977, App
C 298	132	5.8	489	8	US-11-634-620-11	Sequence 11, Appl	371	87.8	3.8	2117	1	US-10-533-069-1059	Sequence 1059, Ap
C 299	132	5.8	3869	1	US-10-533-069-1488	Sequence 1488, Ap	372	85.4	3.7	2818	1	US-10-562-377-79	Sequence 79, Appl
C 300	131.6	5.8	10001	8	US-11-615-454-12	Sequence 12, Appl	373	84.4	3.7	1475	8	US-11-680-414-3	Sequence 3, Appli
C 301	131	5.7	2359	8	US-11-327-695-16	Sequence 16, Appl	374	84.4	3.7	2308	1	US-10-562-377-75	Sequence 75, Appl
C 302	128.2	5.6	1937	1	US-10-533-069-648	Sequence 648, App	375	84.4	3.7	5659	8	US-11-585-666-44	Sequence 44, Appl
C 303	128.2	5.6	1937	1	US-10-533-069-935	Sequence 935, App	376	84.2	3.7	2377	1	US-10-562-377-53	Sequence 53, Appl
C 304	126.6	5.5	2843	8	US-11-257-477-61	Sequence 61, Appl	377	82	3.6	2673	1	US-10-562-377-183	Sequence 183, App
C 305	125.8	5.5	961	8	US-11-632-012-28	Sequence 28, Appl	C 378	81.4	3.6	1363	1	US-10-533-069-1257	Sequence 1257, Ap
C 306	125.4	5.5	3322	1	US-10-533-069-136	Sequence 136, App	379	81.4	3.6	2346	1	US-10-562-377-111	Sequence 111, App
C 307	124.6	5.5	8982	1	US-10-533-069-1708	Sequence 1708, Ap	380	80.8	3.5	2088	8	US-11-625-795-18	Sequence 18, Appl
C 308	124.4	5.4	4321	8	US-11-691-348-6	Sequence 6, Appli	381	80.8	3.5	2274	1	US-10-533-069-1149	Sequence 1149, Ap
C 309	123.4	5.4	2673	1	US-10-562-377-105	Sequence 105, App	382	80	3.5	2818	1	US-10-562-377-157	Sequence 157, App
C 310	123.4	5.4	3319	1	US-10-533-069-566	Sequence 566, App	C 383	79.8	3.5	4674	1	US-10-533-069-55	Sequence 55, Appl
C 311	122.8	5.4	1310	8	US-11-632-012-65	Sequence 65, Appl	384	78.6	3.4	2291	1	US-10-562-377-126	Sequence 126, App
C 312	121.8	5.3	2673	1	US-10-562-377-183	Sequence 183, App	385	78.4	3.4	2345	1	US-10-562-377-47	Sequence 47, Appl
C 313	121.8	5.3	2818	1	US-10-562-377-20	Sequence 20, Appl	386	78.2	3.4	1457	8	US-11-738-671-38	Sequence 38, Appl
C 314	120.6	5.3	3328	1	US-10-533-069-2285	Sequence 2285, Ap	387	78.2	3.4	2346	1	US-10-562-377-189	Sequence 189, App
C 315	120.4	5.3	2535	1	US-10-562-377-35	Sequence 35, Appl	388	77.4	3.4	1701	8	US-11-632-012-31	Sequence 31, Appl
C 316	119.4	5.2	4565	1	US-10-533-069-2135	Sequence 2135, Ap	389	77	3.4	2475	1	US-10-562-377-41	Sequence 41, Appl
C 317	118.8	5.2	2508	1	US-10-562-377-106	Sequence 106, App	390	77	3.4	2475	1	US-10-562-377-45	Sequence 45, Appl

391	77	3.4	3819	8	US-11-552-437-133	Sequence 133, Appl	464	56.8	2.5	836	8	US-11-585-666-12	Sequence 12, Appl
c 392	76.8	3.4	5511	8	US-11-365-630-4	Sequence 4, Appli	465	56.8	2.5	848	8	US-11-585-666-13	Sequence 13, Appl
c 393	76.8	3.4	5511	8	US-11-365-630-11	Sequence 11, Appl	466	56.8	2.5	860	8	US-11-585-666-14	Sequence 14, Appl
394	76	3.3	2377	1	US-10-562-377-131	Sequence 131, App	467	56.6	2.5	1380	8	US-11-632-012-22	Sequence 22, Appl
395	75.2	3.3	711	8	US-11-112-327-16	Sequence 16, Appl	c 468	56.6	2.5	2535	1	US-10-562-377-187	Sequence 187, App
c 396	75.2	3.3	1437	8	US-11-699-229-46	Sequence 46, Appl	469	56.4	2.5	6803	8	US-11-625-795-10	Sequence 10, Appl
397	74.8	3.3	2475	8	US-11-552-437-163	Sequence 163, App	470	55	2.4	1271	1	US-10-533-069-666	Sequence 666, App
c 398	73.6	3.2	2396	1	US-10-562-377-92	Sequence 92, Appl	471	55	2.4	1271	8	US-11-585-666-21	Sequence 21, Appl
c 399	73.6	3.2	3858	8	US-11-655-822-2	Sequence 2, Appli	472	55	2.4	1364	8	US-11-585-666-20	Sequence 20, Appl
c 400	73.6	3.2	3858	8	US-11-655-822-4	Sequence 4, Appli	c 473	55	2.4	5428	1	US-10-533-069-545	Sequence 545, App
c 401	73.6	3.2	3858	8	US-11-655-822-6	Sequence 6, Appli	474	54.6	2.4	1038	8	US-11-728-892-11	Sequence 11, Appl
c 402	73.6	3.2	3858	8	US-11-655-822-8	Sequence 8, Appli	475	54.6	2.4	1107	8	US-11-728-892-84	Sequence 84, Appl
c 403	73.6	3.2	3858	8	US-11-655-822-10	Sequence 10, Appl	476	54.4	2.4	2355	8	US-11-632-012-50	Sequence 50, Appl
c 404	73.6	3.2	3860	8	US-11-655-822-98	Sequence 98, Appl	c 477	54.2	2.4	398	8	US-11-634-620-44	Sequence 44, Appl
c 405	73.6	3.2	3860	8	US-11-655-822-99	Sequence 99, Appl	478	53.8	2.4	3334	1	US-10-533-069-1410	Sequence 1410, Ap
c 406	73.6	3.2	3988	8	US-11-655-822-14	Sequence 14, Appl	c 479	53.6	2.3	2571	1	US-10-533-069-1422	Sequence 1422, Ap
c 407	73.6	3.2	3988	8	US-11-655-822-97	Sequence 97, Appl	c 480	53.4	2.3	3199	8	US-11-112-327-13	Sequence 13, Appl
c 408	73.2	3.2	1885	8	US-11-705-689-15	Sequence 15, Appl	481	52.8	2.3	4357	1	US-10-533-069-2302	Sequence 2302, Ap
c 409	73	3.2	5496	1	US-10-533-069-2005	Sequence 2005, Ap	c 482	52.8	2.3	44728	8	US-11-257-477-23	Sequence 23, Appl
410	72.6	3.2	3516	8	US-11-551-744-161	Sequence 161, App	483	52.6	2.3	501	8	US-11-632-012-55	Sequence 55, Appl
c 411	71.8	3.1	885	1	US-10-533-069-626	Sequence 626, App	c 484	52.2	2.3	1787	1	US-10-533-069-2300	Sequence 2300, Ap
c 412	71.6	3.1	476	8	US-11-634-620-35	Sequence 35, Appl	485	52	2.3	1776	8	US-11-738-671-26	Sequence 26, Appl
413	71.2	3.1	5726	1	US-10-533-069-977	Sequence 977, App	486	51.6	2.3	2688	1	US-10-533-069-1731	Sequence 1731, Ap
c 414	71	3.1	101	8	US-11-640-897-1733	Sequence 1733, Ap	c 487	51.2	2.2	1479	8	US-11-595-320-3	Sequence 3, Appli
c 415	71	3.1	2280	1	US-10-565-626-75	Sequence 75, Appl	488	51	2.2	494	1	US-10-819-557-15	Sequence 15, Appl
416	70.6	3.1	2475	1	US-10-562-377-119	Sequence 119, App	489	50.8	2.2	2883	1	US-10-533-069-1510	Sequence 1510, Ap
417	70.6	3.1	2475	1	US-10-562-377-123	Sequence 123, App	490	50.2	2.2	940	8	US-11-112-327-14	Sequence 14, Appl
c 418	70	3.1	462	8	US-11-634-620-59	Sequence 59, Appl	491	50.2	2.2	2188	1	US-10-533-069-122	Sequence 122, App
419	69.4	3.0	1414	8	US-11-650-478-1	Sequence 64, Appl	c 492	49.8	2.2	2337	1	US-10-533-069-570	Sequence 570, App
420	69.4	3.0	13602	8	US-11-650-478-1	Sequence 1, Appli	c 493	49.4	2.2	1457	8	US-11-738-671-38	Sequence 38, Appl
421	69.4	3.0	13602	8	US-11-650-479-1	Sequence 1, Appli	494	49.4	2.2	2818	1	US-10-562-377-78	Sequence 78, Appl
422	69.4	3.0	17534	8	US-11-650-478-7	Sequence 7, Appli	c 495	49.2	2.2	607	8	US-11-632-012-21	Sequence 21, Appl
423	69.4	3.0	17534	8	US-11-650-479-7	Sequence 7, Appli	496	49	2.1	2818	1	US-10-562-377-156	Sequence 156, App
424	69.4	3.0	30756	8	US-11-650-479-16	Sequence 16, Appl	c 497	48	2.1	2061	1	US-10-533-069-774	Sequence 774, App
425	69.4	3.0	30756	8	US-11-650-479-16	Sequence 16, Appl	498	47.2	2.1	2535	1	US-10-562-377-186	Sequence 186, App
426	68.6	3.0	374	8	US-11-634-620-62	Sequence 62, Appl	499	47	2.1	1070	1	US-10-533-069-1638	Sequence 1638, Ap
c 427	67	2.9	1225	8	US-11-552-437-37	Sequence 37, Appl	c 500	47	2.1	2876	8	US-11-699-229-28	Sequence 28, Appl
428	67	2.9	2446	1	US-10-533-069-1911	Sequence 1911, Ap	c 501	47	2.1	684187	8	US-11-257-477-71	Sequence 71, Appl
429	66.8	2.9	2308	1	US-10-562-377-153	Sequence 153, App	502	46.8	2.0	3335	1	US-10-533-069-986	Sequence 986, App
c 430	66.8	2.9	4975	1	US-10-533-069-321	Sequence 321, App	503	46.6	2.0	450000	1	US-10-650-449-3	Sequence 3, Appli
431	66.4	2.9	7585	1	US-10-533-069-395	Sequence 395, App	504	46.2	2.0	1700	1	US-10-533-069-1788	Sequence 1788, Ap
432	66	2.9	2345	1	US-10-562-377-125	Sequence 125, App	c 505	46.2	2.0	2761	8	US-11-738-671-41	Sequence 41, Appl
433	65	2.8	1415	1	US-10-533-069-543	Sequence 543, App	c 506	45.6	2.0	866	8	US-11-632-012-59	Sequence 59, Appl
434	65	2.8	2319	8	US-11-519-397-48	Sequence 48, Appl	c 507	45.6	2.0	2458	8	US-11-552-437-129	Sequence 129, App
435	65	2.8	2396	1	US-10-562-377-170	Sequence 170, App	c 508	45.4	2.0	2291	1	US-10-562-377-5	Sequence 5, Appli
436	64.2	2.8	2014	1	US-10-533-069-2117	Sequence 2117, Ap	509	45.2	2.0	411	8	US-11-634-620-74	Sequence 74, Appl
c 437	63.8	2.8	2117	1	US-10-533-069-1251	Sequence 1251, Ap	c 510	45	2.0	1313	8	US-11-738-671-31	Sequence 31, Appl
438	63.8	2.8	2337	1	US-10-533-069-570	Sequence 570, App	c 511	45	2.0	44728	8	US-11-257-477-23	Sequence 23, Appl
439	63.8	2.8	2675	1	US-10-533-069-1261	Sequence 1261, Ap	c 512	44.8	2.0	418	8	US-11-738-671-32	Sequence 32, Appl
c 440	63.8	2.8	2745	1	US-10-565-068-100	Sequence 100, App	513	44.6	2.0	115780	8	US-11-257-477-96	Sequence 96, Appl
441	63.8	2.8	2745	1	US-10-581-547-147	Sequence 147, App	514	44.6	2.0	684187	8	US-11-257-477-71	Sequence 71, Appl
c 442	63.4	2.8	2818	1	US-10-562-377-79	Sequence 79, Appl	515	44.4	1.9	224112	8	US-11-257-477-80	Sequence 80, Appl
443	63.2	2.8	3988	8	US-11-655-822-14	Sequence 14, Appl	c 516	43.8	1.9	1926	8	US-11-561-363-81	Sequence 81, Appl
444	63.2	2.8	3988	8	US-11-655-822-97	Sequence 97, Appl	517	43.8	1.9	46030	8	US-11-257-477-1	Sequence 1, Appli
c 445	63	2.8	2196	1	US-10-562-377-37	Sequence 37, Appl	c 518	43.8	1.9	450000	1	US-10-650-449-3	Sequence 3, Appli
c 446	62.8	2.7	1842	8	US-11-725-076-11	Sequence 11, Appl	519	43.4	1.9	2946	1	US-10-567-764-6	Sequence 6, Appli
c 447	62.6	2.7	1493	1	US-10-533-069-1414	Sequence 1414, Ap	520	43.4	1.9	3024	1	US-10-567-764-10	Sequence 10, Appl
448	62.4	2.7	2306	1	US-10-533-069-1830	Sequence 1830, Ap	521	43.4	1.9	3117	1	US-10-567-764-14	Sequence 14, Appl
449	62.4	2.7	2805	1	US-10-533-069-1249	Sequence 1249, Ap	522	43.4	1.9	3210	1	US-10-567-764-18	Sequence 18, Appl
c 450	61.8	2.7	2818	1	US-10-562-377-157	Sequence 157, App	523	43.4	1.9	3303	1	US-10-567-764-22	Sequence 22, Appl
451	61.6	2.7	1510	1	US-10-533-069-1408	Sequence 1408, Ap	524	43.4	1.9	8049	1	US-10-567-764-5	Sequence 5, Appli
c 452	60.8	2.7	454	8	US-11-744-695-32	Sequence 32, Appl	525	43.2	1.9	761	1	US-10-533-069-997	Sequence 997, App
c 453	60.8	2.7	2166	1	US-10-533-069-1923	Sequence 1923, Ap	c 526	43.2	1.9	2883	1	US-10-533-069-1510	Sequence 1510, Ap
c 454	60	2.6	2136	8	US-11-738-671-15	Sequence 15, Appl	527	43.2	1.9	34245	8	US-11-257-477-102	Sequence 102, App
455	59.6	2.6	1855	1	US-10-533-069-2394	Sequence 2394, Ap	528	43	1.9	3385	1	US-10-533-069-9	Sequence 9, Appli
c 456	59.2	2.6	2535	1	US-10-562-377-109	Sequence 109, App	529	43	1.9	80423	8	US-11-257-477-41	Sequence 41, Appl
457	58.8	2.6	1705	1	US-10-533-069-1937	Sequence 1937, Ap	c 530	42.8	1.9	1664	1	US-10-533-069-1616	Sequence 1616, Ap
c 458	58.6	2.6	2233	8	US-11-632-012-29	Sequence 29, Appl	c 531	42.8	1.9	30611	8	US-11-257-477-108	Sequence 108, App
c 459	58.6	2.6	2292	1	US-10-533-069-160	Sequence 160, App	c 532	42	1.8	4040	1	US-10-533-069-624	Sequence 624, App
c 460	58.6	2.6	3335	1	US-10-533-069-986	Sequence 986, App	533	42	1.8	24495	8	US-11-257-477-142	Sequence 142, App
c 461	58.4	2.6	1093	1	US-10-533-069-1742	Sequence 1742, Ap	534	41.8	1.8	480	8	US-11-634-620-16	Sequence 16, Appl
462	58.4	2.6	2535	1	US-10-562-377-108	Sequence 108, App	c 535	41.8	1.8	1242	8	US-11-632-012-48	Sequence 48, Appl
c 463	57.4	2.5	2435	1	US-10-533-069-897	Sequence 897, App	c 536	41.8	1.8	6406	1	US-10-533-069-656	Sequence 656, App



C 537	41.8	1.8	24495	8	US-11-257-477-142	Sequence 142, App
C 538	41.6	1.8	90351	8	US-11-257-477-166	Sequence 166, App
C 539	41.4	1.8	139613	8	US-11-257-477-90	Sequence 90, Appl
C 540	40.4	1.8	918	8	US-11-599-517-12	Sequence 12, Appl
541	40.2	1.8	797	8	US-11-713-768-55845	Sequence 55845, A
542	40	1.8	1282	8	US-11-632-012-16	Sequence 16, Appl
543	40	1.8	1533	8	US-11-713-768-37320	Sequence 37320, A
C 544	40	1.8	37180	8	US-11-257-477-13	Sequence 13, Appl
C 545	40	1.8	80423	8	US-11-257-477-41	Sequence 41, Appl
546	39.8	1.7	1024	8	US-11-599-517-96	Sequence 96, Appl
C 547	39.8	1.7	2271	1	US-10-533-069-244	Sequence 244, App
C 548	39.8	1.7	90351	8	US-11-257-477-166	Sequence 166, App
C 549	39.6	1.7	1445	8	US-11-632-012-38	Sequence 38, Appl
C 550	39.6	1.7	224112	8	US-11-257-477-80	Sequence 80, Appl
551	39.6	1.7	421609	8	US-11-257-477-122	Sequence 122, App
C 552	39.4	1.7	1050	1	US-10-533-069-1756	Sequence 1756, Ap
C 553	39.4	1.7	1301	8	US-11-595-320-7	Sequence 7, Appli
C 554	39	1.7	771	8	US-11-632-012-32	Sequence 32, Appl
555	39	1.7	938	8	US-11-713-768-1268	Sequence 1268, Ap
556	39	1.7	1076	8	US-11-514-704-4118	Sequence 4118, Ap
557	39	1.7	2126	1	US-10-438-246-26985	Sequence 26985, A
558	39	1.7	4080	8	US-11-657-313-4	Sequence 4, Appli
559	39	1.7	5092	8	US-11-657-313-5	Sequence 5, Appli
C 560	38.6	1.7	1678	8	US-11-713-768-43299	Sequence 43299, A
561	38.6	1.7	2085	8	US-11-713-768-72372	Sequence 72372, A
562	38.6	1.7	2154	8	US-11-713-768-71163	Sequence 71163, A
563	38.6	1.7	39084	8	US-11-257-477-35	Sequence 35, Appl
564	38.4	1.7	3289	8	US-11-514-704-21524	Sequence 21524, A
565	38.4	1.7	3925	1	US-10-533-069-939	Sequence 939, App
C 566	38.2	1.7	30304	8	US-11-257-477-128	Sequence 128, App
C 567	38.2	1.7	52637	8	US-11-257-477-186	Sequence 186, App
C 568	38.2	1.7	108845	8	US-11-257-477-7	Sequence 7, Appli
569	38	1.7	1556	8	US-11-514-704-6219	Sequence 6219, Ap
C 570	38	1.7	2866	8	US-11-514-704-23606	Sequence 23606, A
571	38	1.7	3379	8	US-11-514-704-6220	Sequence 6220, Ap
572	37.8	1.7	101	8	US-11-640-897-1466	Sequence 1466, Ap
573	37.8	1.7	52637	8	US-11-257-477-186	Sequence 186, App
574	37.4	1.6	2411	1	US-10-438-246-22503	Sequence 22503, A
C 575	37.4	1.6	46030	1	US-11-257-477-1	Sequence 1, Appli
576	37.2	1.6	1353	1	US-10-596-627-28	Sequence 28, Appl
577	37.2	1.6	1607	8	US-11-514-704-7133	Sequence 7133, Ap
C 578	37.2	1.6	5349	8	US-11-514-704-201	Sequence 201, App
579	37.2	1.6	10535	8	US-11-514-704-3259	Sequence 3259, Ap
580	37.2	1.6	100534	8	US-11-257-477-160	Sequence 160, App
581	37	1.6	795	8	US-11-713-768-111455	Sequence 111455,
C 582	37	1.6	1627	8	US-11-713-768-41129	Sequence 41129, A
583	37	1.6	1956	1	US-10-438-246-13283	Sequence 13283, A
584	37	1.6	2773	8	US-11-649-663A-1465	Sequence 1465, Ap
585	37	1.6	2773	8	US-11-713-768-49006	Sequence 49006, A
586	37	1.6	2791	8	US-11-649-663A-2825	Sequence 2825, Ap
587	37	1.6	2791	8	US-11-713-768-45476	Sequence 45476, A
588	37	1.6	139613	8	US-11-257-477-90	Sequence 90, Appl
589	36.8	1.6	2151	8	US-11-514-704-10912	Sequence 10912, A
590	36.8	1.6	4443	8	US-11-713-768-71358	Sequence 71358, A
591	36.6	1.6	21166	8	US-11-257-477-198	Sequence 198, App
592	36.4	1.6	101	8	US-11-640-897-1203	Sequence 1203, Ap
C 593	36.4	1.6	2943	1	US-10-438-246-561	Sequence 561, App
C 594	36.4	1.6	3310	1	US-10-438-246-550	Sequence 550, App
C 595	36.4	1.6	52138	8	US-11-739-906-75	Sequence 75, Appl
C 596	36.4	1.6	52138	8	US-11-739-872-75	Sequence 75, Appl
C 597	36.4	1.6	100534	8	US-11-257-477-160	Sequence 160, App
C 598	36.2	1.6	21166	8	US-11-257-477-198	Sequence 198, App
599	36.2	1.6	127767	8	US-11-257-477-176	Sequence 176, App
C 600	36.2	1.6	240102	8	US-11-257-477-192	Sequence 192, App
C 601	35.8	1.6	7482	1	US-10-438-246-5333	Sequence 5333, Ap
C 602	35.6	1.6	539	1	US-10-575-829-87	Sequence 87, Appl
C 603	35.6	1.6	539	1	US-10-575-805-87	Sequence 87, Appl
C 604	35.6	1.6	539	1	US-10-576-093-87	Sequence 87, Appl
C 605	35.6	1.6	539	1	US-10-576-094A-87	Sequence 87, Appl
606	35.6	1.6	623	8	US-11-489-234-19	Sequence 19, Appl
607	35.6	1.6	1377	8	US-11-632-012-11	Sequence 11, Appl
608	35.4	1.5	1925	1	US-10-438-246-29150	Sequence 29150, A
C 609	35.4	1.5	4446	1	US-10-438-246-11631	Sequence 11631, A

C 610	35.2	1.5	954	8	US-11-361-092-162	Sequence 162, App
C 611	35.2	1.5	1897	1	US-10-533-069-1339	Sequence 1339, Ap
612	35.2	1.5	2239	1	US-10-596-627-7	Sequence 7, Appli
613	35.2	1.5	2728	1	US-10-562-377-102	Sequence 102, App
C 614	35.2	1.5	39084	8	US-11-257-477-35	Sequence 35, Appl
615	35.2	1.5	152372	8	US-11-361-092-171	Sequence 171, App
616	35	1.5	1549	8	US-11-514-704-12516	Sequence 12516, A
C 617	35	1.5	3823	8	US-11-514-704-23493	Sequence 23493, A
618	34.8	1.5	751	1	US-10-438-246-27956	Sequence 27956, A
C 619	34.8	1.5	2830	1	US-10-438-246-565	Sequence 565, App
C 620	34.8	1.5	3801	8	US-11-514-704-19900	Sequence 19900, A
C 621	34.8	1.5	4377	8	US-11-514-704-23607	Sequence 23607, A
622	34.8	1.5	4572	1	US-10-438-246-15682	Sequence 15682, A
C 623	34.6	1.5	101	8	US-11-640-897-695	Sequence 695, App
624	34.6	1.5	549	8	US-11-713-768-75454	Sequence 75454, A
625	34.6	1.5	855	8	US-11-713-768-38540	Sequence 38540, A
626	34.6	1.5	855	8	US-11-713-768-50066	Sequence 50066, A
627	34.6	1.5	1419	1	US-10-438-246-28743	Sequence 28743, A
628	34.6	1.5	1520	8	US-11-713-768-2243	Sequence 2243, Ap
629	34.6	1.5	1653	8	US-11-514-704-7418	Sequence 7418, Ap
C 630	34.6	1.5	2196	1	US-10-562-377-112	Sequence 112, App
C 631	34.6	1.5	2196	1	US-10-562-377-190	Sequence 190, App
632	34.6	1.5	2406	8	US-11-514-704-21128	Sequence 21128, A
633	34.6	1.5	3271	8	US-11-514-704-5311	Sequence 5311, Ap
C 634	34.6	1.5	421609	8	US-11-257-477-122	Sequence 122, App
635	34.4	1.5	869	8	US-11-713-768-62035	Sequence 62035, A
636	34.4	1.5	1372	8	US-11-713-768-1704	Sequence 1704, Ap
637	34.4	1.5	1721	8	US-11-649-663A-3507	Sequence 3507, Ap
638	34.4	1.5	1966	8	US-11-514-704-18806	Sequence 18806, A
C 639	34.4	1.5	42203	8	US-11-257-477-53	Sequence 53, Appl
C 640	34.2	1.5	525	1	US-10-438-246-11579	Sequence 11579, A
641	34.2	1.5	1353	8	US-11-514-704-12636	Sequence 12636, A
C 642	34.2	1.5	2291	1	US-10-562-377-126	Sequence 126, App
C 643	34.2	1.5	4725	8	US-11-514-704-17007	Sequence 17007, A
C 644	34	1.5	625	8	US-11-684-413-11	Sequence 11, Appl
C 645	34	1.5	625	8	US-11-723-507-9	Sequence 9, Appli
646	34	1.5	1653	8	US-11-713-768-96077	Sequence 96077, A
647	34	1.5	1722	8	US-11-713-768-75614	Sequence 75614, A
648	34	1.5	1749	8	US-11-713-768-87368	Sequence 87368, A
C 649	34	1.5	2343	8	US-11-514-704-8767	Sequence 8767, Ap
C 650	34	1.5	4010	8	US-11-684-413-15	Sequence 15, Appl
C 651	34	1.5	4010	8	US-11-723-507-23	Sequence 23, Appl
652	33.8	1.5	945	8	US-11-713-768-56946	Sequence 56946, A
653	33.8	1.5	963	8	US-11-514-704-23864	Sequence 23864, A
654	33.8	1.5	1000	8	US-11-360-039-59	Sequence 59, Appl
655	33.8	1.5	4306	8	US-11-514-704-6282	Sequence 6282, Ap
656	33.6	1.5	891	1	US-10-438-246-11605	Sequence 11605, A
657	33.6	1.5	1457	1	US-10-438-246-21254	Sequence 21254, A
658	33.6	1.5	2474	8	US-11-514-704-5687	Sequence 5687, Ap
C 659	33.6	1.5	2568	8	US-11-514-704-5863	Sequence 5863, Ap
660	33.6	1.5	2718	8	US-11-514-704-12773	Sequence 12773, A
661	33.6	1.5	2728	1	US-10-562-377-180	Sequence 180, App
662	33.6	1.5	2773	8	US-11-514-704-13991	Sequence 13991, A
663	33.6	1.5	3048	8	US-11-713-768-90578	Sequence 90578, A
664	33.6	1.5	3048	8	US-11-713-768-94334	Sequence 94334, A
665	33.6	1.5	3087	8	US-11-796-730-1629	Sequence 1629, Ap
666	33.6	1.5	7264	8	US-11-514-704-24394	Sequence 24394, A
667	33.6	1.5	37234	8	US-11-257-477-63	Sequence 63, Appl
C 668	33.6	1.5	37234	8	US-11-257-477-63	Sequence 63, Appl
C 669	33.4	1.5	480	8	US-11-634-620-16	Sequence 16, Appl
670	33.4	1.5	682	8	US-11-705-903-53	Sequence 53, Appl
671	33.4	1.5	684	8	US-11-705-903-15	Sequence 15, Appl
672	33.4	1.5	1720	1	US-10-438-246-27762	Sequence 27762, A
C 673	33.4	1.5	1824	1	US-10-533-069-2115	Sequence 2115, Ap
C 674	33.4	1.5	2306	1	US-10-533-069-1830	Sequence 1830, Ap
C 675	33.4	1.5	3248	8	US-11-514-704-17402	Sequence 17402, A
676	33.4	1.5	4578	8	US-11-514-704-7881	Sequence 7881, Ap
677	33.4	1.5	5015	8	US-11-514-704-17480	Sequence 17480, A
678	33.4	1.5	5068	1	US-10-533-069-937	Sequence 937, App
C 679	33.4	1.5	5718	8	US-11-514-704-20708	Sequence 20708, A
C 680	33.2	1.5	354	1	US-10-438-246-28024	Sequence 28024, A
681	33.2	1.5	771	8	US-11-632-012-32	Sequence 32, Appl
682	33.2	1.5	42203	8	US-11-257-477-53	Sequence 53, Appl

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683	33	1.4	1835	8	US-11-514-704-9008	Sequence 9008, Ap	756	31.8	1.4	3293	8	US-11-514-704-18991	Sequence 18991, A
684	33	1.4	3096	8	US-11-514-704-13097	Sequence 13097, A	757	31.8	1.4	3339	8	US-11-514-704-5457	Sequence 5457, Ap
c 685	33	1.4	4106	8	US-11-514-704-20707	Sequence 20707, A	c 758	31.8	1.4	3389	1	US-10-438-246-27995	Sequence 27995, A
686	33	1.4	5850	1	US-10-438-246-15256	Sequence 15256, A	759	31.8	1.4	3794	8	US-11-514-704-20566	Sequence 20566, A
687	33	1.4	5850	1	US-10-438-246-22882	Sequence 22882, A	c 760	31.8	1.4	4085	1	US-10-585-503-3	Sequence 3, Appli
688	32.8	1.4	233	8	US-11-673-456-25	Sequence 25, Appl	761	31.8	1.4	5499	8	US-11-514-704-3073	Sequence 3073, Ap
689	32.8	1.4	1467	8	US-11-649-663A-3187	Sequence 3187, Ap	c 762	31.8	1.4	5694	8	US-11-514-704-22532	Sequence 22532, A
690	32.8	1.4	1718	8	US-11-514-704-11418	Sequence 11418, A	763	31.8	1.4	6226	8	US-11-514-704-18677	Sequence 18677, A
c 691	32.8	1.4	1888	8	US-11-514-704-2729	Sequence 2729, Ap	764	31.8	1.4	6690	1	US-10-438-246-5336	Sequence 5336, Ap
692	32.8	1.4	2410	8	US-11-649-663A-3823	Sequence 3823, Ap	765	31.8	1.4	52138	8	US-11-739-906-75	Sequence 75, Appl
693	32.8	1.4	2623	1	US-10-438-246-27039	Sequence 27039, A	766	31.8	1.4	52138	8	US-11-739-872-75	Sequence 75, Appl
c 694	32.8	1.4	2899	1	US-10-533-069-2350	Sequence 2350, Ap	c 767	31.6	1.4	533	8	US-11-514-704-2457	Sequence 2457, Ap
c 695	32.8	1.4	2923	8	US-11-514-704-7054	Sequence 7054, Ap	768	31.6	1.4	681	8	US-11-796-730-2225	Sequence 2225, Ap
c 696	32.8	1.4	3459	1	US-10-438-246-12905	Sequence 12905, A	769	31.6	1.4	1044	1	US-10-438-246-2081	Sequence 2081, Ap
697	32.8	1.4	3594	1	US-10-438-246-22284	Sequence 22284, A	770	31.6	1.4	1190	1	US-10-438-246-2754	Sequence 2754, Ap
698	32.8	1.4	4642	1	US-10-533-069-1647	Sequence 1647, Ap	771	31.6	1.4	1190	8	US-11-514-704-21068	Sequence 21068, A
c 699	32.8	1.4	5990	8	US-11-514-704-14172	Sequence 14172, A	772	31.6	1.4	1209	8	US-11-649-663A-1609	Sequence 1609, Ap
700	32.8	1.4	18703	1	US-10-650-449-8	Sequence 8, Appli	773	31.6	1.4	1209	8	US-11-713-768-81597	Sequence 81597, A
c 701	32.6	1.4	101	8	US-11-640-897-2340	Sequence 2340, Ap	774	31.6	1.4	1215	1	US-10-438-246-13195	Sequence 13195, A
c 702	32.6	1.4	1377	8	US-11-632-012-11	Sequence 11, Appl	c 775	31.6	1.4	1312	8	US-11-713-768-57601	Sequence 57601, A
703	32.6	1.4	1684	8	US-11-713-768-25966	Sequence 25966, A	776	31.6	1.4	1344	8	US-11-514-704-14371	Sequence 14371, A
704	32.6	1.4	1685	8	US-11-713-768-100603	Sequence 100603, A	c 777	31.6	1.4	1391	8	US-11-713-768-59512	Sequence 59512, A
c 705	32.6	1.4	1774	1	US-10-438-246-1222	Sequence 1222, Ap	c 778	31.6	1.4	1536	1	US-10-438-246-13194	Sequence 13194, A
706	32.6	1.4	1970	8	US-11-514-704-8257	Sequence 8257, Ap	779	31.6	1.4	1642	1	US-10-438-246-22468	Sequence 22468, A
707	32.6	1.4	2044	8	US-11-514-704-8672	Sequence 8672, Ap	780	31.6	1.4	1660	8	US-11-649-663A-2925	Sequence 2925, Ap
c 708	32.6	1.4	2411	8	US-11-713-768-20634	Sequence 20634, A	c 781	31.6	1.4	2082	8	US-11-514-704-16880	Sequence 16880, A
709	32.6	1.4	2588	8	US-11-351-522A-33	Sequence 33, Appl	c 782	31.6	1.4	2119	8	US-11-514-704-553	Sequence 553, App
710	32.6	1.4	2684	8	US-11-514-704-14568	Sequence 14568, A	c 783	31.6	1.4	2290	1	US-10-562-377-87	Sequence 87, Appl
c 711	32.6	1.4	4735	8	US-11-514-704-16570	Sequence 16570, A	784	31.6	1.4	2355	1	US-10-562-377-192	Sequence 192, App
712	32.6	1.4	5635	8	US-11-351-522A-3	Sequence 3, Appli	c 785	31.6	1.4	2429	1	US-10-562-377-83	Sequence 83, Appl
713	32.6	1.4	6382	8	US-11-351-522A-29	Sequence 29, Appl	c 786	31.6	1.4	2556	8	US-11-713-768-70315	Sequence 70315, A
c 714	32.6	1.4	8570	1	US-10-533-069-1572	Sequence 1572, Ap	c 787	31.6	1.4	3278	8	US-11-514-704-23414	Sequence 23414, A
c 715	32.6	1.4	133462	8	US-11-257-477-114	Sequence 114, App	c 788	31.6	1.4	3569	8	US-11-514-704-15131	Sequence 15131, A
c 716	32.4	1.4	761	1	US-10-533-069-997	Sequence 997, App	c 789	31.6	1.4	3683	8	US-11-514-704-24323	Sequence 24323, A
717	32.4	1.4	1140	8	US-11-713-768-69106	Sequence 69106, A	c 790	31.6	1.4	4230	1	US-10-438-246-15250	Sequence 15250, A
c 718	32.4	1.4	1434	8	US-11-713-768-106394	Sequence 106394, A	791	31.6	1.4	4284	1	US-10-438-246-15246	Sequence 15246, A
719	32.4	1.4	2332	8	US-11-514-704-3597	Sequence 3597, Ap	792	31.6	1.4	4326	1	US-10-438-246-15252	Sequence 15252, A
c 720	32.4	1.4	2337	8	US-11-796-730-589	Sequence 589, App	793	31.6	1.4	4381	8	US-11-514-704-21067	Sequence 21067, A
c 721	32.4	1.4	3024	8	US-11-514-704-10800	Sequence 10800, A	794	31.6	1.4	4668	1	US-10-438-246-15694	Sequence 15694, A
c 722	32.4	1.4	3044	8	US-11-514-704-18247	Sequence 18247, A	795	31.6	1.4	4761	1	US-10-438-246-15237	Sequence 15237, A
723	32.4	1.4	21808	8	US-11-257-477-136	Sequence 136, App	796	31.6	1.4	4806	1	US-10-438-246-15233	Sequence 15233, A
724	32.4	1.4	240102	8	US-11-257-477-192	Sequence 192, App	797	31.6	1.4	4806	1	US-10-438-246-15240	Sequence 15240, A
725	32.2	1.4	1045	8	US-11-713-768-1136	Sequence 1136, Ap	798	31.6	1.4	4806	1	US-10-438-246-15241	Sequence 15241, A
726	32.2	1.4	1110	8	US-11-514-704-9950	Sequence 9950, Ap	799	31.6	1.4	4806	1	US-10-438-246-15244	Sequence 15244, A
c 727	32.2	1.4	1410	8	US-11-796-730-1819	Sequence 1819, Ap	800	31.6	1.4	4915	1	US-10-438-246-23313	Sequence 23313, A
728	32.2	1.4	1884	8	US-11-713-768-72191	Sequence 72191, A	801	31.6	1.4	5127	1	US-10-438-246-15686	Sequence 15686, A
729	32.2	1.4	1887	8	US-11-713-768-71857	Sequence 71857, A	802	31.6	1.4	5217	1	US-10-438-246-23457	Sequence 23457, A
730	32.2	1.4	1930	8	US-11-514-704-4182	Sequence 4182, Ap	803	31.6	1.4	5271	1	US-10-438-246-23458	Sequence 23458, A
c 731	32.2	1.4	2093	8	US-11-514-704-18177	Sequence 18177, A	804	31.6	1.4	5311	8	US-11-514-704-14475	Sequence 14475, A
732	32.2	1.4	2354	1	US-10-562-377-136	Sequence 136, App	805	31.6	1.4	5376	1	US-10-438-246-15245	Sequence 15245, A
c 733	32.2	1.4	2437	8	US-11-514-704-20330	Sequence 20330, A	806	31.6	1.4	5484	1	US-10-438-246-15247	Sequence 15247, A
734	32.2	1.4	3087	8	US-11-514-704-8671	Sequence 8671, Ap	807	31.6	1.4	6053	1	US-10-438-246-23315	Sequence 23315, A
c 735	32.2	1.4	4188	1	US-10-533-069-2161	Sequence 2161, Ap	808	31.6	1.4	6216	1	US-10-438-246-11667	Sequence 11667, A
736	32.2	1.4	4467	8	US-11-514-704-12724	Sequence 12724, A	809	31.6	1.4	7710	8	US-11-514-704-3425	Sequence 3425, Ap
737	32.2	1.4	108845	8	US-11-257-477-7	Sequence 7, Appli	810	31.4	1.4	814	1	US-10-438-246-29536	Sequence 29536, A
c 738	32	1.4	1364	8	US-11-514-704-11963	Sequence 11963, A	811	31.4	1.4	1113	8	US-11-713-768-90304	Sequence 90304, A
c 739	32	1.4	1432	8	US-11-514-704-13370	Sequence 13370, A	812	31.4	1.4	1113	8	US-11-713-768-94060	Sequence 94060, A
c 740	32	1.4	2058	8	US-11-514-704-20311	Sequence 20311, A	813	31.4	1.4	1328	8	US-11-713-768-36434	Sequence 36434, A
741	32	1.4	2196	1	US-10-562-377-113	Sequence 113, App	c 814	31.4	1.4	1374	8	US-11-713-768-51528	Sequence 51528, A
742	32	1.4	2196	1	US-10-562-377-191	Sequence 191, App	c 815	31.4	1.4	1595	8	US-11-713-768-53650	Sequence 53650, A
c 743	32	1.4	2870	8	US-11-514-704-21377	Sequence 21377, A	816	31.4	1.4	2251	8	US-11-514-704-18493	Sequence 18493, A
c 744	32	1.4	3112	8	US-11-514-704-24454	Sequence 24454, A	817	31.4	1.4	2253	8	US-11-514-704-10958	Sequence 10958, A
c 745	32	1.4	3181	8	US-11-713-768-76092	Sequence 76092, A	818	31.4	1.4	2403	8	US-11-514-704-5138	Sequence 5138, Ap
c 746	32	1.4	3181	8	US-11-713-768-98308	Sequence 98308, A	819	31.4	1.4	2424	8	US-11-514-704-7902	Sequence 7902, Ap
c 747	31.8	1.4	101	8	US-11-640-897-1520	Sequence 1520, Ap	820	31.4	1.4	2499	8	US-11-514-704-7748	Sequence 7748, Ap
c 748	31.8	1.4	827	8	US-11-713-768-49404	Sequence 49404, A	821	31.4	1.4	3109	8	US-11-514-704-7417	Sequence 7417, Ap
c 749	31.8	1.4	920	1	US-10-438-246-29805	Sequence 29805, A	c 822	31.4	1.4	3212	8	US-11-514-704-21898	Sequence 21898, A
750	31.8	1.4	989	8	US-11-514-704-20891	Sequence 20891, A	823	31.4	1.4	3318	1	US-10-438-246-11282	Sequence 11282, A
c 751	31.8	1.4	1620	8	US-11-713-768-48248	Sequence 48248, A	824	31.4	1.4	3372	1	US-10-438-246-21032	Sequence 21032, A
c 752	31.8	1.4	1620	8	US-11-713-768-50818	Sequence 50818, A	c 825	31.4	1.4	3473	8	US-11-514-704-14808	Sequence 14808, A
c 753	31.8	1.4	2296	8	US-11-514-704-15618	Sequence 15618, A	c 826	31.4	1.4	4865	8	US-11-514-704-19609	Sequence 19609, A
c 754	31.8	1.4	2728	1	US-10-562-377-180	Sequence 180, App	c 827	31.4	1.4	6669	8	US-11-509-784-5	Sequence 5, Appli
c 755	31.8	1.4	3077	8	US-11-514-704-14416	Sequence 14416, A	828	31.2	1.4	291	8	US-11-796-730-928	Sequence 928, App

829	31.2	1.4	513	8	US-11-679-492-51	Sequence 51, Appl	902	30.8	1.3	2435	8	US-11-514-704-9287	Sequence 9287, Ap
830	31.2	1.4	799	1	US-10-438-246-27238	Sequence 27238, A	C 903	30.8	1.3	3443	8	US-11-514-704-13827	Sequence 13827, A
831	31.2	1.4	969	8	US-11-713-768-21119	Sequence 21119, A	904	30.8	1.3	3548	1	US-10-533-069-315	Sequence 315, App
832	31.2	1.4	970	8	US-11-713-768-78164	Sequence 78164, A	C 905	30.8	1.3	3614	1	US-10-438-246-637	Sequence 637, App
C 833	31.2	1.4	1002	8	US-11-514-704-20841	Sequence 20841, A	C 906	30.8	1.3	4044	8	US-11-361-092-158	Sequence 158, App
C 834	31.2	1.4	1198	8	US-11-514-704-17788	Sequence 17788, A	C 907	30.8	1.3	4131	1	US-10-438-246-26553	Sequence 26553, A
C 835	31.2	1.4	1257	8	US-11-559-024-17	Sequence 17, Appl	C 908	30.8	1.3	4376	8	US-11-514-704-17236	Sequence 17236, A
C 836	31.2	1.4	1449	1	US-10-438-246-2495	Sequence 2495, Ap	C 909	30.8	1.3	4660	8	US-11-514-704-13871	Sequence 13871, A
C 837	31.2	1.4	1926	8	US-11-514-704-16080	Sequence 16080, A	C 910	30.8	1.3	5616	8	US-11-514-704-4461	Sequence 4461, Ap
C 838	31.2	1.4	1976	8	US-11-514-704-15594	Sequence 15594, A	911	30.8	1.3	8399	8	US-11-514-704-6949	Sequence 6949, Ap
C 839	31.2	1.4	2237	8	US-11-496-050-11	Sequence 11, Appl	C 912	30.8	1.3	9963	1	US-10-369-909-14	Sequence 14, Appl
C 840	31.2	1.4	2387	1	US-10-562-377-99	Sequence 99, Appl	C 913	30.8	1.3	152372	8	US-11-361-092-171	Sequence 171, App
C 841	31.2	1.4	2387	1	US-10-562-377-177	Sequence 177, App	C 914	30.6	1.3	1017	1	US-10-438-246-15326	Sequence 15326, A
842	31.2	1.4	2390	8	US-11-514-704-8552	Sequence 8552, Ap	915	30.6	1.3	1077	8	US-11-713-768-109951	Sequence 109951,
843	31.2	1.4	2425	1	US-10-562-377-68	Sequence 68, Appl	916	30.6	1.3	1081	1	US-10-438-246-28121	Sequence 28121, A
844	31.2	1.4	2425	1	US-10-562-377-146	Sequence 146, App	C 917	30.6	1.3	1122	1	US-10-438-246-23339	Sequence 23339, A
C 845	31.2	1.4	2628	8	US-11-717-713-127	Sequence 127, App	918	30.6	1.3	1169	1	US-10-438-246-12292	Sequence 12292, A
C 846	31.2	1.4	2631	8	US-11-717-713-125	Sequence 125, App	919	30.6	1.3	1283	8	US-11-713-768-58949	Sequence 58949, A
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C 848	31.2	1.4	2643	8	US-11-717-713-123	Sequence 123, App	C 921	30.6	1.3	2354	1	US-10-562-377-58	Sequence 58, Appl
C 849	31.2	1.4	2708	8	US-11-717-713-131	Sequence 131, App	C 922	30.6	1.3	2354	1	US-10-562-377-136	Sequence 136, App
C 850	31.2	1.4	2739	8	US-11-717-713-115	Sequence 115, App	C 923	30.6	1.3	2413	8	US-11-514-704-11938	Sequence 11938, A
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C 852	31.2	1.4	3647	8	US-11-717-713-134	Sequence 134, App	925	30.6	1.3	2539	8	US-11-514-704-11792	Sequence 11792, A
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C 854	31.2	1.4	4118	8	US-11-514-704-14178	Sequence 14178, A	927	30.6	1.3	2547	1	US-10-438-246-22973	Sequence 22973, A
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C 858	31.2	1.4	5360	1	US-10-533-069-660	Sequence 660, App	C 931	30.6	1.3	2885	8	US-11-514-704-1408	Sequence 1408, Ap
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53	2284	100.0	2284	37	US-09-997-428-514	Sequence 514, App			
67	2284	100.0	2284	47	US-10-429-667-82	Sequence 82, Appl			
68	2284	100.0	2284	50	US-10-677-471-82	Sequence 82, Appl			
69	2284	100.0	2284	50	US-10-677-669-82	Sequence 82, Appl			
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73	2284	100.0	2284	58	US-10-858-993-82	Sequence 82, Appl			
74	2284	100.0	2284	58	US-10-899-671-82	Sequence 82, Appl			
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243	386.8	16.9	422	19	US-09-036-522-46	Sequence 46, Appl	316	257.6	11.3	532	30	US-09-726-790-1598	Sequence 1598, Ap
244	386.8	16.9	422	22	US-09-343-566-46	Sequence 46, Appl	317	256.8	11.2	280	25	US-09-539-331D-33139	Sequence 33139, A
245	386	16.9	386	21	US-09-293-972-28031	Sequence 28031, A	c	254.4	11.1	330	25	US-09-540-229-29577	Sequence 29577, A
246	386	16.9	386	34	US-09-904-939-28031	Sequence 28031, A		253.2	11.1	388	76	US-11-443-428A-576439	Sequence 576439, A
247	383.2	16.8	390	22	US-09-332-782-11182	Sequence 11182, A		252	11.0	252	16	US-08-782-035-1334	Sequence 1334, Ap
248	383.2	16.8	390	24	US-09-515-694-11182	Sequence 11182, A	321	252	11.0	252	25	US-09-534-856-24642	Sequence 24642, A
249	368.4	16.1	383	28	US-09-649-163-2508	Sequence 2508, Ap	322	250.8	11.0	262	16	US-08-748-106-1202	Sequence 1202, Ap
250	368.4	16.1	383	28	US-09-652-916-3749	Sequence 3749, Ap	323	250.8	11.0	262	25	US-09-540-766-3913	Sequence 3913, Ap
251	368	16.1	368	85	US-60-185-215-2729	Sequence 2729, Ap	c	248.4	10.9	12351	61	US-10-990-328-96640	Sequence 96640, A
252	363.6	15.9	438	22	US-09-362-510-1230	Sequence 1230, Ap		248.4	10.9	12351	61	US-10-990-328A-96640	Sequence 96640, A
253	363.6	15.9	438	22	US-09-362-510A-1230	Sequence 1230, Ap		248.4	10.9	14034	61	US-10-990-328-96760	Sequence 96760, A
254	363.6	15.9	438	34	US-09-904-013-1230	Sequence 1230, Ap	c	248.4	10.9	14034	61	US-10-990-328A-96760	Sequence 96760, A
255	359.4	15.7	445	24	US-09-528-409-42767	Sequence 42767, A		246.4	10.8	307	30	US-09-726-806-2237	Sequence 2237, Ap
256	359.4	15.7	445	34	US-09-933-524-42767	Sequence 42767, A		245.6	10.8	324	12	US-08-337-601A-5664	Sequence 5664, Ap
257	359.4	15.7	445	35	US-09-933-524A-42767	Sequence 42767, A	330	245.6	10.8	324	14	US-08-530-112A-5664	Sequence 5664, Ap
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259	359	15.7	428	35	US-09-943-143-16987	Sequence 16987, A		244	10.7	29930	60	US-10-940-774A-15326	Sequence 15326, A
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261	353.2	15.5	358	23	US-09-489-036-22888	Sequence 22888, A	c	244	10.7	38779	59	US-10-932-349-19348	Sequence 19348, A
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267	334.8	14.7	562	87	US-60-252-833-27421	Sequence 27421, A	340	243.4	10.7	478	22	US-09-332-782-32190	Sequence 32190, A
268	332.2	14.5	367	23	US-09-489-036-17525	Sequence 17525, A	341	243.4	10.7	478	30	US-09-737-223-32190	Sequence 32190, A
269	332.2	14.5	367	35	US-09-943-143-17525	Sequence 17525, A	342	243.4	10.7	478	34	US-09-918-995-32190	Sequence 32190, A
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271	324	14.2	360	69	US-11-266-748A-460080	Sequence 460080, A	344	243.2	10.6	146776	87	US-60-248-505-474	Sequence 474, App
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273	323.2	14.2	352	46	US-10-349-781-52754	Sequence 52754, A	346	243	10.6	1000	44	US-10-301-480B-155646	Sequence 155646, A
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518	237.4	10.4	461086	58	US-10-896-891-623	Sequence 623, App		591	236.8	10.4	251664	61	US-10-990-328-94156	Sequence 94156, A
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c 525	237.2	10.4	214475	89	US-60-465-241-51534	Sequence 51534, A		598	236.6	10.4	100463	60	US-10-940-774A-12511	Sequence 12511, A
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c 529	237	10.4	601	35	US-09-948-933-3827	Sequence 3827, Ap		602	236.6	10.4	118488	61	US-10-990-328A-98050	Sequence 98050, A
c 530	237	10.4	601	35	US-09-949-003C-10405	Sequence 10405, A		603	236.6	10.4	126488	48	US-10-573-332-463	Sequence 463, App
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c 532	237	10.4	601	59	US-10-902-387-1403	Sequence 1403, Ap		605	236.6	10.4	155782	59	US-10-932-349-19245	Sequence 19245, A
c 533	237	10.4	601	59	US-10-902-387-3827	Sequence 3827, Ap		606	236.6	10.4	155782	91	US-60-500-337-19245	Sequence 19245, A
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c 535	237	10.4	601	62	US-11-033-545-5643	Sequence 5643, Ap		608	236.4	10.4	238	13	US-08-416-401-3033	Sequence 3033, Ap
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c 550	237	10.4	38009	59	US-10-940-774-13617	Sequence 13617, A		623	236.4	10.4	2088	38	US-10-027-632-98072	Sequence 98072, A
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558	237	10.4	107507	90	US-60-495-114-16290	Sequence 16290, A		631	236.4	10.4	1093019	3	PCT-US04-37982-980	Sequence 980, App
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561	237	10.4	140197	57	US-10-796-307-8811	Sequence 8811, Ap		634	236.2	10.3	111414	61	US-10-990-328A-95449	Sequence 95449, A
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565	237	10.4	140213	90	US-60-466-412-86999	Sequence 86999, A		638	236.2	10.3	175288	87	US-60-258-251-32	Sequence 32, Appl1
c 566	237	10.4	150780	59	US-10-940-774-14711	Sequence 14711, A		c 639	236.2	10.3	183265	89	US-60-465-241-52888	Sequence 52888, A
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c 568	237	10.4	453407	90	US-60-466-412-84558	Sequence 84558, A		c 641	236.2	10.3	323767	62	US-11-033-056A-36170	Sequence 36170, A
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c 570	237	10.4	453737	61	US-10-990-328A-94083	Sequence 94083, A		c 643	236.2	10.3	337843	61	US-10-990-328A-95702	Sequence 95702, A
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c 572	237	10.4	1452321	35	US-09-947-911-267	Sequence 267, App		645	236.2	10.3	5401257	35	US-09-947-916-209	Sequence 209, App
c 573	237	10.4	15105345	35	US-09-948-128-55	Sequence 55, Appl1		c 646	236	10.3	841	43	US-10-301-480A-214542	Sequence 214542,
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c 581	236.8	10.4	20901	59	US-10-940-774-11866	Sequence 11866, A		c 654	236	10.3	13186	1	PCT-US02-09370-1145	Sequence 1145, Ap
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c 583	236.8	10.4	28666	87	US-60-243-468-574	Sequence 574, App		c 656	236	10.3	13186	35	US-09-950-083-8476	Sequence 8476, Ap
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C 662	236	10.3	13186	47	US-10-472-965-664	Sequence 664, App	C 735	235.8	10.3	2300	80	US-11-636-385A-4745	Sequence 4745, Ap
C 663	236	10.3	13186	58	US-10-868-184-7497	Sequence 7497, Ap	C 736	235.8	10.3	2300	93	US-60-762-056-4745	Sequence 4745, Ap
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C 672	236	10.3	13186	58	US-10-868-184D-8476	Sequence 8476, Ap	745	235.8	10.3	32198	40	US-10-217-651-723	Sequence 723, App
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C 675	236	10.3	13186	58	US-10-896-164-7497	Sequence 7497, Ap	748	235.8	10.3	51469	1	PCT-US01-01354-24134	Sequence 24134, A
C 676	236	10.3	13186	58	US-10-896-164-8476	Sequence 8476, Ap	749	235.8	10.3	51469	1	PCT-US01-01354-25082	Sequence 25082, A
C 677	236	10.3	13862	1	PCT-US02-09257-663	Sequence 663, App	750	235.8	10.3	51469	1	PCT-US01-01354-33625	Sequence 33625, A
C 678	236	10.3	13862	1	PCT-US02-09370-1144	Sequence 1144, Ap	751	235.8	10.3	51469	31	US-09-764-905-24134	Sequence 24134, A
C 679	236	10.3	13862	35	US-09-950-083-7496	Sequence 7496, Ap	752	235.8	10.3	51469	31	US-09-764-905-25082	Sequence 25082, A
C 680	236	10.3	13862	35	US-09-950-083-8475	Sequence 8475, Ap	753	235.8	10.3	51469	31	US-09-764-905-33625	Sequence 33625, A
C 681	236	10.3	13862	35	US-09-950-083-11223	Sequence 11223, A	754	235.8	10.3	51469	38	US-10-092-399-24134	Sequence 24134, A
C 682	236	10.3	13862	35	US-09-950-083B-7496	Sequence 7496, Ap	755	235.8	10.3	51469	38	US-10-092-399-25082	Sequence 25082, A
C 683	236	10.3	13862	35	US-09-950-083B-8475	Sequence 8475, Ap	756	235.8	10.3	51469	38	US-10-092-399-33625	Sequence 33625, A
C 684	236	10.3	13862	35	US-09-950-083B-11223	Sequence 11223, A	757	235.8	10.3	58881	59	US-10-932-349-19853	Sequence 19853, A
C 685	236	10.3	13862	39	US-10-105-299-9647	Sequence 9647, Ap	C 758	235.8	10.3	58881	91	US-60-500-337-19853	Sequence 19853, A
C 686	236	10.3	13862	39	US-10-105-299-10626	Sequence 10626, A	759	235.8	10.3	62546	89	US-60-465-241-51910	Sequence 51910, A
C 687	236	10.3	13862	39	US-10-105-299-13374	Sequence 13374, A	760	235.8	10.3	62546	90	US-60-466-412-85101	Sequence 85101, A
C 688	236	10.3	13862	47	US-10-472-963-1144	Sequence 1144, Ap	761	235.8	10.3	62546	90	US-60-487-610-19475	Sequence 19475, A
C 689	236	10.3	13862	47	US-10-472-965-663	Sequence 663, App	762	235.8	10.3	62546	91	US-60-582-609-19475	Sequence 19475, A
C 690	236	10.3	13862	58	US-10-868-184-7496	Sequence 7496, Ap	763	235.8	10.3	62555	2	PCT-US03-40978-17630	Sequence 17630, A
C 691	236	10.3	13862	58	US-10-868-184-8475	Sequence 8475, Ap	764	235.8	10.3	62555	56	US-10-741-600-17630	Sequence 17630, A
C 692	236	10.3	13862	58	US-10-868-184-11223	Sequence 11223, A	765	235.8	10.3	62555	91	US-60-548-091-5623	Sequence 5623, Ap
C 693	236	10.3	13862	58	US-10-868-184A-7496	Sequence 7496, Ap	C 766	235.8	10.3	97600	87	US-60-236-804-129	Sequence 129, App
C 694	236	10.3	13862	58	US-10-868-184A-8475	Sequence 8475, Ap	C 767	235.8	10.3	105168	59	US-10-940-774-13296	Sequence 13296, A
C 695	236	10.3	13862	58	US-10-868-184A-11223	Sequence 11223, A	C 768	235.8	10.3	105168	60	US-10-940-774A-13296	Sequence 13296, A
C 696	236	10.3	13862	58	US-10-868-184B-7496	Sequence 7496, Ap	C 769	235.8	10.3	120955	57	US-10-756-149-4579	Sequence 4579, Ap
C 697	236	10.3	13862	58	US-10-868-184B-8475	Sequence 8475, Ap	C 770	235.8	10.3	121167	2	PCT-US03-41389-710	Sequence 710, App
C 698	236	10.3	13862	58	US-10-868-184B-11223	Sequence 11223, A	C 771	235.8	10.3	121167	46	US-10-330-773-710	Sequence 710, App
C 699	236	10.3	13862	58	US-10-868-184C-7496	Sequence 7496, Ap	C 772	235.8	10.3	121167	46	US-10-330-773A-710	Sequence 710, App
C 700	236	10.3	13862	58	US-10-868-184C-8475	Sequence 8475, Ap	C 773	235.8	10.3	121167	48	US-10-540-898-710	Sequence 710, App
C 701	236	10.3	13862	58	US-10-868-184C-11223	Sequence 11223, A	C 774	235.8	10.3	121167	75	US-11-403-116-710	Sequence 710, App
C 702	236	10.3	13862	58	US-10-868-184D-7496	Sequence 7496, Ap	775	235.8	10.3	3710966	35	US-09-948-128-368	Sequence 368, App
C 703	236	10.3	13862	58	US-10-868-184D-8475	Sequence 8475, Ap	C 776	235.6	10.3	309	69	US-11-202-542A-28	Sequence 28, Appl
C 704	236	10.3	13862	58	US-10-868-184D-11223	Sequence 11223, A	C 777	235.6	10.3	660	43	US-10-301-480A-188122	Sequence 188122, A
C 705	236	10.3	13862	58	US-10-868-194B-7496	Sequence 7496, Ap	C 778	235.6	10.3	660	44	US-10-301-480B-188122	Sequence 188122, A
C 706	236	10.3	13862	58	US-10-868-194B-8475	Sequence 8475, Ap	C 779	235.6	10.3	660	45	US-10-301-480C-188122	Sequence 188122, A
C 707	236	10.3	13862	58	US-10-868-194B-11223	Sequence 11223, A	C 780	235.6	10.3	6000	94	US-60-873-739-3514	Sequence 3514, Ap
C 708	236	10.3	13862	58	US-10-896-164-7496	Sequence 7496, Ap	C 781	235.6	10.3	6000	94	US-60-873-882-4361	Sequence 4361, Ap
C 709	236	10.3	13862	58	US-10-896-164-8475	Sequence 8475, Ap	C 782	235.6	10.3	25452	89	US-60-465-241-52186	Sequence 52186, A
C 710	236	10.3	13862	58	US-10-896-164-11223	Sequence 11223, A	783	235.6	10.3	29145	62	US-11-033-056A-37595	Sequence 37595, A
711	236	10.3	32215	86	US-60-212-655-149	Sequence 149, App	784	235.6	10.3	29145	62	US-11-033-056A-37596	Sequence 37596, A
712	236	10.3	39243	62	US-11-066-316A-10009	Sequence 10009, A	C 785	235.6	10.3	32659	38	US-10-085-117-208	Sequence 208, App
713	236	10.3	62267	61	US-10-990-328-94216	Sequence 94216, A	786	235.6	10.3	42993	90	US-60-466-412-85969	Sequence 85969, A
714	236	10.3	62267	61	US-10-990-328A-94216	Sequence 94216, A	C 787	235.6	10.3	70683	89	US-60-465-241-53100	Sequence 53100, A
715	236	10.3	79278	89	US-60-465-241-51894	Sequence 51894, A	C 788	235.6	10.3	70683	90	US-60-466-412-87167	Sequence 87167, A
716	236	10.3	79278	90	US-60-466-412-85087	Sequence 85087, A	789	235.6	10.3	71574	59	US-10-940-774-15580	Sequence 15580, A
717	236	10.3	79278	90	US-60-470-166-8833	Sequence 8833, Ap	790	235.6	10.3	71574	60	US-11-266-748A-24186	Sequence 24186, A
C 718	236	10.3	108364	62	US-11-033-056A-35821	Sequence 35821, A	C 791	235.6	10.3	142707	69	US-11-266-748A-24186	Sequence 24186, A
719	236	10.3	168174	1	PCT-US02-03546-63	Sequence 63, Appl	792	235.6	10.3	171414	90	US-60-466-412-84914	Sequence 84914, A
720	236	10.3	168174	59	US-10-914-799-63	Sequence 63, Appl	793	235.6	10.3	901438	91	US-60-568-845-2861	Sequence 2861, Ap
721	236	10.3	168273	1	PCT-US02-03546-2	Sequence 2, Appl	C 794	235.6	10.3	3710966	35	US-09-948-128-368	Sequence 368, App
722	236	10.3	168273	59	US-10-914-799-2	Sequence 2, Appl	C 795	235.4	10.3	256	25	US-09-540-229-27106	Sequence 27106, A
723	236	10.3	184475	87	US-60-243-468-477	Sequence 477, App	C 796	235.4	10.3	787	43	US-10-301-480A-312808	Sequence 312808, A
724	236	10.3	184475	87	US-60-243-742-76	Sequence 76, Appl	C 797	235.4	10.3	787	44	US-10-301-480B-312808	Sequence 312808, A
725	236	10.3	189199	62	US-11-066-316A-9942	Sequence 9942, Ap	C 798	235.4	10.3	787	45	US-10-301-480C-312808	Sequence 312808, A
C 726	236	10.3	208209	50	US-10-674-575-64	Sequence 64, Appl	C 799	235.4	10.3	18968	32	US-09-814-353-20301	Sequence 20301, A
727	236	10.3	334918	87	US-60-248-499-12	Sequence 12, Appl	800	235.4	10.3	18968	32	US-09-814-353A-20301	Sequence 20301, A
C 728	236	10.3	2307596	35	US-09-948-128-334	Sequence 334, App	801	235.4	10.3	55650	87	US-60-243-468-312	Sequence 312, App
C 729	235.8	10.3	773	1	PCT-US01-01354-36204	Sequence 36204, A	802	235.4	10.3	58397	59	US-10-940-774-14469	Sequence 14469, A
C 730	235.8	10.3	773	31	US-09-764-905-36204	Sequence 36204, A	803	235.4	10.3	58397	60	US-10-940-774A-14469	Sequence 14469, A
C 731	235.8	10.3	773	38	US-10-092-399-36204	Sequence 36204, A	804	235.4	10.3	59076	59	US-10-940-774-15097	Sequence 15097, A
732	235.8	10.3	1000	69	US-11-266-748A-211062	Sequence 211062, A	805	235.4	10.3	59076	60	US-10-940-774A-15097	Sequence 15097, A

806	235.4	10.3	63962	61	US-10-990-328-95230	Sequence 95230, A	879	235	10.3	202100	1	PCT-US02-34679-484	Sequence 484, App
807	235.4	10.3	63962	61	US-10-990-328A-95230	Sequence 95230, A	880	235	10.3	202100	40	US-10-282-174-484	Sequence 484, App
808	235.4	10.3	67293	90	US-60-466-412-84196	Sequence 84196, A	881	235	10.3	202100	49	US-10-600-009-484	Sequence 484, App
C 809	235.4	10.3	80505	87	US-60-242-679-379	Sequence 379, App	C 882	235	10.3	5401257	35	US-09-947-916-209	Sequence 209, App
810	235.4	10.3	87859	87	US-60-242-679-688	Sequence 688, App	C 883	234.8	10.3	994	42	US-10-301-480-594433	Sequence 594433,
811	235.4	10.3	93435	90	US-60-466-412-87963	Sequence 87963, A	C 884	234.8	10.3	994	42	US-10-301-480-1207842	Sequence 1207842,
C 812	235.4	10.3	100608	47	US-10-417-375-108	Sequence 108, App	C 885	234.8	10.3	994	43	US-10-301-480A-970502	Sequence 970502,
C 813	235.4	10.3	100608	47	US-10-417-375A-108	Sequence 108, App	C 886	234.8	10.3	994	44	US-10-301-480B-970502	Sequence 970502,
C 814	235.4	10.3	100608	47	US-10-417-375B-108	Sequence 108, App	C 887	234.8	10.3	994	45	US-10-301-480C-970502	Sequence 970502,
C 815	235.4	10.3	925175	35	US-09-947-911-61	Sequence 61, Appl	C 888	234.8	10.3	5872	76	US-11-443-428A-313692	Sequence 313692,
C 816	235.2	10.3	993	43	US-10-301-480A-3063	Sequence 3063, Ap	C 889	234.8	10.3	5952	76	US-11-443-428A-313690	Sequence 313690,
C 817	235.2	10.3	993	43	US-10-301-480A-304111	Sequence 304111,	C 890	234.8	10.3	6491	76	US-11-443-428A-313691	Sequence 313691,
C 818	235.2	10.3	993	44	US-10-301-480B-3063	Sequence 3063, Ap	C 891	234.8	10.3	7085	76	US-11-443-428A-313688	Sequence 313688,
C 819	235.2	10.3	993	44	US-10-301-480B-304111	Sequence 304111,	C 892	234.8	10.3	7250	76	US-11-443-428A-313687	Sequence 313687,
C 820	235.2	10.3	993	45	US-10-301-480C-3063	Sequence 3063, Ap	C 893	234.8	10.3	7252	76	US-11-443-428A-313682	Sequence 313682,
C 821	235.2	10.3	993	45	US-10-301-480C-304111	Sequence 304111,	C 894	234.8	10.3	7252	76	US-11-443-428A-313683	Sequence 313683,
C 822	235.2	10.3	994	43	US-10-301-480A-3064	Sequence 3064, Ap	C 895	234.8	10.3	7252	76	US-11-443-428A-313684	Sequence 313684,
C 823	235.2	10.3	994	44	US-10-301-480B-3064	Sequence 3064, Ap	C 896	234.8	10.3	7269	76	US-11-443-428A-313679	Sequence 313679,
C 824	235.2	10.3	994	45	US-10-301-480C-3064	Sequence 3064, Ap	C 897	234.8	10.3	7278	76	US-11-443-428A-313680	Sequence 313680,
825	235.2	10.3	2300	3	PCT-US06-46920-7190	Sequence 7190, Ap	C 898	234.8	10.3	7306	76	US-11-443-428A-313678	Sequence 313678,
826	235.2	10.3	2300	80	US-11-636-385-7190	Sequence 7190, Ap	C 899	234.8	10.3	7306	76	US-11-443-428A-313685	Sequence 313685,
827	235.2	10.3	2300	80	US-11-636-385A-7190	Sequence 7190, Ap	900	234.8	10.3	15278	35	US-09-948-941-638	Sequence 638, App
828	235.2	10.3	2300	93	US-60-762-056-7190	Sequence 7190, Ap	901	234.8	10.3	15278	58	US-10-896-891-638	Sequence 638, App
C 829	235.2	10.3	4178	76	US-11-443-428A-313693	Sequence 313693,	902	234.8	10.3	23277	89	US-60-465-241-52125	Sequence 52125, A
C 830	235.2	10.3	34051	61	US-10-990-328-96624	Sequence 96624, A	903	234.8	10.3	23277	90	US-60-466-412-85573	Sequence 85573, A
C 831	235.2	10.3	34051	61	US-10-990-328A-96624	Sequence 96624, A	C 904	234.8	10.3	28398	86	US-60-207-315-127	Sequence 127, App
832	235.2	10.3	62386	59	US-10-940-774-12823	Sequence 12823, A	905	234.8	10.3	31277	38	US-10-087-192-1510	Sequence 1510, Ap
833	235.2	10.3	62386	60	US-10-940-774A-12823	Sequence 12823, A	906	234.8	10.3	32351	61	US-10-990-328-93698	Sequence 93698, A
834	235.2	10.3	113464	59	US-60-500-337-19435	Sequence 19435, A	C 907	234.8	10.3	32351	61	US-10-990-328A-93698	Sequence 93698, A
835	235.2	10.3	113464	91	US-60-500-337-19435	Sequence 19435, A	C 908	234.8	10.3	100557	90	US-60-466-412-86678	Sequence 86678, A
836	235.2	10.3	176956	86	US-60-212-664-142	Sequence 142, App	909	234.8	10.3	141646	91	US-60-550-051-3063	Sequence 3063, Ap
837	235.2	10.3	188788	59	US-10-932-349-19179	Sequence 19179, A	910	234.8	10.3	187583	76	US-11-443-428A-735343	Sequence 735343,
838	235.2	10.3	188788	91	US-60-500-337-19179	Sequence 19179, A	911	234.8	10.3	187664	76	US-11-443-428A-735317	Sequence 735317,
839	235.2	10.3	223320	87	US-60-242-679-528	Sequence 528, App	912	234.8	10.3	187679	76	US-11-443-428A-735342	Sequence 735342,
C 840	235.2	10.3	238417	47	US-10-461-862-98	Sequence 98, Appl	913	234.8	10.3	187746	76	US-11-443-428A-735330	Sequence 735330,
841	235.2	10.3	4925599	35	US-09-948-128-259	Sequence 259, App	914	234.8	10.3	187760	76	US-11-443-428A-735316	Sequence 735316,
C 842	235	10.3	601	59	US-10-940-774-94321	Sequence 94321, A	915	234.8	10.3	187779	76	US-11-443-428A-735290	Sequence 735290,
C 843	235	10.3	601	59	US-10-940-774-94322	Sequence 94322, A	916	234.8	10.3	187827	76	US-11-443-428A-735304	Sequence 735304,
C 844	235	10.3	601	60	US-10-940-774A-94321	Sequence 94321, A	917	234.8	10.3	187842	76	US-11-443-428A-735329	Sequence 735329,
C 845	235	10.3	601	60	US-10-940-774A-94322	Sequence 94322, A	918	234.8	10.3	187842	76	US-11-443-428A-735341	Sequence 735341,
846	235	10.3	936	43	US-10-301-480A-159147	Sequence 159147,	919	234.8	10.3	187860	76	US-11-443-428A-735291	Sequence 735291,
847	235	10.3	936	44	US-10-301-480B-159147	Sequence 159147,	920	234.8	10.3	187923	76	US-11-443-428A-735303	Sequence 735303,
848	235	10.3	936	45	US-60-873-883-1823	Sequence 159147,	921	234.8	10.3	187923	76	US-11-443-428A-735315	Sequence 735315,
849	235	10.3	6000	94	US-60-873-883-1823	Sequence 1823, Ap	922	234.8	10.3	188005	76	US-11-443-428A-735328	Sequence 735328,
850	235	10.3	11173	1	PCT-US02-21090-10	Sequence 10, Appl	923	234.8	10.3	188013	76	US-11-443-428A-735338	Sequence 735338,
851	235	10.3	11173	33	US-09-898-556A-10	Sequence 10, Appl	924	234.8	10.3	188056	76	US-11-443-428A-735339	Sequence 735339,
852	235	10.3	11173	33	US-10-772-542-10	Sequence 10, Appl	925	234.8	10.3	188086	76	US-11-443-428A-735302	Sequence 735302,
C 853	235	10.3	13619	61	US-10-990-328-96037	Sequence 96037, A	926	234.8	10.3	188094	76	US-11-443-428A-735312	Sequence 735312,
C 854	235	10.3	13619	61	US-10-990-328A-96037	Sequence 96037, A	927	234.8	10.3	188134	76	US-11-443-428A-735337	Sequence 735337,
C 855	235	10.3	24177	61	US-10-990-328-96993	Sequence 96993, A	928	234.8	10.3	188137	76	US-11-443-428A-735313	Sequence 735313,
C 856	235	10.3	24177	61	US-10-990-328A-96993	Sequence 96993, A	929	234.8	10.3	188140	76	US-11-443-428A-735333	Sequence 735333,
857	235	10.3	58773	87	US-60-243-468-692	Sequence 692, App	930	234.8	10.3	188158	76	US-11-443-428A-735340	Sequence 735340,
C 858	235	10.3	76838	62	US-11-033-056A-37312	Sequence 37312, A	931	234.8	10.3	188176	76	US-11-443-428A-735325	Sequence 735325,
C 859	235	10.3	128034	1	PCT-US02-34679-186	Sequence 186, App	932	234.8	10.3	188177	76	US-11-443-428A-735336	Sequence 735336,
C 860	235	10.3	128034	1	PCT-US02-34679-187	Sequence 187, App	933	234.8	10.3	188183	76	US-11-443-428A-735334	Sequence 735334,
C 861	235	10.3	128034	40	US-10-282-174-186	Sequence 186, App	934	234.8	10.3	188215	76	US-11-443-428A-735311	Sequence 735311,
C 862	235	10.3	128034	40	US-10-282-174-187	Sequence 187, App	935	234.8	10.3	188219	76	US-11-443-428A-735326	Sequence 735326,
C 863	235	10.3	128034	49	US-10-600-009-186	Sequence 186, App	936	234.8	10.3	188221	76	US-11-443-428A-735307	Sequence 735307,
C 864	235	10.3	128034	49	US-10-600-009-187	Sequence 187, App	937	234.8	10.3	188239	76	US-11-443-428A-735314	Sequence 735314,
C 865	235	10.3	134469	59	US-10-918-754-16364	Sequence 16364, A	938	234.8	10.3	188257	76	US-11-443-428A-735299	Sequence 735299,
C 866	235	10.3	134469	90	US-60-495-114-16364	Sequence 16364, A	939	234.8	10.3	188258	76	US-11-443-428A-735310	Sequence 735310,
C 867	235	10.3	135173	1	PCT-US00-27620-76	Sequence 76, Appl	940	234.8	10.3	188261	76	US-11-443-428A-735332	Sequence 735332,
868	235	10.3	179790	35	US-09-948-941-716	Sequence 716, App	941	234.8	10.3	188264	76	US-11-443-428A-735308	Sequence 735308,
869	235	10.3	179790	58	US-10-896-891-716	Sequence 716, App	942	234.8	10.3	188285	76	US-11-443-428A-735335	Sequence 735335,
870	235	10.3	187790	89	US-60-465-241-52660	Sequence 52660, A	943	234.8	10.3	188297	76	US-11-443-428A-735324	Sequence 735324,
871	235	10.3	187790	90	US-60-466-412-87780	Sequence 87780, A	944	234.8	10.3	188300	76	US-11-443-428A-735300	Sequence 735300,
872	235	10.3	187790	90	US-60-485-450-12163	Sequence 12163, A	945	234.8	10.3	188303	76	US-11-443-428A-735320	Sequence 735320,
873	235	10.3	187790	91	US-60-563-440-12163	Sequence 12163, A	946	234.8	10.3	188304	76	US-11-443-428A-735331	Sequence 735331,
874	235	10.3	187790	92	US-60-659-397-12163	Sequence 12163, A	947	234.8	10.3	188321	76	US-11-443-428A-735327	Sequence 735327,
875	235	10.3	190138	59	US-10-932-333-11946	Sequence 11946, A	948	234.8	10.3	188340	76	US-11-443-428A-735323	Sequence 735323,
876	235	10.3	190138	91	US-60-500-315-11946	Sequence 11946, A	949	234.8	10.3	188342	76	US-11-443-428A-735306	Sequence 735306,
877	235	10.3	190138	91	US-60-505-218-7472	Sequence 1472, Ap	950	234.8	10.3	188346	76	US-11-443-428A-735321	Sequence 735321,
878	235	10.3	198138	3	PCT-US04-37982-1087	Sequence 1087, Ap	951	234.8	10.3	188366	76	US-11-443-428A-735309	Sequence 735309,



952	234.8	10.3	188378	76	US-11-443-428A-735298	Sequence 735298,	1025	234.2	10.3	32768	86	US-60-207-954-3	Sequence 3, Appli
953	234.8	10.3	188384	76	US-11-443-428A-735294	Sequence 735294,	1026	234.2	10.3	32768	86	US-60-208-586-3	Sequence 3, Appli
954	234.8	10.3	188385	76	US-11-443-428A-735305	Sequence 735305,	1027	234.2	10.3	32768	86	US-60-212-354-7	Sequence 7, Appli
955	234.8	10.3	188402	76	US-11-443-428A-735301	Sequence 735301,	1028	234.2	10.3	32768	86	US-60-213-164-6	Sequence 6, Appli
956	234.8	10.3	188421	76	US-11-443-428A-735297	Sequence 735297,	1029	234.2	10.3	36799	3	PCT-US04-37982-1416	Sequence 1416, Ap
957	234.8	10.3	188424	76	US-11-443-428A-735319	Sequence 735319,	c1030	234.2	10.3	50836	59	US-10-940-774-16722	Sequence 16722, A
958	234.8	10.3	188427	76	US-11-443-428A-735295	Sequence 735295,	c1031	234.2	10.3	50836	60	US-10-940-774A-16722	Sequence 16722, A
959	234.8	10.3	188448	76	US-11-443-428A-735322	Sequence 735322,	1032	234.2	10.3	67228	61	US-10-990-328-94343	Sequence 94343, A
960	234.8	10.3	188467	76	US-11-443-428A-735318	Sequence 735318,	1033	234.2	10.3	67228	61	US-10-990-328A-94343	Sequence 94343, A
961	234.8	10.3	188505	76	US-11-443-428A-735293	Sequence 735293,	1034	234.2	10.3	125001	92	US-60-660-589-35	Sequence 35, Appl
962	234.8	10.3	188529	76	US-11-443-428A-735296	Sequence 735296,	1035	234.2	10.3	127369	38	US-10-087-192-238	Sequence 238, Appl
963	234.8	10.3	188548	76	US-11-443-428A-735292	Sequence 735292,	1036	234.2	10.3	128978	1	PCT-US01-17423-6	Sequence 6, Appli
C 964	234.8	10.3	400438	3	PCT-US04-07141-8717	Sequence 8717, Ap	1037	234.2	10.3	128978	1	PCT-US02-17423-6	Sequence 6, Appli
C 965	234.8	10.3	400438	57	US-10-796-280-12229	Sequence 12229, A	1038	234.2	10.3	128978	1	PCT-US02-25766-4301	Sequence 4301, Ap
C 966	234.8	10.3	400438	57	US-10-796-307-8717	Sequence 8717, Ap	1039	234.2	10.3	128978	3	PCT-US04-24424-1791	Sequence 1791, Ap
967	234.8	10.3	2556324	35	US-09-947-911-95	Sequence 95, Appl	1040	234.2	10.3	128978	39	US-10-161-453-6	Sequence 6, Appli
968	234.8	10.3	2813043	35	US-09-947-911-103	Sequence 103, Appl	1041	234.2	10.3	128978	48	US-10-567-867-1791	Sequence 1791, Ap
969	234.8	10.3	4604723	35	US-09-947-916-240	Sequence 240, App	1042	234.2	10.3	128978	57	US-10-775-169-345	Sequence 345, App
970	234.6	10.3	6000	94	US-60-873-739-1321	Sequence 1321, Ap	1043	234.2	10.3	128978	57	US-10-775-169A-345	Sequence 345, App
C 971	234.6	10.3	13624	61	US-10-990-328-94132	Sequence 94132, A	1044	234.2	10.3	128978	69	US-11-266-748A-61436	Sequence 61436, A
C 972	234.6	10.3	13624	61	US-10-990-328A-94132	Sequence 94132, A	1045	234.2	10.3	128978	74	US-11-378-923-6	Sequence 6, Appli
C 973	234.6	10.3	33830	61	US-10-990-328-95071	Sequence 95071, A	1046	234.2	10.3	128978	89	US-60-446-133-345	Sequence 345, App
974	234.6	10.3	33830	61	US-10-990-328A-95071	Sequence 95071, A	1047	234.2	10.3	128978	90	US-60-490-890-1791	Sequence 1791, Ap
975	234.6	10.3	58791	90	US-60-466-412-87409	Sequence 87409, A	1048	234.2	10.3	154001	86	US-60-212-664-40	Sequence 40, Appl
C 976	234.6	10.3	60550	61	US-10-990-328-96238	Sequence 96238, A	1049	234.2	10.3	214066	90	US-60-485-450-12239	Sequence 12239, A
C 977	234.6	10.3	60550	61	US-10-990-328A-96238	Sequence 96238, A	1050	234.2	10.3	214066	91	US-60-563-440-12239	Sequence 12239, A
C 978	234.6	10.3	134199	89	US-60-461-762-3394	Sequence 3394, Ap	1051	234.2	10.3	214066	92	US-60-659-397-12239	Sequence 12239, A
C 979	234.6	10.3	134199	90	US-60-466-412-84515	Sequence 84515, A	1052	234.2	10.3	232641	61	US-10-990-328-93650	Sequence 93650, A
C 980	234.6	10.3	134199	90	US-60-470-166-8783	Sequence 8783, Ap	1053	234.2	10.3	232641	61	US-10-990-328A-93650	Sequence 93650, A
C 981	234.6	10.3	146361	61	US-10-990-328-93202	Sequence 93202, A	1054	234.2	10.3	5506356	35	US-09-948-128-429	Sequence 429, App
C 982	234.6	10.3	146361	61	US-10-990-328A-93202	Sequence 93202, A	c1055	234	10.2	966	43	US-10-301-480A-122405	Sequence 122405,
983	234.6	10.3	179024	86	US-60-212-664-182	Sequence 182, App	c1056	234	10.2	966	44	US-10-301-480B-122405	Sequence 122405,
984	234.4	10.3	595	43	US-10-301-480A-301161	Sequence 301161,	c1057	234	10.2	966	45	US-10-301-480C-122405	Sequence 122405,
985	234.4	10.3	595	44	US-10-301-480B-301161	Sequence 301161,	1058	234	10.2	24299	59	US-10-940-774-15452	Sequence 15452, A
986	234.4	10.3	595	45	US-10-301-480C-301161	Sequence 301161,	1059	234	10.2	24299	60	US-10-940-774A-15452	Sequence 15452, A
987	234.4	10.3	6000	94	US-60-873-738-760	Sequence 760, App	1060	234	10.2	31871	1	PCT-US01-01322-1403	Sequence 1403, Ap
988	234.4	10.3	70509	50	US-10-676-684-336	Sequence 336, App	1061	234	10.2	31871	30	US-09-764-847-1403	Sequence 1403, Ap
989	234.4	10.3	169495	66	US-11-121-086-61	Sequence 61, Appl	1062	234	10.2	31871	38	US-10-092-154-1403	Sequence 1403, Ap
990	234.4	10.3	462586	47	US-10-476-264-420	Sequence 420, App	1063	234	10.2	40742	1	PCT-US01-01354-22901	Sequence 22901, A
C 991	234.4	10.3	3037227	35	US-09-947-911-286	Sequence 286, App	1064	234	10.2	40742	1	PCT-US01-01354-34698	Sequence 34698, A
C 992	234.2	10.3	991	43	US-10-301-480A-256275	Sequence 256275,	1065	234	10.2	40742	31	US-09-764-905-22901	Sequence 22901, A
C 993	234.2	10.3	991	44	US-10-301-480B-256275	Sequence 256275,	1066	234	10.2	40742	31	US-09-764-905-34698	Sequence 34698, A
C 994	234.2	10.3	991	45	US-10-301-480C-256275	Sequence 256275,	1067	234	10.2	40742	38	US-10-092-399-22901	Sequence 22901, A
C 995	234.2	10.3	992	43	US-10-301-480A-256276	Sequence 256276,	1068	234	10.2	40742	38	US-10-092-399-34698	Sequence 34698, A
C 996	234.2	10.3	992	44	US-10-301-480B-256276	Sequence 256276,	c1069	234	10.2	67300	87	US-60-243-468-691	Sequence 691, App
C 997	234.2	10.3	992	45	US-10-301-480C-256276	Sequence 256276,	1070	234	10.2	74361	50	US-10-676-684-409	Sequence 409, App
C 998	234.2	10.3	993	42	US-10-301-480-600145	Sequence 600145,	1071	234	10.2	77195	35	US-09-949-003C-4193	Sequence 4193, Ap
C 999	234.2	10.3	993	42	US-10-301-480-1213554	Sequence 1213554,	1072	234	10.2	77695	35	US-09-949-003C-5324	Sequence 5324, Ap
c1000	234.2	10.3	993	43	US-10-301-480A-976214	Sequence 976214,	1073	234	10.2	86164	90	US-60-466-412-87401	Sequence 87401, A
c1001	234.2	10.3	993	44	US-10-301-480B-976214	Sequence 976214,	1074	234	10.2	86361	2	PCT-US03-40977-5702	Sequence 5702, Ap
c1002	234.2	10.3	993	45	US-10-301-480C-976214	Sequence 976214,	1075	234	10.2	86361	2	PCT-US03-40978-17803	Sequence 17803, A
1003	234.2	10.3	5819	59	US-10-940-774-14050	Sequence 14050, A	1076	234	10.2	86361	56	US-10-741-600-17803	Sequence 17803, A
1004	234.2	10.3	5819	60	US-10-940-774A-14050	Sequence 14050, A	1077	234	10.2	86361	56	US-10-741-601-5702	Sequence 5702, Ap
c1005	234.2	10.3	6200	80	US-11-664-374-45	Sequence 45, Appl	1078	234	10.2	86361	61	US-10-995-561-13364	Sequence 13364, A
1006	234.2	10.3	9822	59	US-10-940-774-15697	Sequence 15697, A	1079	234	10.2	86361	91	US-60-524-882-9257	Sequence 9257, Ap
1007	234.2	10.3	9822	59	US-10-940-774A-15697	Sequence 15697, A	1080	234	10.2	135173	1	PCT-US00-27620-76	Sequence 76, Appl
1008	234.2	10.3	9822	60	US-10-940-774A-15697	Sequence 83234, A	1081	234	10.2	143389	66	US-11-112-908-30	Sequence 30, Appl
c1009	234.2	10.3	13818	90	US-60-466-412-83234	Sequence 7492, Ap	1082	234	10.2	143389	93	US-60-724-067-30	Sequence 30, Appl
c1010	234.2	10.3	13970	35	US-09-950-083-7492	Sequence 7492, Ap	1083	234	10.2	143389	93	US-60-725-677-30	Sequence 30, Appl
c1011	234.2	10.3	13970	35	US-09-950-083B-7492	Sequence 9643, Ap	1084	234	10.2	143389	93	US-60-725-989-30	Sequence 30, Appl
c1012	234.2	10.3	13970	39	US-10-105-299-9643	Sequence 7492, Ap	1085	234	10.2	143389	93	US-60-726-029-30	Sequence 30, Appl
c1013	234.2	10.3	13970	58	US-10-868-184-7492	Sequence 7492, Ap	1086	234	10.2	143389	93	US-60-726-030-30	Sequence 30, Appl
c1014	234.2	10.3	13970	58	US-10-868-184B-7492	Sequence 7492, Ap	1087	234	10.2	143389	93	US-60-726-063-30	Sequence 30, Appl
c1015	234.2	10.3	13970	58	US-10-868-184C-7492	Sequence 7492, Ap	1088	234	10.2	150314	66	US-11-112-908-24	Sequence 24, Appl
c1016	234.2	10.3	13970	58	US-10-868-184D-7492	Sequence 7492, Ap	1089	234	10.2	150314	93	US-60-724-067-24	Sequence 24, Appl
c1017	234.2	10.3	13970	58	US-10-868-194B-7492	Sequence 7492, Ap	1090	234	10.2	150314	93	US-60-725-677-24	Sequence 24, Appl
c1018	234.2	10.3	13970	58	US-10-896-164-7492	Sequence 7492, Ap	1091	234	10.2	150314	93	US-60-725-989-24	Sequence 24, Appl
1019	234.2	10.3	17436	90	US-60-466-412-82879	Sequence 82879, A	1092	234	10.2	150314	93	US-60-726-029-24	Sequence 24, Appl
1020	234.2	10.3	17841	90	US-60-466-412-86472	Sequence 86472, A	1093	234	10.2	150314	93	US-60-726-030-24	Sequence 24, Appl
1021	234.2	10.3	17880	59	US-10-932-349-19378	Sequence 19378, A	1094	234	10.2	150314	93	US-60-726-063-24	Sequence 24, Appl
1022	234.2	10.3	17880	91	US-60-500-337-19378	Sequence 36084, A	1095	234	10.2	220895	57	US-10-756-149-723	Sequence 723, App
c1023	234.2	10.3	29331	62	US-11-033-056A-36084	Sequence 36084, A	1096	234	10.2	220895	57	US-10-775-169-88	Sequence 88, Appl
1024	234.2	10.3	32768	86	US-60-207-421-8	Sequence 8, Appli	1097	234	10.2	220895	57	US-10-775-169A-88	Sequence 88, Appl



1098	234	10.2	220895	89	US-60-446-133-88	Sequence 88, Appl	c1171	233.4	10.2	17526	90	US-60-466-412-83077	Sequence 83077, A
c1099	234	10.2	312453	62	US-11-033-056A-36041	Sequence 36041, A	1172	233.4	10.2	18836	86	US-60-212-358-80	Sequence 80, Appl
c1100	234	10.2	4057573	35	US-09-948-128-219	Sequence 219, App	1173	233.4	10.2	19739	61	US-10-990-328-97775	Sequence 97775, A
1101	233.8	10.2	601	59	US-10-940-774-18060	Sequence 18060, A	1174	233.4	10.2	19739	61	US-10-990-328A-97775	Sequence 97775, A
1102	233.8	10.2	601	59	US-10-940-774-197087	Sequence 197087, A	c1175	233.4	10.2	27702	59	US-10-940-774-11795	Sequence 11795, A
1103	233.8	10.2	601	60	US-10-940-774A-18060	Sequence 18060, A	c1176	233.4	10.2	27702	60	US-10-940-774A-11795	Sequence 11795, A
1104	233.8	10.2	601	60	US-10-940-774A-197087	Sequence 197087, A	1177	233.4	10.2	32278	59	US-10-940-774-14575	Sequence 14575, A
1105	233.8	10.2	2300	3	PCT-US06-46920-29032	Sequence 29032, A	1178	233.4	10.2	32278	60	US-10-940-774A-14575	Sequence 14575, A
1106	233.8	10.2	2300	80	US-11-636-385-29032	Sequence 29032, A	c1179	233.4	10.2	32768	86	US-60-208-084-7	Sequence 7, Appli
1107	233.8	10.2	2300	80	US-11-636-385A-29032	Sequence 29032, A	c1180	233.4	10.2	32768	86	US-60-208-596-9	Sequence 9, Appli
1108	233.8	10.2	2300	93	US-60-762-056-29032	Sequence 29032, A	c1181	233.4	10.2	32768	86	US-60-208-596-10	Sequence 10, Appl
1109	233.8	10.2	6000	94	US-60-873-738-1055	Sequence 1055, Ap	1182	233.4	10.2	32768	86	US-60-212-413-98	Sequence 98, Appl
c1110	233.8	10.2	6000	94	US-60-873-739-1001	Sequence 1001, Ap	1183	233.4	10.2	32768	86	US-60-213-162-32	Sequence 32, Appl
c1111	233.8	10.2	6000	94	US-60-873-883-690	Sequence 690, App	1184	233.4	10.2	32768	86	US-60-213-177-285	Sequence 285, App
1112	233.8	10.2	7001	2	PCT-US03-37493-17	Sequence 17, Appl	c1185	233.4	10.2	32768	86	US-60-229-512-56	Sequence 56, Appl
1113	233.8	10.2	7001	45	US-10-304-116-15	Sequence 15, Appl	1186	233.4	10.2	32768	86	US-60-230-445-193	Sequence 193, App
1114	233.8	10.2	17803	59	US-10-918-754-16912	Sequence 16912, A	1187	233.4	10.2	32768	86	US-60-230-445-673	Sequence 673, App
1115	233.8	10.2	17803	90	US-60-495-114-16912	Sequence 16912, A	1188	233.4	10.2	32768	86	US-60-233-644-16	Sequence 16, Appl
1116	233.8	10.2	17825	89	US-60-465-241-51905	Sequence 51905, A	c1189	233.4	10.2	42697	86	US-60-212-664-214	Sequence 214, App
1117	233.8	10.2	17825	90	US-60-466-412-85094	Sequence 85094, A	c1190	233.4	10.2	112046	35	US-09-949-003C-4143	Sequence 4143, Ap
1118	233.8	10.2	18032	59	US-10-932-349-19145	Sequence 19145, A	c1191	233.4	10.2	160576	86	US-60-212-664-300	Sequence 300, App
1119	233.8	10.2	18032	91	US-60-500-337-19145	Sequence 19145, A	1192	233.4	10.2	215281	2	PCT-US04-02652-10745	Sequence 10745, A
1120	233.8	10.2	23256	35	US-09-949-003C-4354	Sequence 4354, Ap	1193	233.4	10.2	215281	57	US-10-767-471-10745	Sequence 10745, A
1121	233.8	10.2	24573	90	US-60-466-412-83548	Sequence 83548, A	1194	233.4	10.2	232234	61	US-10-990-328-93684	Sequence 93684, A
1122	233.8	10.2	25284	61	US-10-990-328-93630	Sequence 93630, A	1195	233.4	10.2	232234	61	US-10-990-328A-93684	Sequence 93684, A
1123	233.8	10.2	25284	61	US-10-990-328A-93630	Sequence 93630, A	c1196	233.4	10.2	2132949	62	US-11-033-056A-38500	Sequence 38500, A
c1124	233.8	10.2	32636	86	US-60-229-518-189	Sequence 189, App	c1197	233.4	10.2	3436920	35	US-09-947-911-49	Sequence 49, Appl
c1125	233.8	10.2	32674	86	US-60-212-413-133	Sequence 133, App	c1198	233.4	10.2	3928194	35	US-09-947-911-317	Sequence 317, App
c1126	233.8	10.2	43172	3	PCT-US04-37982-1095	Sequence 1095, Ap	1199	233.4	10.2	8885655	35	US-09-947-916-97	Sequence 97, Appl
c1127	233.8	10.2	103665	2	PCT-US03-41389-680	Sequence 680, App	c1200	233.2	10.2	444	24	US-09-528-409-82728	Sequence 82728, A
c1128	233.8	10.2	103665	46	US-10-330-773-680	Sequence 680, App	c1201	233.2	10.2	444	34	US-09-933-524-82728	Sequence 82728, A
c1129	233.8	10.2	103665	46	US-10-330-773A-680	Sequence 680, App	c1202	233.2	10.2	444	35	US-09-933-524A-82728	Sequence 82728, A
c1130	233.8	10.2	103665	48	US-10-540-898-680	Sequence 680, App	1203	233.2	10.2	477	29	US-09-698-010-9384	Sequence 9384, Ap
c1131	233.8	10.2	103665	75	US-11-403-116-680	Sequence 680, App	c1204	233.2	10.2	711	43	US-10-301-480A-374494	Sequence 374494,
1132	233.8	10.2	104073	62	US-11-033-056A-37679	Sequence 37679, A	c1205	233.2	10.2	711	44	US-10-301-480B-374494	Sequence 374494,
1133	233.8	10.2	104073	62	US-11-033-056A-37958	Sequence 37958, A	c1206	233.2	10.2	711	45	US-10-301-480C-374494	Sequence 374494,
c1134	233.8	10.2	107603	3	PCT-US05-10257-315	Sequence 315, App	1207	233.2	10.2	1701	80	US-11-641-626-9	Sequence 9, Appli
1135	233.8	10.2	177528	89	US-60-449-629-846	Sequence 846, App	c1208	233.2	10.2	2300	3	PCT-US06-46920-10226	Sequence 10226, A
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1	238.2	10.4 155470 6	US-10-910-811B-373 Sequence 373, App
2	238.2	10.4 155470 6	US-10-945-565B-373 Sequence 373, App
3	231.4	10.1 267966 7	US-11-852-912-1 Sequence 1, Appli
C 4	225.2	9.9 6000 1	PCT-US07-13803-146 Sequence 146, App
C 5	221.6	9.7 408 7	US-11-881-406-1278 Sequence 1278, Ap
C 6	221.6	9.7 3102 7	US-11-574-839-13 Sequence 13, Appl
C 7	221	9.7 74424 7	US-11-829-279-153 Sequence 153, App
C 8	220	9.6 6000 1	PCT-US07-13803-189 Sequence 189, App
9	219.2	9.6 1254 7	US-11-781-665-1823 Sequence 1823, Ap
C 10	219	9.6 6000 1	PCT-US06-25800-39 Sequence 39, Appl
11	218.4	9.6 130001 1	PCT-US07-13803-226 Sequence 226, App
12	217.8	9.5 6000 1	US-11-757-860-1 Sequence 1, Appli
13	217.6	9.5 11190 7	US-10-590-043-1 Sequence 1, Appli
14	217.2	9.5 5687 6	US-10-590-043-1 Sequence 9, Appli
15	217.2	9.5 24255 8	US-11-781-665-770 Sequence 770, App
16	217	9.5 1154 7	US-11-781-665-15 Sequence 15, Appl
C 17	217	9.5 6000 1	PCT-US07-13803-15 Sequence 253, App
C 18	217	9.5 6000 1	PCT-US07-13803-253 Sequence 556, App
C 19	216.4	9.5 2996 7	US-11-884-496-556 Sequence 29, Appl
20	216	9.5 6000 1	PCT-US07-13803-29 Sequence 256, App
21	216	9.5 6000 1	PCT-US07-13803-256 Sequence 2139, Ap
22	216	9.5 6928 7	US-11-490-374A-2139 Sequence 1, Appli
C 23	214.8	9.4 267966 7	US-11-852-912-1 Sequence 2560, Ap
C 24	214.6	9.4 1586 7	US-11-781-665-2560 Sequence 2561, Ap
C 25	214.6	9.4 1703 7	US-11-781-665-2561 Sequence 7, Appli
26	214.6	9.4 14001 7	US-11-851-267-7 Sequence 7, Appli

C 27	214.2	9.4	986	7	US-11-781-665-2842	Sequence 2842, Ap
C 28	214	9.4	1292	7	US-11-781-665-2507	Sequence 2507, Ap
C 29	214	9.4	1292	7	US-11-781-665-2508	Sequence 2508, Ap
C 30	214	9.4	155470	6	US-10-910-811B-373	Sequence 373, App
C 31	214	9.4	155470	6	US-10-945-565B-373	Sequence 373, App
C 32	213.8	9.4	92384	7	US-11-328-881A-80	Sequence 80, Appl
C 33	213.6	9.4	130001	1	PCT-US06-25800-39	Sequence 39, Appl
34	213.4	9.3	6907	7	US-11-490-374A-2138	Sequence 2138, Ap
35	213	9.3	28001	7	US-11-889-507-3	Sequence 3, Appli
36	212.8	9.3	6000	1	PCT-US07-13803-262	Sequence 262, App
37	212.4	9.3	6000	1	PCT-US07-13803-71	Sequence 71, Appl
C 38	212.4	9.3	11190	7	US-11-757-860-1	Sequence 1, Appli
C 39	212.2	9.3	6000	1	PCT-US07-13803-217	Sequence 217, App
40	211.8	9.3	173637	7	US-11-060-659A-37	Sequence 37, Appl
C 41	211.4	9.3	1001	7	US-11-881-406-1948	Sequence 1948, Ap
C 42	211.2	9.2	6000	1	PCT-US07-13803-53	Sequence 53, Appl
C 43	210.8	9.2	2314	7	US-11-781-665-3059	Sequence 3059, Ap
C 44	210.2	9.2	6000	1	PCT-US07-13803-127	Sequence 127, App
45	210.2	9.2	165589	7	US-11-328-881A-81	Sequence 81, Appl
C 46	210	9.2	6000	1	PCT-US07-13803-50	Sequence 50, Appl
C 47	210	9.2	24255	8	US-60-970-396-9	Sequence 9, Appli
C 48	210	9.2	74424	7	US-11-829-279-153	Sequence 153, App
C 49	209.6	9.2	1134	7	US-11-781-665-1744	Sequence 1744, Ap
C 50	209.6	9.2	6000	1	PCT-US07-13803-165	Sequence 165, App
C 51	209.6	9.2	8456	1	PCT-US07-13803-415	Sequence 415, App
C 52	209.2	9.2	6000	1	PCT-US07-13803-51	Sequence 51, Appl
53	209	9.2	6000	1	PCT-US07-13803-169	Sequence 169, App
C 54	209	9.2	79666	7	US-11-881-406-1	Sequence 1, Appli
C 55	209	9.2	89728	7	US-11-328-881A-83	Sequence 83, Appl
56	208.6	9.1	6000	1	PCT-US07-13803-106	Sequence 106, App
57	208.4	9.1	6000	1	PCT-US07-13803-236	Sequence 236, App
58	208.4	9.1	6000	1	PCT-US07-13803-249	Sequence 249, App
59	208	9.1	2001	7	US-11-881-406-3829	Sequence 3829, Ap
60	208	9.1	2001	7	US-11-881-406-3833	Sequence 3833, Ap
C 61	208	9.1	6000	1	PCT-US07-13803-55	Sequence 55, Appl
C 62	208	9.1	165589	7	US-11-328-881A-81	Sequence 81, Appl
63	207.8	9.1	382	7	US-11-881-406-2415	Sequence 2415, Ap
64	207.6	9.1	1504	7	US-11-235-701A-350	Sequence 350, App
C 65	207.6	9.1	6670	7	US-11-782-310-34	Sequence 34, Appl
C 66	207.6	9.1	60401	1	PCT-US06-25800-36	Sequence 36, Appl
67	207.4	9.1	2001	7	US-11-881-406-3889	Sequence 3889, Ap
68	207.4	9.1	2001	7	US-11-881-406-3890	Sequence 3890, Ap
C 69	207.2	9.1	1839	7	US-11-781-665-560	Sequence 560, App
C 70	207.2	9.1	173637	7	US-11-060-659A-37	Sequence 37, Appl
C 71	207	9.1	2148	7	US-11-781-665-1183	Sequence 1183, Ap
C 72	207	9.1	5466	7	US-11-490-374A-1510	Sequence 1510, Ap
C 73	207	9.1	6000	1	PCT-US07-13803-6	Sequence 6, Appli
74	207	9.1	6000	1	PCT-US07-13803-16	Sequence 16, Appl
C 75	207	9.1	6000	1	PCT-US07-13803-163	Sequence 163, App
76	207	9.1	6000	1	PCT-US07-13803-265	Sequence 265, App
C 77	207	9.1	21001	1	PCT-US07-75297-3	Sequence 3, Appli
78	206.8	9.1	1001	7	US-11-781-665-193	Sequence 193, App
C 79	206.8	9.1	6000	1	PCT-US07-13803-58	Sequence 58, Appl
C 80	206.8	9.1	6000	1	PCT-US07-13803-149	Sequence 149, App
C 81	206.8	9.1	6000	1	PCT-US07-13803-158	Sequence 158, App
C 82	206.6	9.0	6000	1	PCT-US07-13803-86	Sequence 86, Appl
C 83	206.6	9.0	6000	1	PCT-US07-13803-204	Sequence 204, Appl
C 84	206.2	9.0	735	7	US-11-781-665-1535	Sequence 1535, Ap
C 85	206	9.0	6000	1	PCT-US07-13803-197	Sequence 197, App
86	205.8	9.0	322	6	US-10-594-597-99	Sequence 99, Appl
C 87	205.8	9.0	929	7	US-11-781-665-918	Sequence 918, App
88	205.8	9.0	6000	1	PCT-US07-13803-233	Sequence 233, App
C 89	205.8	9.0	14001	7	US-11-851-267-7	Sequence 7, Appli
C 90	205.6	9.0	2446	1	PCT-US07-13803-494	Sequence 494, App
C 91	205.6	9.0	6000	1	PCT-US07-13803-126	Sequence 126, App
C 92	205.6	9.0	167253	7	US-11-328-881A-82	Sequence 82, Appl
C 93	205.6	9.0	168323	7	US-11-328-881A-84	Sequence 84, Appl
C 94	205.2	9.0	1270	7	US-11-781-665-605	Sequence 605, App
C 95	205.2	9.0	6000	1	PCT-US07-13803-62	Sequence 62, Appl
96	205.2	9.0	6000	1	PCT-US07-13803-220	Sequence 220, App
97	205.2	9.0	79666	7	US-11-881-406-1	Sequence 1, Appli
98	205	9.0	6000	1	PCT-US07-13803-124	Sequence 124, App
99	205	9.0	6000	1	PCT-US07-13803-170	Sequence 170, App

C 100	204.8	9.0	1538	7	US-11-781-665-568	Sequence 568, App	C 173	200.6	8.8	2129	7	US-11-781-665-1677	Sequence 1677, Ap
C 101	204.8	9.0	1572	7	US-11-831-404-48	Sequence 48, Appl	174	200.4	8.8	6000	1	PCT-US07-13803-248	Sequence 248, App
C 102	204.8	9.0	1932	7	US-11-781-665-1962	Sequence 1962, Ap	175	200	8.8	4121	7	US-11-885-002-1	Sequence 1, Appli
C 103	204.8	9.0	3682	7	US-11-831-404-38	Sequence 38, Appl	176	200	8.8	5225	7	US-11-734-562-3	Sequence 3, Appli
C 104	204.6	9.0	748	7	US-11-781-665-2057	Sequence 2057, Ap	C 177	199.8	8.7	825	7	US-11-781-665-2185	Sequence 2185, Ap
C 105	204.4	8.9	787	7	US-11-781-665-2273	Sequence 2273, Ap	C 178	199.8	8.7	1139	7	US-11-781-665-774	Sequence 774, App
C 106	204.4	8.9	1277	7	US-11-781-665-214	Sequence 214, App	C 179	199.8	8.7	1600	7	US-11-781-665-2966	Sequence 2966, Ap
C 107	204.4	8.9	3347	1	PCT-US07-13803-296	Sequence 296, App	180	199.8	8.7	6000	1	PCT-US07-13803-15	Sequence 15, Appl
C 108	204.4	8.9	3347	1	PCT-US07-13803-441	Sequence 441, App	181	199.8	8.7	6000	1	PCT-US07-13803-253	Sequence 253, App
C 109	204.4	8.9	6000	1	PCT-US07-13803-189	Sequence 189, App	182	199.8	8.7	6594	1	PCT-US07-13803-509	Sequence 509, App
C 110	204.4	8.9	6000	1	PCT-US07-13803-257	Sequence 257, App	C 183	199.6	8.7	798	7	US-11-781-665-2933	Sequence 2933, Ap
C 111	204.4	8.9	33780	6	US-10-148-848D-4	Sequence 4, Appli	C 184	199.4	8.7	6000	1	PCT-US07-13803-235	Sequence 235, App
C 112	204.2	8.9	415	7	US-11-881-406-1457	Sequence 1457, Ap	C 185	199.2	8.7	6000	1	PCT-US07-13803-10	Sequence 10, Appl
C 113	204.2	8.9	812	7	US-11-781-665-2567	Sequence 2567, Ap	C 186	199.2	8.7	28001	7	US-11-889-507-3	Sequence 3, Appli
C 114	204.2	8.9	1487	7	US-11-235-701A-351	Sequence 351, App	C 187	199	8.7	1036	7	US-11-781-665-1682	Sequence 1682, Ap
C 115	204.2	8.9	6000	1	PCT-US07-13803-232	Sequence 232, App	C 188	199	8.7	3620	7	US-11-781-665-1912	Sequence 1912, Ap
C 116	204	8.9	776	7	US-11-781-665-2968	Sequence 2968, Ap	189	199	8.7	3627	6	US-10-858-887A-6	Sequence 6, Appli
C 117	204	8.9	6000	1	PCT-US07-13803-172	Sequence 172, App	190	199	8.7	6000	1	PCT-US07-13803-6	Sequence 6, Appli
C 118	204	8.9	7239	7	US-11-794-690-28	Sequence 28, Appl	C 191	199	8.7	6000	1	PCT-US07-13803-239	Sequence 239, App
C 119	204	8.9	13001	1	PCT-US06-25800-38	Sequence 38, Appl	C 192	199	8.7	6000	1	PCT-US07-13803-257	Sequence 257, App
C 120	204	8.9	89728	7	US-11-328-881A-83	Sequence 83, Appl	C 193	199	8.7	6000	1	PCT-US07-13803-264	Sequence 264, App
C 121	203.8	8.9	901	7	US-11-781-665-322	Sequence 322, App	194	198.6	8.7	6000	1	PCT-US07-13803-230	Sequence 230, App
C 122	203.8	8.9	6000	1	PCT-US07-13803-12	Sequence 12, Appl	195	198.4	8.7	6000	1	PCT-US07-13803-200	Sequence 200, App
C 123	203.8	8.9	6000	1	PCT-US07-13803-82	Sequence 82, Appl	C 196	198.2	8.7	390	7	US-11-881-406-3398	Sequence 3398, Ap
C 124	203.8	8.9	6000	1	PCT-US07-13803-139	Sequence 139, App	197	198.2	8.7	392	7	US-11-881-406-3174	Sequence 3174, Ap
C 125	203.6	8.9	389	7	US-11-881-406-1668	Sequence 1668, Ap	198	198.2	8.7	2001	7	US-11-881-406-3178	Sequence 3178, Ap
C 126	203.6	8.9	1733	7	US-11-781-665-557	Sequence 557, App	C 199	198.2	8.7	6000	1	PCT-US07-13803-109	Sequence 109, App
C 127	203.4	8.9	824	7	US-11-781-665-2707	Sequence 2707, Ap	200	198.2	8.7	6000	1	PCT-US07-13803-224	Sequence 224, App
C 128	203.4	8.9	16015	7	US-11-885-002-74	Sequence 74, Appl	C 201	198	8.7	1753	7	US-11-781-665-2603	Sequence 2603, Ap
C 129	203	8.9	2887	7	US-11-825-627-350	Sequence 350, App	202	198	8.7	6000	1	PCT-US07-13803-12	Sequence 12, Appl
C 130	203	8.9	6000	1	PCT-US07-13803-40	Sequence 40, Appl	203	198	8.7	6000	1	PCT-US07-13803-82	Sequence 82, Appl
C 131	203	8.9	6000	1	PCT-US07-13803-178	Sequence 178, App	C 204	197.8	8.7	695	7	US-11-781-665-2543	Sequence 2543, Ap
C 132	203	8.9	6000	1	PCT-US07-13803-241	Sequence 241, App	C 205	197.8	8.7	1440	7	US-11-781-665-2970	Sequence 2970, Ap
C 133	202.8	8.9	1862	7	US-11-781-665-2597	Sequence 2597, Ap	C 206	197.8	8.7	1796	7	US-11-781-665-1624	Sequence 1624, Ap
C 134	202.8	8.9	6000	1	PCT-US07-13803-260	Sequence 260, App	C 207	197.8	8.7	6000	1	PCT-US07-13803-22	Sequence 22, Appl
C 135	202.6	8.9	6000	1	PCT-US07-13803-269	Sequence 269, App	C 208	197.8	8.7	6000	1	PCT-US07-13803-23	Sequence 23, Appl
C 136	202.4	8.9	6000	1	PCT-US07-13803-258	Sequence 258, App	C 209	197.8	8.7	6000	1	PCT-US07-13803-77	Sequence 77, Appl
C 137	202.2	8.9	721	7	US-11-781-665-403	Sequence 403, App	210	197.8	8.7	6000	1	PCT-US07-13803-117	Sequence 117, App
C 138	202.2	8.9	1298	7	US-11-781-665-2962	Sequence 2962, Ap	C 211	197.6	8.7	868	7	US-11-781-665-1862	Sequence 1862, Ap
C 139	202.2	8.9	6000	1	PCT-US07-13803-69	Sequence 69, Appl	C 212	197.6	8.7	6000	1	PCT-US07-13803-93	Sequence 93, Appl
C 140	202.2	8.9	6000	1	PCT-US07-13803-73	Sequence 73, Appl	C 213	197.4	8.6	779	7	US-11-781-665-1794	Sequence 1794, Ap
C 141	202	8.8	6000	1	PCT-US07-13803-39	Sequence 39, Appl	C 214	197.4	8.6	1325	7	US-11-881-406-3440	Sequence 3440, Ap
C 142	201.8	8.8	924	7	US-11-781-665-1110	Sequence 1110, Ap	215	197.4	8.6	1585	7	US-11-781-665-628	Sequence 628, App
C 143	201.8	8.8	1092	7	US-11-781-665-2633	Sequence 2633, Ap	C 216	197.4	8.6	2001	7	US-11-881-406-3437	Sequence 3437, App
C 144	201.8	8.8	3497	7	US-11-816-601-791	Sequence 791, App	217	197.4	8.6	2001	7	US-11-881-406-3441	Sequence 3441, Ap
C 145	201.8	8.8	5077	7	US-11-781-665-2326	Sequence 2326, Ap	218	197.2	8.6	421	7	US-11-881-406-1370	Sequence 1370, Ap
C 146	201.8	8.8	6000	1	PCT-US07-13803-39	Sequence 39, Appl	219	197	8.6	6000	1	PCT-US07-13803-217	Sequence 217, App
C 147	201.8	8.8	6000	1	PCT-US07-13803-121	Sequence 121, App	C 220	196.8	8.6	6000	1	PCT-US07-13803-252	Sequence 252, App
C 148	201.8	8.8	6000	1	PCT-US07-13803-140	Sequence 140, App	C 221	196.8	8.6	7468	1	PCT-US07-73799-2	Sequence 2, Appli
C 149	201.8	8.8	6000	1	PCT-US07-13803-207	Sequence 207, App	C 222	196.8	8.6	8194	7	US-11-797-156-15	Sequence 15, Appl
C 150	201.6	8.8	1388	7	US-11-781-665-1127	Sequence 1127, Ap	C 223	196.8	8.6	8194	7	US-11-745-857-15	Sequence 15, Appl
C 151	201.6	8.8	5687	6	US-10-590-043-1	Sequence 1, Appli	C 224	196.8	8.6	13001	1	PCT-US06-25800-38	Sequence 38, Appl
C 152	201.4	8.8	640	7	US-11-781-665-2356	Sequence 2356, Ap	225	196.6	8.6	1786	7	US-11-781-665-890	Sequence 890, App
C 153	201.4	8.8	1475	7	US-11-781-665-2174	Sequence 2174, Ap	C 226	196.6	8.6	4145	7	US-11-816-601-28	Sequence 28, Appl
C 154	201.4	8.8	6000	1	PCT-US07-13803-181	Sequence 181, App	C 227	196.6	8.6	6000	1	PCT-US07-13803-28	Sequence 28, Appl
C 155	201.2	8.8	1133	7	US-11-781-665-2829	Sequence 2829, Ap	C 228	196.6	8.6	6000	1	PCT-US07-13803-268	Sequence 268, App
C 156	201.2	8.8	1467	7	US-11-235-701A-352	Sequence 352, App	229	196.6	8.6	7392	7	US-11-060-659A-55	Sequence 55, Appl
C 157	201.2	8.8	3177	7	US-11-884-496-709	Sequence 709, App	230	196.6	8.6	167253	7	US-11-328-881A-82	Sequence 82, Appl
C 158	201.2	8.8	3177	7	US-11-908-114-4	Sequence 4, Appli	C 231	196.4	8.6	1551	7	US-11-781-665-812	Sequence 812, App
C 159	201	8.8	1345	7	US-11-781-665-772	Sequence 772, App	232	196.4	8.6	6000	1	PCT-US07-13803-254	Sequence 254, App
C 160	201	8.8	5170	7	US-11-733-861-62	Sequence 62, Appl	C 233	196.2	8.6	420	7	US-11-881-406-2349	Sequence 2349, Ap
C 161	201	8.8	6000	1	PCT-US07-13803-42	Sequence 42, Appl	C 234	196.2	8.6	1309	7	US-11-781-665-1437	Sequence 1437, Ap
C 162	201	8.8	6000	1	PCT-US07-13803-54	Sequence 54, Appl	235	196.2	8.6	2020	7	US-11-816-601-92	Sequence 92, Appl
C 163	201	8.8	6000	1	PCT-US07-13803-88	Sequence 88, Appl	C 236	196	8.6	2242	1	PCT-US07-13803-409	Sequence 409, App
C 164	201	8.8	6000	1	PCT-US07-13803-89	Sequence 89, Appl	237	196	8.6	6000	1	PCT-US07-13803-27	Sequence 27, Appl
C 165	201	8.8	6000	1	PCT-US07-13803-90	Sequence 90, Appl	238	196	8.6	6000	1	PCT-US07-13803-41	Sequence 41, Appl
C 166	201	8.8	6000	1	PCT-US07-13803-153	Sequence 153, App	239	196	8.6	6000	1	PCT-US07-13803-132	Sequence 132, App
C 167	201	8.8	6000	1	PCT-US07-13803-159	Sequence 159, App	C 240	195.8	8.6	1671	7	US-11-781-665-1694	Sequence 1694, Ap
C 168	201	8.8	6000	1	PCT-US07-13803-165	Sequence 165, App	C 241	195.8	8.6	2001	7	US-11-881-406-3652	Sequence 3652, Ap
C 169	201	8.8	6000	1	PCT-US07-13803-208	Sequence 208, App	C 242	195.8	8.6	2001	7	US-11-881-406-3653	Sequence 3653, Ap
C 170	201	8.8	33780	6	US-10-148-848D-4	Sequence 4, Appli	C 243	195.8	8.6	2001	7	US-11-881-406-3654	Sequence 3654, Ap
C 171	200.8	8.8	6000	1	PCT-US07-13803-176	Sequence 176, App	C 244	195.8	8.6	2001	7	US-11-881-406-3655	Sequence 3655, Ap
C 172	200.8	8.8	6000	1	PCT-US07-13803-201	Sequence 201, App	245	195.8	8.6	2310	7	US-11-781-665-2433	Sequence 2433, Ap

c 246	195.8	8.6	6000	1	PCT-US07-13803-194	Sequence 194, App	Sequence 194, App
c 247	195.6	8.6	653	7	US-11-781-665-2228	Sequence 2228, Ap	Sequence 2228, Ap
248	195.6	8.6	6000	1	PCT-US07-13803-17	Sequence 17, Appl	Sequence 7, Appli
c 249	195.6	8.6	6000	1	PCT-US07-13803-150	Sequence 150, App	Sequence 205, App
250	195.6	8.6	6000	1	PCT-US07-13803-251	Sequence 251, App	Sequence 1098, Ap
c 251	195.4	8.6	421	7	US-11-881-406-2046	Sequence 2046, Ap	Sequence 208, App
c 252	195.2	8.5	1090	7	US-11-781-665-2840	Sequence 2840, Ap	Sequence 261, App
c 253	195.2	8.5	2259	7	US-11-781-665-2852	Sequence 2852, Ap	Sequence 2418, Ap
254	195	8.5	4038	7	US-11-781-665-1741	Sequence 1741, Ap	Sequence 83, Appl
c 255	194.8	8.5	1157	7	US-11-781-665-2202	Sequence 2202, Ap	Sequence 79, Appl
c 256	194.8	8.5	1528	7	US-11-781-665-1993	Sequence 1993, Ap	Sequence 81, Appl
c 257	194.8	8.5	2632	7	US-11-781-665-206	Sequence 206, App	Sequence 368, App
c 258	194.8	8.5	3599	7	US-11-908-113-5	Sequence 5, Appli	Sequence 170, App
259	194.8	8.5	3599	7	US-11-908-114-17	Sequence 17, Appl	Sequence 2916, Ap
c 260	194.8	8.5	6000	1	PCT-US07-13803-68	Sequence 68, Appl	Sequence 701, App
c 261	194.8	8.5	6000	1	PCT-US07-13803-205	Sequence 205, App	Sequence 1657, Ap
c 262	194.6	8.5	1075	7	US-11-781-665-2903	Sequence 2903, Ap	Sequence 1951, Ap
c 263	194.6	8.5	2253	7	US-11-781-665-2079	Sequence 2079, Ap	Sequence 218, App
264	194.6	8.5	6000	1	PCT-US07-13803-186	Sequence 186, App	Sequence 218, App
c 265	194.4	8.5	1149	7	US-11-781-665-2265	Sequence 2265, Ap	Sequence 1788, Ap
c 266	194.4	8.5	1425	7	US-11-781-665-874	Sequence 874, App	Sequence 2047, Ap
c 267	194.4	8.5	1634	7	US-11-781-665-2327	Sequence 2327, Ap	Sequence 6, Appli
c 268	194.4	8.5	1780	7	US-11-781-665-916	Sequence 916, App	Sequence 16, Appl
c 269	194.2	8.5	759	7	US-11-781-665-2206	Sequence 2206, Ap	Sequence 1725, Ap
c 270	194.2	8.5	1325	7	US-11-781-665-2832	Sequence 2832, Ap	Sequence 22, Appl
c 271	194.2	8.5	2859	7	US-11-848-462-5	Sequence 5, Appli	Sequence 23, Appl
c 272	194.2	8.5	4517	6	US-10-514-040B-3	Sequence 3, Appli	Sequence 636, App
c 273	194	8.5	908	7	US-11-781-665-364	Sequence 364, App	Sequence 2918, Ap
274	194	8.5	1377	7	US-11-781-665-1441	Sequence 1441, Ap	Sequence 914, App
c 275	194	8.5	2001	7	US-11-881-406-3800	Sequence 3800, Ap	Sequence 58, Appl
c 276	194	8.5	6000	1	PCT-US07-13803-31	Sequence 31, Appl	Sequence 158, App
c 277	194	8.5	6000	1	PCT-US07-13803-255	Sequence 255, App	Sequence 3953, Ap
c 278	193.8	8.5	822	7	US-11-881-406-3828	Sequence 3828, Ap	Sequence 2215, Ap
c 279	193.8	8.5	1399	7	US-11-781-665-2892	Sequence 2892, Ap	Sequence 2556, Ap
c 280	193.8	8.5	1572	7	US-11-781-665-2059	Sequence 2059, Ap	Sequence 179, App
c 281	193.8	8.5	1593	7	US-11-781-665-2607	Sequence 2607, Ap	Sequence 3776, Ap
c 282	193.8	8.5	1891	7	US-11-781-665-64	Sequence 64, Appl	Sequence 184, App
c 283	193.8	8.5	6000	1	PCT-US07-13803-121	Sequence 121, App	Sequence 2222, Ap
c 284	193.6	8.5	2001	7	US-11-881-406-3619	Sequence 3619, Ap	Sequence 511, App
c 285	193.6	8.5	2001	7	US-11-881-406-3620	Sequence 3620, Ap	Sequence 106, App
c 286	193.6	8.5	2001	7	US-11-881-406-3656	Sequence 3656, Ap	Sequence 994, App
c 287	193.6	8.5	2339	4	US-08-444-791C-3	Sequence 3, Appli	Sequence 116, App
c 288	193.6	8.5	8194	7	US-11-797-156-15	Sequence 15, Appl	Sequence 303, App
c 289	193.6	8.5	8194	7	US-11-745-857-15	Sequence 15, Appl	Sequence 1, Appli
c 290	193.4	8.5	909	7	US-11-781-665-1936	Sequence 1936, Ap	Sequence 147, App
c 291	193.4	8.5	1446	7	US-11-781-665-1781	Sequence 1781, Ap	Sequence 721, App
c 292	193.4	8.5	6000	1	PCT-US07-13803-96	Sequence 96, Appl	Sequence 80, Appl
c 293	193.2	8.5	788	7	US-11-781-665-1327	Sequence 1327, Ap	Sequence 1829, Ap
c 294	193.2	8.5	3610	7	US-11-908-113-4	Sequence 4, Appli	Sequence 1145, Ap
c 295	193.2	8.5	6000	1	PCT-US07-13803-11	Sequence 11, Appl	Sequence 2108, Ap
c 296	193.2	8.5	6000	1	PCT-US07-13803-54	Sequence 54, Appl	Sequence 2110, Ap
c 297	193.2	8.5	6000	1	PCT-US07-13803-60	Sequence 60, Appl	Sequence 3872, Ap
c 298	193.2	8.5	6042	7	US-11-302-202A-34	Sequence 34, Appl	Sequence 76, Appl
c 299	193	8.5	6000	1	PCT-US07-13803-32	Sequence 32, Appl	Sequence 195, App
c 300	193	8.5	6000	1	PCT-US07-13803-266	Sequence 266, App	Sequence 202, App
c 301	193	8.5	6000	1	PCT-US07-13803-267	Sequence 267, App	Sequence 946, App
c 302	192.8	8.4	1319	7	US-11-781-665-1971	Sequence 1971, Ap	Sequence 2150, Ap
c 303	192.8	8.4	2001	7	US-11-881-406-3282	Sequence 3282, Ap	Sequence 1057, Ap
c 304	192.8	8.4	6000	1	PCT-US07-13803-24	Sequence 24, Appl	Sequence 2516, Ap
c 305	192.8	8.4	6000	1	PCT-US07-13803-71	Sequence 71, Appl	Sequence 2907, Ap
c 306	192.8	8.4	6000	1	PCT-US07-13803-86	Sequence 86, Appl	Sequence 10, Appl
c 307	192.8	8.4	6000	1	PCT-US07-13803-174	Sequence 174, App	Sequence 3, Appli
c 308	192.8	8.4	6000	1	PCT-US07-13803-182	Sequence 182, App	Sequence 2833, Ap
c 309	192.6	8.4	405	7	US-11-881-406-1876	Sequence 1876, Ap	Sequence 2407, Ap
c 310	192.6	8.4	1472	7	US-11-781-665-2955	Sequence 2955, Ap	Sequence 539, App
c 311	192.6	8.4	5225	7	US-11-734-562-3	Sequence 3, Appli	Sequence 107, App
c 312	192.6	8.4	6000	1	PCT-US07-13803-227	Sequence 227, App	Sequence 107, App
c 313	192.6	8.4	6000	1	PCT-US07-13803-250	Sequence 250, App	Sequence 259, App
c 314	192.4	8.4	1148	7	US-11-781-665-939	Sequence 939, App	Sequence 3786, Ap
c 315	192.4	8.4	1879	7	US-11-881-406-2011	Sequence 2011, Ap	Sequence 154, App
c 316	192.4	8.4	2001	7	US-11-881-406-2012	Sequence 2012, Ap	Sequence 243, App
c 317	192.4	8.4	6000	1	PCT-US07-13803-50	Sequence 50, Appl	Sequence 2555, Ap
c 318	192.4	8.4	6000	1	PCT-US07-13803-105	Sequence 105, App	Sequence 108, App



C 392	188.8	8.3	6000	1	PCT-US07-13803-262	Sequence 262, App	465	185.4	8.1	6000	1	PCT-US07-13803-231	Sequence 231, App
C 393	188.6	8.3	1320	7	US-11-781-665-2734	Sequence 2734, Ap	466	185.2	8.1	2001	7	US-11-881-406-3582	Sequence 3582, Ap
C 394	188.6	8.3	1380	7	US-11-781-665-643	Sequence 643, App	467	185.2	8.1	6000	1	PCT-US07-13803-38	Sequence 38, Appl
C 395	188.6	8.3	1847	6	US-10-910-811B-374	Sequence 374, App	C 468	185.2	8.1	6000	1	PCT-US07-13803-140	Sequence 140, App
C 396	188.6	8.3	1847	6	US-10-945-565B-374	Sequence 374, App	C 469	185	8.1	1190	7	US-11-781-665-270	Sequence 270, App
C 397	188.6	8.3	2520	7	US-11-832-009-50	Sequence 50, Appl	C 470	185	8.1	1408	7	US-11-781-665-2652	Sequence 2652, Ap
C 398	188.6	8.3	6000	1	PCT-US07-13803-179	Sequence 179, App	471	185	8.1	2194	1	PCT-US07-13803-453	Sequence 453, App
C 399	188.4	8.2	403	7	US-11-881-406-1885	Sequence 1885, Ap	472	185	8.1	6000	1	PCT-US07-13803-31	Sequence 31, Appl
C 400	188.4	8.2	1010	7	US-11-781-665-72	Sequence 72, Appl	473	185	8.1	6000	1	PCT-US07-13803-255	Sequence 255, App
C 401	188.4	8.2	1583	7	US-11-781-665-2608	Sequence 2608, Ap	C 474	184.8	8.1	1776	1	PCT-US07-75115-3	Sequence 3, Appli
C 402	188.4	8.2	1614	7	US-11-781-665-164	Sequence 164, App	C 475	184.8	8.1	6000	1	PCT-US07-13803-45	Sequence 45, Appl
C 403	188.4	8.2	2286	7	US-11-781-665-950	Sequence 950, App	C 476	184.8	8.1	6000	1	PCT-US07-13803-92	Sequence 92, Appl
C 404	188.4	8.2	5518	7	US-11-884-496-547	Sequence 547, App	C 477	184.6	8.1	878	7	US-11-781-665-1428	Sequence 1428, Ap
C 405	188.4	8.2	6444	7	US-11-831-404-85	Sequence 85, Appl	C 478	184.6	8.1	1308	7	US-11-781-665-63	Sequence 63, Appl
C 406	188.2	8.2	1647	7	US-11-781-665-809	Sequence 809, App	479	184.6	8.1	1401	7	US-11-798-002-1	Sequence 1, Appli
C 407	188.2	8.2	2154	7	US-11-781-665-1747	Sequence 1747, Ap	C 480	184.6	8.1	6000	1	PCT-US07-13803-122	Sequence 122, App
C 408	188.2	8.2	5879	7	US-11-816-601-166	Sequence 166, App	C 481	184.6	8.1	6683	1	PCT-US07-13803-493	Sequence 493, App
C 409	188.2	8.2	6000	1	PCT-US07-13803-46	Sequence 46, Appl	C 482	184.4	8.1	657	7	US-11-781-665-2845	Sequence 2845, Ap
C 410	188.2	8.2	6000	1	PCT-US07-13803-107	Sequence 107, App	483	184.4	8.1	4567	7	US-11-847-733-82	Sequence 82, Appl
C 411	188.2	8.2	168323	7	US-11-328-881A-84	Sequence 84, Appl	C 484	184.2	8.1	5144	7	US-11-490-374A-1684	Sequence 1684, Ap
C 412	188	8.2	414	7	US-11-881-406-1272	Sequence 1272, Ap	C 485	184.2	8.1	6000	1	PCT-US07-13803-19	Sequence 19, Appl
C 413	188	8.2	1697	7	US-11-781-665-607	Sequence 607, App	C 486	184.2	8.1	6000	1	PCT-US07-13803-57	Sequence 57, Appl
C 414	188	8.2	1779	7	US-11-781-665-1673	Sequence 1673, Ap	C 487	184.2	8.1	6000	1	PCT-US07-13803-229	Sequence 229, App
C 415	187.8	8.2	5508	7	US-11-490-374A-2137	Sequence 2137, Ap	488	184	8.1	2001	7	US-11-881-406-3537	Sequence 3537, Ap
C 416	187.8	8.2	6000	1	PCT-US07-13803-1	Sequence 1, Appli	C 489	183.8	8.0	851	7	US-11-781-665-2553	Sequence 2553, Ap
C 417	187.8	8.2	6000	1	PCT-US07-13803-18	Sequence 18, Appl	C 490	183.8	8.0	1104	7	US-11-781-665-2587	Sequence 2587, Ap
C 418	187.8	8.2	6000	1	PCT-US07-13803-53	Sequence 53, Appl	C 491	183.6	8.0	859	7	US-11-781-665-1551	Sequence 1551, Ap
C 419	187.8	8.2	6000	1	PCT-US07-13803-111	Sequence 111, App	492	183.6	8.0	6000	1	PCT-US07-13803-88	Sequence 88, Appl
C 420	187.8	8.2	6000	1	PCT-US07-13803-130	Sequence 130, App	493	183.6	8.0	6000	1	PCT-US07-13803-90	Sequence 90, Appl
C 421	187.6	8.2	1245	7	US-11-781-665-650	Sequence 650, App	494	183.6	8.0	6000	1	PCT-US07-13803-228	Sequence 228, App
C 422	187.6	8.2	2612	7	US-11-781-665-2090	Sequence 2090, Ap	495	183.6	8.0	6000	1	US-11-881-406-2206	Sequence 2206, Ap
C 423	187.6	8.2	6000	1	PCT-US07-13803-167	Sequence 167, App	C 496	183.4	8.0	418	7	US-11-832-009-54	Sequence 54, Appl
C 424	187.6	8.2	6000	1	PCT-US07-13803-203	Sequence 203, App	C 497	183.4	8.0	1182	7	US-11-781-665-2721	Sequence 2721, Ap
C 425	187.4	8.2	824	7	US-11-781-665-707	Sequence 707, App	498	183.4	8.0	1733	7	US-11-781-665-2615	Sequence 2615, Ap
C 426	187.4	8.2	1268	7	US-11-781-665-2081	Sequence 2081, Ap	C 499	183.2	8.0	1501	7	US-11-781-665-891	Sequence 891, App
C 427	187.4	8.2	1948	7	US-11-781-665-807	Sequence 807, App	C 500	183.2	8.0	1688	7	US-11-881-406-39	Sequence 39, Appl
C 428	187.4	8.2	6000	1	PCT-US07-13803-139	Sequence 139, App	C 501	183.2	8.0	7028	7	US-11-881-406-927	Sequence 927, App
C 429	187.2	8.2	865	7	US-11-781-665-2588	Sequence 2588, Ap	C 502	183	8.0	419	7	US-11-881-406-2918	Sequence 2918, Ap
C 430	187.2	8.2	2075	7	US-11-831-404-99	Sequence 99, Appl	503	183	8.0	430	7	PCT-US07-13803-336	Sequence 336, App
C 431	187.2	8.2	6433	7	US-11-490-374A-1949	Sequence 1949, Ap	504	183	8.0	4642	1	PCT-US07-13803-75	Sequence 75, Appl
C 432	187.2	8.2	6433	7	US-11-490-374A-1950	Sequence 1950, Ap	505	183	8.0	6000	1	PCT-US07-13803-254	Sequence 254, App
C 433	187.2	8.2	6433	7	US-11-490-374A-1951	Sequence 1951, Ap	C 506	183	8.0	6000	1	US-11-881-406-3694	Sequence 3694, Ap
C 434	187.2	8.2	6444	7	US-11-831-404-85	Sequence 85, Appl	C 507	182.8	8.0	425	7	US-11-781-665-2205	Sequence 2205, Ap
C 435	187	8.2	1430	7	US-11-781-665-1085	Sequence 1085, Ap	C 508	182.8	8.0	1162	7	US-60-970-396-7	Sequence 7, Appli
C 436	187	8.2	6000	1	PCT-US07-13803-264	Sequence 264, App	509	182.6	8.0	5019	8	US-11-781-665-302	Sequence 302, App
C 437	187	8.2	6883	7	US-11-490-374A-1494	Sequence 1494, Ap	510	182.6	8.0	1156	7	US-11-781-665-367	Sequence 367, App
C 438	186.8	8.2	420	7	US-11-881-406-1847	Sequence 1847, Ap	C 511	182.6	8.0	1158	7	US-11-781-665-920	Sequence 920, App
C 439	186.8	8.2	1227	7	US-11-781-665-2388	Sequence 2388, Ap	C 512	182.6	8.0	1718	7	PCT-US07-13803-57	Sequence 57, Appl
C 440	186.8	8.2	1278	7	US-11-781-665-551	Sequence 551, App	513	182.6	8.0	6000	1	US-11-881-406-3993	Sequence 3993, Ap
C 441	186.8	8.2	6000	1	PCT-US07-13803-92	Sequence 92, Appl	514	182.4	8.0	409	7	US-11-781-665-2357	Sequence 2357, Ap
C 442	186.8	8.2	13602	1	PCT-US07-06371-1	Sequence 1, Appli	C 515	182.4	8.0	706	7	US-11-781-665-1527	Sequence 1527, Ap
C 443	186.8	8.2	17534	1	PCT-US07-06371-7	Sequence 7, Appli	516	182.4	8.0	1141	7	US-11-781-665-1543	Sequence 1543, Ap
C 444	186.8	8.2	30756	1	PCT-US07-06371-16	Sequence 16, Appl	C 517	182.4	8.0	1158	7	US-11-881-406-40	Sequence 40, Appl
C 445	186.4	8.2	467	7	US-11-884-496-705	Sequence 705, App	C 518	182.4	8.0	5096	7	PCT-US07-13803-200	Sequence 200, App
C 446	186.4	8.2	2845	7	US-11-884-496-643	Sequence 643, App	C 519	182.4	8.0	6000	1	PCT-US07-13803-227	Sequence 227, App
C 447	186.2	8.2	953	7	US-11-781-665-2515	Sequence 2515, Ap	520	182.4	8.0	6000	1	US-11-781-665-160	Sequence 160, App
C 448	186.2	8.2	1256	7	PCT-US07-13803-147	Sequence 147, App	C 521	182.2	8.0	2168	7	PCT-US07-13803-60	Sequence 60, Appl
C 449	186.2	8.2	6000	1	PCT-US07-13803-187	Sequence 187, App	C 522	182.2	8.0	6000	1	PCT-US07-13803-502	Sequence 502, App
C 450	186.2	8.2	6000	1	US-11-781-665-1438	Sequence 1438, Ap	C 523	182.2	8.0	7367	1	US-11-781-665-366	Sequence 366, App
C 451	186	8.1	910	7	US-11-781-665-2824	Sequence 2824, Ap	C 524	182.2	8.0	1157	7	US-11-781-665-446	Sequence 446, App
C 452	186	8.1	1803	7	PCT-US07-13803-142	Sequence 142, App	C 525	182	8.0	1444	7	US-11-781-665-239	Sequence 239, App
C 453	185.8	8.1	6000	1	US-11-881-406-1962	Sequence 1962, Ap	C 526	182	8.0	1842	7	US-11-832-009-24	Sequence 24, Appl
C 454	185.6	8.1	379	7	US-11-781-665-3009	Sequence 3009, Ap	C 527	182	8.0	2495	7	US-11-781-665-801	Sequence 801, App
C 455	185.6	8.1	772	7	US-11-781-665-723	Sequence 723, App	C 528	182	8.0	2520	7	US-11-781-665-1686	Sequence 1686, Ap
C 456	185.6	8.1	1118	7	US-11-781-665-241	Sequence 241, App	C 529	182	8.0	2702	7	US-11-881-406-3935	Sequence 3935, Ap
C 457	185.6	8.1	1768	7	PCT-US07-13803-126	Sequence 126, App	C 530	181.8	8.0	430	7	US-11-781-665-1440	Sequence 1440, Ap
C 458	185.6	8.1	6000	1	PCT-US07-13803-188	Sequence 188, App	C 531	181.8	8.0	837	7	US-11-781-665-2547	Sequence 2547, Ap
C 459	185.6	8.1	6000	1	US-11-881-406-1393	Sequence 1393, Ap	C 532	181.8	8.0	1288	7	US-11-781-665-1708	Sequence 1708, Ap
C 460	185.4	8.1	422	7	US-11-781-665-1280	Sequence 1280, Ap	C 533	181.8	8.0	1601	7	PCT-US07-13803-44	Sequence 44, Appl
C 461	185.4	8.1	850	7	PCT-US07-13803-104	Sequence 104, App	C 534	181.8	8.0	6000	1	US-11-881-406-1361	Sequence 1361, Ap
C 462	185.4	8.1	6000	1	PCT-US07-13803-152	Sequence 152, App	C 535	181.6	8.0	800	7	US-11-781-665-60	Sequence 60, Appl
C 463	185.4	8.1	6000	1	PCT-US07-13803-204	Sequence 204, App	C 536	181.6	8.0	1076	7		
C 464	185.4	8.1	6000	1			C 537	181.6	8.0				

C 538	181.6	8.0	1181	7	US-11-781-665-228	Sequence 228, App
C 539	181.6	8.0	6000	1	PCT-US07-13803-49	Sequence 49, Appl
C 540	181.6	8.0	7468	1	PCT-US07-73799-2	Sequence 2, Appl1
C 541	181.4	7.9	390	7	US-11-881-406-3065	Sequence 3065, Ap
C 542	181.4	7.9	430	7	US-11-881-406-2510	Sequence 2510, Ap
C 543	181.4	7.9	2043	7	US-11-781-665-2661	Sequence 2661, Ap
C 544	181.2	7.9	1633	7	US-11-781-665-407	Sequence 407, App
C 545	181.2	7.9	1693	7	US-11-781-665-1282	Sequence 1282, Ap
C 546	181.2	7.9	1790	7	US-11-781-665-1611	Sequence 1611, Ap
C 547	181.2	7.9	1797	7	US-11-781-665-2915	Sequence 2915, Ap
C 548	181	7.9	394	7	US-11-881-406-1032	Sequence 1032, Ap
C 549	181	7.9	983	7	US-11-881-406-41	Sequence 41, Appl
C 550	181	7.9	1001	7	US-11-881-406-3751	Sequence 3751, Ap
C 551	180.8	7.9	1166	7	US-11-781-665-1983	Sequence 1983, Ap
C 552	180.8	7.9	1302	7	US-11-682-135-1	Sequence 1, Appli
C 553	180.8	7.9	1566	7	US-11-781-665-1852	Sequence 1852, Ap
C 554	180.8	7.9	6000	1	PCT-US07-13803-136	Sequence 136, App
C 555	180.6	7.9	1384	7	US-11-781-665-1930	Sequence 1930, Ap
C 556	180.6	7.9	1535	7	US-11-781-665-1826	Sequence 1826, Ap
C 557	180.6	7.9	1583	7	US-11-884-496-660	Sequence 660, App
C 558	180.6	7.9	6000	1	PCT-US07-13803-113	Sequence 13, Appl
C 559	180.6	7.9	6000	1	PCT-US07-13803-174	Sequence 174, App
C 560	180.6	7.9	6000	1	PCT-US07-13803-214	Sequence 214, App
C 561	180.6	7.9	17483	6	US-10-751-606A-1	Sequence 1, Appli
C 562	180.4	7.9	409	7	US-11-881-406-2657	Sequence 2657, Ap
C 563	180.4	7.9	7063	6	US-10-148-848D-1	Sequence 1, Appli
C 564	180.4	7.9	12050	1	PCT-US07-13803-347	Sequence 347, App
C 565	180.2	7.9	1725	7	US-11-781-665-1987	Sequence 1987, Ap
C 566	180.2	7.9	4868	7	US-11-490-374A-1594	Sequence 1594, Ap
C 567	180.2	7.9	5333	7	US-11-490-374A-1596	Sequence 1596, Ap
C 568	180.2	7.9	5441	7	US-11-490-374A-1595	Sequence 1595, Ap
C 569	180.2	7.9	6000	1	PCT-US07-13803-13	Sequence 13, Appl
C 570	180.2	7.9	6000	1	PCT-US07-13803-78	Sequence 78, Appl
C 571	180.2	7.9	6000	1	PCT-US07-13803-214	Sequence 214, App
C 572	180	7.9	1035	7	US-11-781-665-1881	Sequence 1881, Ap
C 573	180	7.9	1472	7	US-11-781-665-2913	Sequence 2913, Ap
C 574	180	7.9	6000	1	PCT-US07-13803-197	Sequence 197, App
C 575	179.8	7.9	1491	7	US-11-781-665-1260	Sequence 1260, Ap
C 576	179.8	7.9	1759	7	US-11-781-665-1684	Sequence 1684, Ap
C 577	179.8	7.9	6000	1	PCT-US07-13803-72	Sequence 72, Appl
C 578	179.8	7.9	6666	1	PCT-US07-13803-504	Sequence 504, App
C 579	179.6	7.9	1520	7	US-11-781-665-191	Sequence 191, App
C 580	179.6	7.9	6000	1	PCT-US07-13803-222	Sequence 222, App
C 581	179.6	7.9	6000	1	PCT-US07-13803-223	Sequence 223, App
C 582	179.4	7.9	1102	7	US-11-781-665-535	Sequence 535, App
C 583	179.4	7.9	1635	7	US-11-781-665-1064	Sequence 1064, Ap
C 584	179.4	7.9	2414	7	US-11-781-665-1255	Sequence 1255, Ap
C 585	179.4	7.9	3915	7	US-11-847-733-49	Sequence 49, Appl
C 586	179.4	7.9	6000	1	PCT-US07-13803-35	Sequence 35, Appl
C 587	179.4	7.9	6000	1	PCT-US07-13803-63	Sequence 63, Appl
C 588	179.2	7.8	1639	7	US-11-781-665-1680	Sequence 1680, Ap
C 589	179	7.8	636	7	US-11-781-665-2188	Sequence 2188, Ap
C 590	179	7.8	4220	7	US-11-816-601-149	Sequence 149, App
C 591	178.8	7.8	3234	7	US-11-816-601-13	Sequence 13, Appl
C 592	178.8	7.8	3234	7	US-11-816-601-293	Sequence 293, App
C 593	178.6	7.8	1104	7	US-11-781-665-2823	Sequence 2823, Ap
C 594	178.6	7.8	1162	7	US-11-781-665-754	Sequence 754, App
C 595	178.6	7.8	2001	7	US-11-881-406-901	Sequence 901, App
C 596	178.6	7.8	2001	7	US-11-881-406-3343	Sequence 3343, Ap
C 597	178.6	7.8	6000	1	PCT-US07-13803-45	Sequence 45, Appl
C 598	178.4	7.8	990	7	US-11-881-406-3842	Sequence 3842, Ap
C 599	178.4	7.8	1724	7	US-11-781-665-284	Sequence 284, App
C 600	178.4	7.8	6000	1	PCT-US07-13803-24	Sequence 24, Appl
C 601	178.4	7.8	6000	1	PCT-US07-13803-182	Sequence 182, App
C 602	178.4	7.8	6000	1	PCT-US07-13803-210	Sequence 210, App
C 603	178.4	7.8	6000	1	PCT-US07-13803-260	Sequence 260, App
C 604	178.4	7.8	9648	7	US-11-847-733-64	Sequence 64, Appl
C 605	178.2	7.8	898	7	US-11-781-665-2568	Sequence 2568, Ap
C 606	178.2	7.8	1230	7	US-11-781-665-852	Sequence 852, App
C 607	178.2	7.8	1295	7	US-11-781-665-1445	Sequence 1445, Ap
C 608	178.2	7.8	2085	7	US-11-781-665-503	Sequence 503, App
C 609	178.2	7.8	2085	7	US-11-781-665-503	Sequence 503, App
C 610	178.2	7.8	2284	7	US-11-781-665-1980	Sequence 1980, Ap

C 611	178	7.8	1262	7	US-11-832-009-30	Sequence 30, Appl
C 612	178	7.8	1986	7	US-11-781-665-3038	Sequence 3038, Ap
C 613	177.8	7.8	1200	7	US-11-781-665-465	Sequence 465, App
C 614	177.8	7.8	1683	1	PCT-US07-13803-325	Sequence 325, App
C 615	177.8	7.8	2007	7	US-11-781-665-230	Sequence 230, App
C 616	177.8	7.8	4015	7	US-11-851-267-8	Sequence 8, Appli
C 617	177.8	7.8	4015	7	US-11-851-267-15	Sequence 15, Appl
C 618	177.8	7.8	4356	7	US-11-852-912-10	Sequence 10, Appl
C 619	177.8	7.8	6000	1	PCT-US07-13803-75	Sequence 75, Appl
C 620	177.8	7.8	6000	1	PCT-US07-13803-261	Sequence 261, App
C 621	177.6	7.8	410	7	US-11-881-406-2445	Sequence 2445, Ap
C 622	177.6	7.8	2015	1	PCT-US07-13803-521	Sequence 521, App
C 623	177.6	7.8	2141	7	US-11-781-665-2001	Sequence 2001, Ap
C 624	177.4	7.8	958	7	US-11-781-665-670	Sequence 670, App
C 625	177.4	7.8	1901	7	US-11-781-665-1269	Sequence 1269, Ap
C 626	177.4	7.8	3271	7	US-11-816-601-124	Sequence 124, App
C 627	177.4	7.8	3271	7	US-11-816-601-273	Sequence 273, App
C 628	177.4	7.8	5001	7	US-11-885-002-23	Sequence 23, Appl
C 629	177.4	7.8	92384	7	US-11-328-881A-80	Sequence 80, Appl
C 630	177.2	7.8	1079	7	US-11-781-665-2781	Sequence 2781, Ap
C 631	177.2	7.8	2572	1	PCT-US07-13803-500	Sequence 500, App
C 632	177	7.7	1272	7	US-11-781-665-2259	Sequence 2259, Ap
C 633	177	7.7	1851	7	US-11-781-665-2960	Sequence 2960, Ap
C 634	176	7.7	3382	7	US-11-781-665-2651	Sequence 2651, Ap
C 635	176	7.7	3775	7	US-11-847-733-71	Sequence 71, Appl
C 636	176.8	7.7	2001	7	US-11-881-406-3875	Sequence 3875, Ap
C 637	176.8	7.7	2001	7	US-11-881-406-3876	Sequence 3876, Ap
C 638	176.8	7.7	3708	1	PCT-US07-77281-17	Sequence 17, Appl
C 639	176.8	7.7	5045	1	PCT-US07-77281-19	Sequence 19, Appl
C 640	176.6	7.7	10240	8	US-60-970-396-5	Sequence 5, Appli
C 641	176.4	7.7	6000	1	PCT-US07-13803-93	Sequence 93, Appl
C 642	176.2	7.7	3121	7	US-11-781-665-2419	Sequence 2419, Ap
C 643	176.2	7.7	6000	1	PCT-US07-13803-59	Sequence 59, Appl
C 644	176.2	7.7	6000	1	PCT-US07-13803-70	Sequence 70, Appl
C 645	176	7.7	788	7	US-11-781-665-363	Sequence 363, App
C 646	176	7.7	1750	7	US-11-781-665-2630	Sequence 2630, Ap
C 647	176	7.7	2001	7	US-11-881-406-2196	Sequence 2196, Ap
C 648	176	7.7	2521	7	US-11-235-701A-462	Sequence 462, App
C 649	176	7.7	3628	7	US-11-235-701A-463	Sequence 463, App
C 650	176	7.7	3856	7	US-11-235-701A-460	Sequence 460, App
C 651	175.8	7.7	390	7	US-11-881-406-2106	Sequence 2106, Ap
C 652	175.8	7.7	1305	7	US-11-490-374A-1810	Sequence 1810, Ap
C 653	175.8	7.7	2101	7	US-11-490-374A-1808	Sequence 1808, Ap
C 654	175.8	7.7	6000	1	PCT-US07-13803-146	Sequence 146, App
C 655	175.6	7.7	996	7	US-11-781-665-876	Sequence 876, App
C 656	175.6	7.7	1156	7	US-11-781-665-2437	Sequence 2437, Ap
C 657	175.6	7.7	1592	7	US-11-781-665-575	Sequence 575, App
C 658	175.6	7.7	2393	7	US-11-781-665-3062	Sequence 3062, Ap
C 659	175.6	7.7	6000	1	PCT-US07-13803-55	Sequence 55, Appl
C 660	175.6	7.7	6000	1	PCT-US07-13803-247	Sequence 247, App
C 661	175.4	7.7	1686	7	US-11-781-665-579	Sequence 579, App
C 662	175.2	7.7	557	7	US-11-781-665-569	Sequence 569, App
C 663	175.2	7.7	974	7	US-11-781-665-2016	Sequence 2016, Ap
C 664	175.2	7.7	2288	7	US-11-781-665-2436	Sequence 2436, Ap
C 665	175.2	7.7	5518	7	US-11-884-496-547	Sequence 547, App
C 666	175.2	7.7	6000	1	PCT-US07-13803-145	Sequence 145, App
C 667	175	7.7	1450	7	US-11-781-665-2605	Sequence 2605, Ap
C 668	175	7.7	2280	7	US-11-781-665-884	Sequence 884, App
C 669	175	7.7	4964	7	US-11-884-496-680	Sequence 680, App
C 670	175	7.7	5508	7	US-11-490-374A-1939	Sequence 1939, Ap
C 671	175	7.7	6000	1	PCT-US07-13803-161	Sequence 161, App
C 672	175	7.7	6000	1	PCT-US07-13803-211	Sequence 211, App
C 673	175	7.7	18524	1	PCT-US07-06371-12	Sequence 12, Appl
C 674	174.8	7.7	1742	7	US-11-781-665-1488	Sequence 1488, Ap
C 675	174.8	7.7	2778	7	US-11-781-665-2904	Sequence 2904, Ap
C 676	174.8	7.7	3536	7	US-11-825-627-354	Sequence 354, App
C 677	174.8	7.7	10876	1	PCT-US07-16656-6	Sequence 6, Appli
C 678	174.6	7.6	1302	7	US-11-781-665-1478	Sequence 1478, Ap
C 679	174.6	7.6	1626	7	US-11-781-665-2580	Sequence 2580, Ap
C 680	174.6	7.6	2157	7	US-11-781-665-627	Sequence 627, App
C 681	174.4	7.6	1461	7	US-11-781-665-844	Sequence 844, App
C 682	174.4	7.6	4122	1	PCT-US07-13803-280	Sequence 280, App
C 683	174.4	7.6	4122	1	PCT-US07-13803-365	Sequence 365, App

C 684	174.4	7.6	6221	7	US-11-908-114-27	Sequence 27, Appl	C 757	170.4	7.5	890	7	US-11-781-665-2820	Sequence 2820, Ap
C 685	174.2	7.6	1167	7	US-11-781-665-2799	Sequence 2799, Ap	C 758	170.4	7.5	2001	7	US-11-881-406-3890	Sequence 3890, Ap
C 686	174.2	7.6	1347	7	US-11-781-665-2131	Sequence 2131, Ap	C 759	170.4	7.5	3754	7	US-11-816-601-737	Sequence 737, App
C 687	174.2	7.6	6000	1	PCT-US07-13803-180	Sequence 180, App	C 760	170.4	7.5	3754	7	US-11-816-601-813	Sequence 813, App
C 688	174.2	7.6	6000	1	PCT-US07-13803-269	Sequence 269, App	C 761	170.4	7.5	6000	1	PCT-US07-13803-19	Sequence 19, Appl
C 689	174	7.6	1125	7	US-11-781-665-2572	Sequence 2572, Ap	C 762	170.4	7.5	6000	1	PCT-US07-13803-229	Sequence 229, App
C 690	174	7.6	1864	7	US-11-884-496-655	Sequence 655, App	C 763	170.2	7.5	2001	7	US-11-881-406-3382	Sequence 3382, Ap
C 691	173.8	7.6	978	7	US-11-781-665-3893	Sequence 3893, Ap	C 764	170.2	7.5	2001	7	US-11-881-406-3383	Sequence 3383, Ap
C 692	173.8	7.6	1255	7	US-11-781-665-1267	Sequence 1267, Ap	C 765	170.2	7.5	2001	7	US-11-881-406-3384	Sequence 3384, Ap
C 693	173.8	7.6	1311	7	US-11-781-665-1487	Sequence 1487, Ap	C 766	170.2	7.5	2001	7	US-11-881-406-3385	Sequence 3385, Ap
C 694	173.8	7.6	1369	7	US-11-781-665-2026	Sequence 2026, Ap	C 767	170.2	7.5	2001	7	US-11-881-406-3389	Sequence 3389, Ap
C 695	173.8	7.6	6000	1	PCT-US07-13803-192	Sequence 192, App	C 768	170.2	7.5	6000	1	PCT-US07-13803-105	Sequence 105, App
C 696	173.8	7.6	6000	1	PCT-US07-13803-230	Sequence 230, App	C 769	170	7.4	1598	7	US-11-781-665-2706	Sequence 2706, Ap
C 697	173.6	7.6	399	7	US-11-881-406-2276	Sequence 2276, Ap	C 770	170	7.4	1603	7	US-11-781-665-1481	Sequence 1481, Ap
C 698	173.6	7.6	416	7	US-11-881-406-2091	Sequence 2091, Ap	C 771	170	7.4	1877	7	US-11-781-665-2947	Sequence 2947, Ap
C 699	173.6	7.6	2272	7	US-11-794-690-22	Sequence 22, Appl	C 772	170	7.4	1927	7	US-11-825-627-246	Sequence 246, App
C 700	173.4	7.6	979	7	US-11-781-665-2631	Sequence 2631, Ap	C 773	170	7.4	1927	7	US-11-825-627-248	Sequence 248, App
C 701	173.2	7.6	1309	7	US-11-781-665-1967	Sequence 1967, Ap	C 774	170	7.4	2001	7	US-11-881-406-3889	Sequence 3889, Ap
C 702	173.2	7.6	1320	7	US-11-781-665-2387	Sequence 2387, Ap	C 775	170	7.4	6000	1	PCT-US07-13803-123	Sequence 123, App
C 703	173.2	7.6	1406	7	US-11-781-665-1486	Sequence 1486, Ap	C 776	169.8	7.4	1547	7	US-11-781-665-123	Sequence 123, App
C 704	173.2	7.6	1554	7	US-11-781-665-3024	Sequence 3024, Ap	C 777	169.8	7.4	2235	7	US-11-832-009-34	Sequence 34, Appl
C 705	173.2	7.6	2459	7	US-11-847-733-57	Sequence 57, Appl	C 778	169.8	7.4	4421	7	US-11-847-733-16	Sequence 16, Appl
C 706	173	7.6	2001	7	US-11-881-406-2280	Sequence 2280, Ap	C 779	169.6	7.4	4356	7	US-11-852-912-10	Sequence 10, Appl
C 707	173	7.6	2399	7	US-11-781-665-2071	Sequence 2071, Ap	C 780	169.6	7.4	4520	7	US-11-847-733-62	Sequence 62, Appl
C 708	173	7.6	6000	1	PCT-US07-13803-1	Sequence 1, Appli	C 781	169.6	7.4	6000	1	PCT-US07-13803-52	Sequence 52, Appl
C 709	173	7.6	6000	1	PCT-US07-13803-96	Sequence 96, Appl	C 782	169.6	7.4	6000	1	PCT-US07-13803-84	Sequence 84, Appl
C 710	173	7.6	6000	1	PCT-US07-13803-184	Sequence 184, App	C 783	169.4	7.4	3396	1	PCT-US07-13803-519	Sequence 519, App
C 711	172.8	7.6	824	7	US-11-781-665-1471	Sequence 1471, Ap	C 784	169.2	7.4	2014	7	US-11-781-665-1443	Sequence 1443, Ap
C 712	172.6	7.6	6000	1	PCT-US07-13803-97	Sequence 97, Appl	C 785	169.2	7.4	5182	6	US-10-910-811B-395	Sequence 395, App
C 713	172.6	7.6	6000	1	PCT-US07-13803-119	Sequence 119, App	C 786	169.2	7.4	5182	6	US-10-945-565B-395	Sequence 395, App
C 714	172.4	7.5	1998	7	US-11-832-009-47	Sequence 47, Appl	C 787	169.2	7.4	6000	1	PCT-US07-13803-115	Sequence 115, App
C 715	172.4	7.5	2001	7	US-11-881-406-3296	Sequence 3296, Ap	C 788	169.2	7.4	6000	1	PCT-US07-13803-209	Sequence 209, App
C 716	172.4	7.5	6000	1	PCT-US07-13803-168	Sequence 168, App	C 789	169.2	7.4	6000	1	PCT-US07-13803-223	Sequence 223, App
C 717	172.4	7.5	6004	7	US-11-235-701A-401	Sequence 401, App	C 790	169	7.4	411	7	US-11-881-406-2298	Sequence 2298, Ap
C 718	172.4	7.5	6004	7	US-11-235-701A-403	Sequence 403, App	C 791	169	7.4	2001	7	US-11-881-406-3562	Sequence 3562, Ap
C 719	172.4	7.5	6017	7	US-11-235-701A-402	Sequence 402, App	C 792	169	7.4	2001	7	US-11-881-406-3569	Sequence 3569, Ap
C 720	172.2	7.5	1692	7	US-11-781-665-2581	Sequence 2581, Ap	C 793	169	7.4	2251	7	US-11-852-219-13	Sequence 13, Appl
C 721	172.2	7.5	2001	7	US-11-881-406-3762	Sequence 3762, Ap	C 794	169	7.4	2587	7	US-11-852-219-1	Sequence 1, Appli
C 722	172.2	7.5	2001	7	US-11-881-406-3763	Sequence 3763, Ap	C 795	169	7.4	2587	7	US-11-852-219-3	Sequence 3, Appli
C 723	172.2	7.5	2001	7	US-11-881-406-3764	Sequence 3764, Ap	C 796	169	7.4	2587	7	US-11-852-219-5	Sequence 5, Appli
C 724	172.2	7.5	2693	7	US-11-881-406-1737	Sequence 1737, Ap	C 797	169	7.4	2587	7	US-11-852-219-7	Sequence 7, Appli
C 725	172.2	7.5	8122	7	US-11-847-733-87	Sequence 87, Appl	C 798	169	7.4	2587	7	US-11-852-219-9	Sequence 9, Appli
C 726	172	7.5	2783	7	US-11-781-665-3066	Sequence 3066, Ap	C 799	169	7.4	2587	7	US-11-852-219-11	Sequence 11, Appl
C 727	172	7.5	4220	7	US-11-816-601-149	Sequence 149, App	C 800	169	7.4	2593	7	US-11-852-219-17	Sequence 17, Appl
C 728	172	7.5	6000	1	PCT-US07-13803-84	Sequence 84, Appl	C 801	169	7.4	2623	7	US-11-852-219-15	Sequence 15, Appl
C 729	172	7.5	6000	1	PCT-US07-13803-207	Sequence 207, App	C 802	169	7.4	4978	6	US-10-571-511-19	Sequence 19, Appl
C 730	171.8	7.5	1899	7	US-11-881-406-1303	Sequence 1303, Ap	C 803	169	7.4	5631	1	PCT-US07-13803-390	Sequence 390, App
C 731	171.8	7.5	2001	7	US-11-881-406-3687	Sequence 3687, Ap	C 804	169	7.4	6000	1	PCT-US07-13803-157	Sequence 157, App
C 732	171.6	7.5	1276	7	US-11-781-665-1219	Sequence 1219, Ap	C 805	168.8	7.4	1332	7	US-11-781-665-1676	Sequence 1676, Ap
C 733	171.6	7.5	1502	7	US-11-781-665-1566	Sequence 1566, Ap	C 806	168.8	7.4	5184	7	US-11-235-701A-509	Sequence 509, App
C 734	171.4	7.5	1541	7	US-11-781-665-1963	Sequence 1963, Ap	C 807	168.8	7.4	6000	1	PCT-US07-13803-62	Sequence 62, Appl
C 735	171.4	7.5	2001	7	US-11-881-406-3366	Sequence 3366, Ap	C 808	168.6	7.4	421	7	US-11-881-406-1237	Sequence 1237, Ap
C 736	171.4	7.5	2036	7	US-11-781-665-148	Sequence 148, App	C 809	168.6	7.4	776	7	US-11-781-665-382	Sequence 382, App
C 737	171.4	7.5	6000	1	PCT-US07-13803-61	Sequence 61, Appl	C 810	168.6	7.4	853	7	US-11-781-665-827	Sequence 827, App
C 738	171.4	7.5	6000	1	PCT-US07-13803-97	Sequence 97, Appl	C 811	168.6	7.4	1316	7	US-11-781-665-195	Sequence 195, App
C 739	171.4	7.5	6000	1	PCT-US07-13803-98	Sequence 98, Appl	C 812	168.6	7.4	1907	7	US-11-781-665-1679	Sequence 1679, Ap
C 740	171.4	7.5	6683	1	PCT-US07-13803-493	Sequence 493, App	C 813	168.6	7.4	3337	7	US-11-832-009-51	Sequence 51, Appl
C 741	171.2	7.5	423	7	US-11-881-406-1097	Sequence 1097, Ap	C 814	168.6	7.4	6000	1	PCT-US07-13803-133	Sequence 133, App
C 742	171.2	7.5	429	7	US-11-881-406-2116	Sequence 2116, Ap	C 815	168.6	7.4	6000	1	PCT-US07-13803-225	Sequence 225, App
C 743	171.2	7.5	1195	7	US-11-781-665-2219	Sequence 2219, Ap	C 816	168.2	7.4	847	7	US-11-781-665-1231	Sequence 1231, Ap
C 744	171	7.5	416	7	US-11-881-406-3234	Sequence 3234, Ap	C 817	168.2	7.4	2001	7	US-11-881-406-3365	Sequence 3365, Ap
C 745	171	7.5	2945	7	US-11-781-665-282	Sequence 282, App	C 818	168.2	7.4	6000	1	PCT-US07-13803-99	Sequence 99, Appl
C 746	171	7.5	6000	1	PCT-US07-13803-247	Sequence 247, App	C 819	168	7.4	1605	7	US-11-832-009-42	Sequence 42, Appl
C 747	170.8	7.5	408	7	US-11-881-406-2710	Sequence 2710, Ap	C 820	168	7.4	2001	7	US-11-881-406-3798	Sequence 3798, Ap
C 748	170.8	7.5	2033	7	US-11-884-496-651	Sequence 651, App	C 821	168	7.4	2001	7	US-11-881-406-3799	Sequence 3799, Ap
C 749	170.8	7.5	6000	1	PCT-US07-13803-87	Sequence 87, Appl	C 822	167.8	7.3	2001	7	US-11-881-406-3787	Sequence 3787, Ap
C 750	170.6	7.5	427	7	US-11-881-406-2681	Sequence 2681, Ap	C 823	167.8	7.3	5312	7	US-11-816-601-740	Sequence 740, App
C 751	170.6	7.5	1586	7	US-11-781-665-2560	Sequence 2560, Ap	C 824	167.6	7.3	3655	7	US-11-490-374A-1818	Sequence 1818, Ap
C 752	170.6	7.5	1634	7	US-11-781-665-2313	Sequence 2313, Ap	C 825	167.6	7.3	3724	7	US-11-490-374A-1819	Sequence 1819, Ap
C 753	170.6	7.5	2141	7	US-11-781-665-1254	Sequence 1254, Ap	C 826	167.6	7.3	6000	1	PCT-US07-13803-212	Sequence 212, App
C 754	170.6	7.5	6000	1	PCT-US07-13803-30	Sequence 30, Appl	C 827	167.4	7.3	401	7	US-11-881-406-3793	Sequence 3793, Ap
C 755	170.6	7.5	6000	1	PCT-US07-13803-185	Sequence 185, App	C 828	167.4	7.3	793	7	US-11-781-665-2836	Sequence 2836, Ap
C 756	170.6	7.5	6000	1	PCT-US07-13803-195	Sequence 195, App	C 829	167.4	7.3	1141	7	US-11-781-665-1555	Sequence 1555, Ap



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C 831 167.4 7.3 3455 7 US-11-829-279-154 Sequence 154, App  
C 832 167.4 7.3 6000 1 PCT-US07-13803-192 Sequence 192, App  
C 833 167.2 7.3 1726 7 US-11-781-665-2329 Sequence 2329, App  
C 834 167.2 7.3 6000 1 PCT-US07-13803-263 Sequence 263, App  
C 835 167 7.3 2511 7 US-11-884-496-624 Sequence 624, App  
C 836 167 7.3 5667 7 US-11-847-733-84 Sequence 84, Appl  
C 837 166.8 7.3 811 7 US-11-781-665-656 Sequence 656, App  
C 838 166.8 7.3 859 7 US-11-781-665-168 Sequence 168, App  
C 839 166.8 7.3 888 7 US-11-781-665-767 Sequence 767, App  
C 840 166.8 7.3 1847 7 US-11-781-665-2049 Sequence 2049, App  
C 841 166.8 7.3 6000 1 PCT-US07-13803-56 Sequence 56, Appl  
C 842 166.8 7.3 6000 1 PCT-US07-13803-233 Sequence 233, App  
C 843 166.6 7.3 1349 1 PCT-US07-13803-356 Sequence 356, App  
C 844 166.4 7.3 1714 7 US-11-781-665-866 Sequence 866, App  
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C 848 165.8 7.3 1448 7 US-11-781-665-2040 Sequence 2040, App  
C 849 165.8 7.3 1699 7 US-11-781-665-1414 Sequence 1414, App  
C 850 165.6 7.3 924 7 US-11-781-665-2018 Sequence 2018, App  
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C 852 165.6 7.3 6000 1 PCT-US07-13803-228 Sequence 228, App  
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C 856 165.4 7.2 14177 7 US-11-569-756-4 Sequence 4, Appli  
C 857 165.2 7.2 1363 7 US-11-781-665-1477 Sequence 1477, App  
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C 859 165 7.2 6000 1 PCT-US07-13803-151 Sequence 151, App  
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C 861 164.8 7.2 374 7 US-11-881-406-2639 Sequence 2639, App  
C 862 164.8 7.2 1380 7 US-11-781-665-894 Sequence 894, App  
C 863 164.8 7.2 1552 7 US-11-781-665-341 Sequence 341, App  
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C 865 164.6 7.2 2230 6 US-10-511-989B-25 Sequence 25, Appl  
C 866 164.4 7.2 1610 7 US-11-781-665-2487 Sequence 2487, App  
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C 868 164.2 7.2 1830 7 US-11-781-665-848 Sequence 848, App  
C 869 164.2 7.2 2001 7 US-11-881-406-3557 Sequence 3557, App  
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C 873 163.6 7.2 773 7 US-11-781-665-2949 Sequence 2949, App  
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C 875 163.6 7.2 6000 1 PCT-US07-13803-239 Sequence 239, App  
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C 878 163.2 7.1 2640 7 US-11-885-002-45 Sequence 45, Appl  
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C 880 163.2 7.1 3534 6 US-10-699-597B-8 Sequence 8, Appli  
C 881 163.2 7.1 3534 6 US-10-699-597B-9 Sequence 9, Appli  
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C 900 162 7.1 7216 1 PCT-US07-13803-507 Sequence 507, App  
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C 902 161.6 7.1 1887 7 US-11-781-665-141 Sequence 141, App

C 903 161.6 7.1 1887 7 US-11-781-665-142 Sequence 142, App  
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C 915 161 7.0 6000 1 PCT-US07-13803-265 Sequence 265, App  
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C 921 160.8 7.0 2001 7 US-11-881-406-3389 Sequence 3389, App  
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C 926 160.6 7.0 2180 7 US-11-781-665-2510 Sequence 2510, App  
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C 930 160.2 7.0 2099 7 US-11-781-665-1420 Sequence 1420, App  
C 931 160 7.0 5001 7 US-11-885-002-23 Sequence 23, Appl  
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C 933 160 7.0 6000 1 PCT-US07-13803-67 Sequence 67, Appl  
C 934 159.8 7.0 6000 1 PCT-US07-13803-191 Sequence 191, App  
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C 936 159.6 7.0 403 7 US-11-881-406-964 Sequence 964, App  
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C 938 159.6 7.0 6000 1 PCT-US07-13803-148 Sequence 148, App  
C 939 159.4 7.0 430 7 US-11-881-406-4108 Sequence 4108, App  
C 940 159.4 7.0 6000 1 PCT-US07-13803-164 Sequence 164, App  
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C 947 158.8 7.0 1472 7 US-11-781-665-2913 Sequence 2913, App  
C 948 158.8 7.0 1861 7 US-11-781-665-487 Sequence 487, App  
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C 953 158.4 6.9 686 7 US-11-781-665-1503 Sequence 1503, App  
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C 955 158.2 6.9 1228 7 US-11-781-665-571 Sequence 571, App  
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C 958 158 6.9 1301 7 US-11-781-665-2725 Sequence 2725, App  
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C 962 157.8 6.9 1092 7 US-11-781-665-2170 Sequence 2170, App  
C 963 157.8 6.9 1710 7 US-11-781-665-2610 Sequence 2610, App  
C 964 157.6 6.9 1277 7 US-11-781-665-1453 Sequence 1453, App  
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C 966 157.6 6.9 6000 1 PCT-US07-13803-258 Sequence 258, App  
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C 968 157.4 6.9 2001 7 US-11-881-406-3914 Sequence 3914, App  
C 969 157.4 6.9 2001 7 US-11-881-406-3915 Sequence 3915, App  
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C 972 157.2 6.9 1647 7 US-11-781-665-1482 Sequence 1482, App  
C 973 157 6.9 1435 7 US-11-781-665-494 Sequence 494, App  
C 974 157 6.9 1453 7 US-11-781-665-1469 Sequence 1469, App  
C 975 157 6.9 5001 7 US-11-885-002-22 Sequence 22, Appl

976	156.8	6.9	423	7	US-11-881-406-4180	Sequence 4180, Ap	cl1049	149.6	6.5	1904	7	US-11-781-665-2905	Sequence 2905, Ap
c 977	156.8	6.9	2220	7	US-11-781-665-1685	Sequence 1685, Ap	cl1050	149.6	6.5	4421	7	US-11-847-733-16	Sequence 16, Appl
c 978	156.8	6.9	6000	1	PCT-US07-13803-133	Sequence 133, App	cl1051	149.4	6.5	1280	7	US-11-781-665-565	Sequence 565, App
c 979	156.8	6.9	6000	1	PCT-US07-13803-193	Sequence 193, App	cl1052	149.4	6.5	1485	7	US-11-781-665-2401	Sequence 2401, Ap
c 980	156.6	6.9	1074	7	US-11-781-665-2821	Sequence 2821, Ap	1053	149.4	6.5	6000	1	PCT-US07-13803-81	Sequence 81, Appl
c 981	156.4	6.8	2001	7	US-11-881-406-3950	Sequence 3950, Ap	1054	149.2	6.5	424	7	US-11-881-406-2937	Sequence 2937, Ap
c 982	156.2	6.8	6000	1	PCT-US07-13803-152	Sequence 152, App	1055	149.2	6.5	559	7	US-11-881-406-3879	Sequence 3879, Ap
c 983	156.2	6.8	6000	1	PCT-US07-13803-198	Sequence 198, App	1056	149.2	6.5	1236	7	US-11-781-665-189	Sequence 189, App
c 984	156	6.8	1520	7	US-11-781-665-2495	Sequence 2495, Ap	1057	149.2	6.5	6000	1	PCT-US07-13803-151	Sequence 151, App
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c 986	156	6.8	2001	7	US-11-881-406-3766	Sequence 3766, Ap	cl1059	148.8	6.5	698	7	US-11-781-665-1732	Sequence 1732, Ap
c 987	156	6.8	2001	7	US-11-881-406-3767	Sequence 3767, Ap	cl1060	148.4	6.5	1612	7	US-11-781-665-1415	Sequence 1415, Ap
c 988	156	6.8	2001	7	US-11-881-406-3768	Sequence 3768, Ap	1061	148.4	6.5	6000	1	PCT-US07-13803-246	Sequence 246, App
c 989	155.8	6.8	360	7	US-11-757-860-12	Sequence 12, Appl	cl1062	148.2	6.5	373	7	US-11-881-406-1002	Sequence 1002, Ap
c 990	155.8	6.8	1545	7	US-11-825-627-342	Sequence 342, App	cl1063	148	6.5	2858	7	US-11-908-114-6	Sequence 6, Appl1
c 991	155.8	6.8	6000	1	PCT-US07-13803-220	Sequence 220, App	cl1064	147.8	6.5	1058	7	US-11-781-665-1618	Sequence 1618, Ap
c 992	155.6	6.8	1316	7	US-11-781-665-1877	Sequence 1877, Ap	cl1065	147.8	6.5	1160	7	US-11-781-665-452	Sequence 452, App
c 993	155.6	6.8	1383	7	US-11-781-665-2056	Sequence 2056, Ap	cl1066	147.4	6.5	766	7	US-11-781-665-1937	Sequence 1937, Ap
c 994	155.6	6.8	2647	7	US-11-781-665-2494	Sequence 2494, Ap	cl1067	147.4	6.5	2185	7	US-11-781-665-2344	Sequence 2344, Ap
c 995	155.6	6.8	6000	1	PCT-US07-13803-49	Sequence 49, Appl	cl1068	147.4	6.5	6000	1	PCT-US07-13803-18	Sequence 18, Appl
c 996	155.2	6.8	1455	7	US-11-781-665-2895	Sequence 2895, Ap	cl1069	147.4	6.5	6000	1	PCT-US07-13803-130	Sequence 130, App
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c 998	155	6.8	486	7	US-11-881-406-864	Sequence 864, App	1071	147	6.4	1300	7	US-11-781-665-1037	Sequence 1037, Ap
c 999	155	6.8	2284	7	US-11-781-665-756	Sequence 756, App	cl1072	147	6.4	1302	7	US-11-781-665-671	Sequence 671, App
cl1000	155	6.8	6000	1	PCT-US07-13803-98	Sequence 98, Appl	cl1073	147	6.4	1501	7	US-11-781-665-2604	Sequence 2604, Ap
cl1001	155	6.8	6000	1	PCT-US07-13803-248	Sequence 248, App	cl1074	147	6.4	1628	7	US-11-781-665-2973	Sequence 2973, Ap
cl1002	154.8	6.8	781	7	US-11-781-665-714	Sequence 714, App	cl1075	147	6.4	6000	1	PCT-US07-13803-64	Sequence 64, Appl
1003	154.8	6.8	969	7	US-11-881-406-2016	Sequence 2016, Ap	cl1076	147	6.4	6000	1	PCT-US07-13803-231	Sequence 231, App
1004	154.8	6.8	1798	7	US-11-881-406-2015	Sequence 2015, Ap	cl1077	146.8	6.4	386	7	US-11-881-406-2763	Sequence 2763, Ap
1005	154.8	6.8	6000	1	PCT-US07-13803-199	Sequence 199, App	1078	146.8	6.4	569	7	US-11-781-665-2128	Sequence 2128, Ap
cl1006	154.6	6.8	1359	7	US-11-781-665-88	Sequence 88, Appl	cl1079	146.8	6.4	1668	7	US-11-781-665-902	Sequence 902, App
cl1007	154.4	6.8	2063	7	US-11-490-374A-2179	Sequence 2179, Ap	cl1080	146.8	6.4	1669	7	US-11-781-665-901	Sequence 901, App
cl1008	154.4	6.8	6000	1	PCT-US07-13803-145	Sequence 145, App	cl1081	146.8	6.4	2708	7	US-11-490-374A-1814	Sequence 1814, Ap
cl1009	154.4	6.8	6000	1	PCT-US07-13803-241	Sequence 241, App	cl1082	146.6	6.4	1913	7	US-11-781-665-1214	Sequence 1214, Ap
cl1010	154.2	6.8	1237	7	US-11-781-665-27	Sequence 27, Appl	1083	146.4	6.4	1659	7	US-11-881-406-3497	Sequence 3497, Ap
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cl1012	153.8	6.7	805	7	US-11-781-665-2735	Sequence 2735, Ap	cl1085	145.8	6.4	1030	7	US-11-781-665-1519	Sequence 1519, Ap
1013	153.8	6.7	5399	7	US-11-884-496-692	Sequence 692, App	cl1086	145.4	6.4	1684	7	US-11-490-374A-1637	Sequence 1637, Ap
cl1014	153.6	6.7	6000	1	PCT-US07-13803-169	Sequence 169, App	1087	145.4	6.4	3470	7	US-11-272-833C-3	Sequence 3, Appli
cl1015	153.4	6.7	11779	8	US-60-970-396-3	Sequence 3, Appli	1088	145.4	6.4	4828	7	US-11-725-402A-7	Sequence 7, Appli
cl1016	153	6.7	1127	7	US-11-781-665-3008	Sequence 3008, Ap	cl1089	145.2	6.4	674	7	US-11-781-665-699	Sequence 699, App
cl1017	153	6.7	6926	7	US-11-490-374A-1345	Sequence 1345, Ap	cl1090	145.2	6.4	1647	7	US-11-781-665-167	Sequence 167, App
cl1018	153	6.7	6980	7	US-11-490-374A-1338	Sequence 1338, Ap	1091	145.2	6.4	2001	7	US-11-881-406-3747	Sequence 3747, Ap
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cl1020	152.8	6.7	231	6	US-10-587-791-653	Sequence 653, App	1093	145.2	6.4	2001	7	US-11-881-406-3749	Sequence 3749, Ap
cl1021	152.8	6.7	782	7	US-11-781-665-1704	Sequence 1704, Ap	1094	145.2	6.4	2001	7	US-11-881-406-3750	Sequence 3750, Ap
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1023	152.6	6.7	334	7	US-11-881-406-4183	Sequence 4183, Ap	cl1096	144.8	6.3	2207	7	US-11-781-665-868	Sequence 868, App
1024	152.6	6.7	1893	7	US-11-781-665-850	Sequence 850, App	1097	144.8	6.3	2281	7	US-11-490-374A-1965	Sequence 1965, Ap
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cl1026	152.4	6.7	419	7	US-11-881-406-2323	Sequence 2323, Ap	1099	144.6	6.3	999	7	US-11-881-406-3109	Sequence 3109, Ap
cl1027	152	6.7	1545	7	US-11-781-665-1001	Sequence 1001, Ap	cl1100	144.6	6.3	1162	7	US-11-781-665-1688	Sequence 1688, Ap
1028	151.8	6.6	1551	7	US-11-781-665-812	Sequence 812, App	cl1101	144.6	6.3	2204	7	US-11-832-009-46	Sequence 46, Appl
1029	151.6	6.6	1076	7	US-11-781-665-1646	Sequence 1646, Ap	cl1102	144.4	6.3	1392	7	US-11-881-406-2522	Sequence 2522, Ap
1030	151.4	6.6	1645	7	US-11-781-665-1973	Sequence 1973, Ap	cl1103	144.2	6.3	1267	7	US-11-781-665-1114	Sequence 1114, Ap
1031	151.4	6.6	2001	7	US-11-881-406-3786	Sequence 3786, Ap	cl1104	144.2	6.3	2719	7	US-11-781-665-1199	Sequence 1199, Ap
cl1032	151.4	6.6	2521	7	US-11-781-665-2173	Sequence 2173, Ap	cl1105	144.2	6.3	6000	1	PCT-US07-13803-162	Sequence 162, App
1033	151.4	6.6	5871	1	PCT-US07-13803-405	Sequence 405, App	cl1106	144	6.3	810	7	US-11-781-665-1031	Sequence 1031, Ap
cl1034	151.2	6.6	424	7	US-11-881-406-4156	Sequence 4156, Ap	cl1107	144	6.3	2212	7	US-11-884-496-723	Sequence 723, App
1035	151.2	6.6	2075	7	US-11-781-665-574	Sequence 574, App	cl1108	143.8	6.3	428	7	US-11-881-406-2122	Sequence 2122, Ap
1036	151.2	6.6	6000	1	PCT-US07-13803-162	Sequence 162, App	cl1109	143.8	6.3	1063	7	US-11-781-665-120	Sequence 120, App
cl1037	151	6.6	3161	7	US-11-781-665-1205	Sequence 1205, Ap	1110	143.8	6.3	1309	7	US-11-781-665-2351	Sequence 2351, Ap
cl1038	150.8	6.6	1305	7	US-11-781-665-1941	Sequence 1941, Ap	1111	143.8	6.3	2689	7	US-11-781-665-1818	Sequence 1818, Ap
cl1039	150.8	6.6	2190	7	US-11-781-665-2490	Sequence 2490, Ap	1112	143.8	6.3	2778	7	US-11-781-665-2904	Sequence 2904, Ap
1040	150.8	6.6	3633	7	US-11-884-496-678	Sequence 678, App	1113	143.8	6.3	2945	7	US-11-781-665-282	Sequence 282, App
1041	150.8	6.6	4290	7	US-11-884-496-653	Sequence 653, App	cl1114	143.8	6.3	4284	1	PCT-US07-13803-444	Sequence 444, App
cl1042	150.6	6.6	1479	7	US-11-781-665-2838	Sequence 2838, Ap	cl1115	143.6	6.3	1174	7	US-11-781-665-2111	Sequence 2111, Ap
cl1043	150.2	6.6	879	7	US-11-831-468-73	Sequence 73, Appl	cl1116	143.4	6.3	1541	7	US-11-781-665-2434	Sequence 2434, Ap
1044	150.2	6.6	2324	7	US-11-781-665-1612	Sequence 1612, Ap	cl1117	143.4	6.3	1577	7	US-11-781-665-1666	Sequence 1666, Ap
cl1045	150	6.6	971	7	US-11-781-665-2854	Sequence 2854, Ap	cl1118	143	6.3	2048	7	US-11-781-665-279	Sequence 279, App
1046	150	6.6	6000	1	PCT-US07-13803-119	Sequence 119, App	cl1119	142.8	6.3	754	7	US-11-781-665-617	Sequence 617, App
1047	150	6.6	6000	1	PCT-US07-13803-150	Sequence 150, App	1120	142.6	6.2	6000	1	PCT-US07-13803-114	Sequence 114, App
cl1048	149.6	6.5	1647	7	US-11-781-665-2355	Sequence 2355, Ap	cl1121	142.6	6.2	6000	1	PCT-US07-13803-155	Sequence 155, App

c1122	142.4	6.2	1467	7	US-11-781-665-2552	Sequence 2552, Ap
1123	142.2	6.2	915	7	US-11-781-665-301	Sequence 301, App
c1124	142	6.2	1061	7	US-11-781-665-1800	Sequence 1800, Ap
1125	142	6.2	1344	7	US-11-235-701A-373	Sequence 373, App
1126	141.8	6.2	936	7	US-11-781-665-1731	Sequence 1731, Ap
1127	141.8	6.2	1501	7	US-11-781-665-2604	Sequence 2604, Ap
1128	141.8	6.2	6000	1	PCT-US07-13803-95	Sequence 95, Appl
c1129	141.8	6.2	6000	1	PCT-US07-13803-226	Sequence 226, App
c1130	141.6	6.2	1120	7	US-11-781-665-2135	Sequence 2135, Ap
c1131	141.6	6.2	5727	7	US-11-490-374A-1306	Sequence 1306, Ap
c1132	141.6	6.2	5947	7	US-11-490-374A-1305	Sequence 1305, Ap
c1133	141.2	6.2	876	7	US-11-781-665-626	Sequence 626, App
1134	141.2	6.2	3644	7	US-11-847-733-25	Sequence 25, Appl
c1135	141	6.2	1125	7	US-11-884-496-636	Sequence 636, App
c1136	141	6.2	1138	7	US-11-781-665-2248	Sequence 2248, Ap
1137	141	6.2	2001	7	US-11-881-406-3771	Sequence 3771, Ap
1138	141	6.2	2001	7	US-11-881-406-3772	Sequence 3772, Ap
1139	141	6.2	2001	7	US-11-881-406-3773	Sequence 3773, Ap
c1140	140.8	6.2	1075	7	US-11-781-665-2542	Sequence 2542, Ap
1141	140.8	6.2	1544	7	US-11-781-665-2971	Sequence 2971, Ap
c1142	140.8	6.2	6000	1	PCT-US07-13803-191	Sequence 191, App
c1143	140.4	6.1	1020	7	US-11-781-665-1923	Sequence 1923, Ap
c1144	140.2	6.1	883	7	US-11-781-665-1024	Sequence 1024, Ap
1145	140.2	6.1	4232	7	US-11-781-905-1	Sequence 1, Appli
1146	140.2	6.1	5775	7	US-11-839-314-6	Sequence 6, Appli
1147	140.2	6.1	6641	7	US-11-816-601-718	Sequence 718, App
1148	140.2	6.1	6641	7	US-11-235-701A-328	Sequence 328, App
1149	140	6.1	428	7	US-11-881-406-1656	Sequence 1656, Ap
c1150	140	6.1	813	7	US-11-781-665-1942	Sequence 1942, Ap
1151	139.8	6.1	1679	7	US-11-881-406-3553	Sequence 3553, Ap
1152	139.8	6.1	1698	7	US-11-781-665-1493	Sequence 1493, Ap
1153	139.8	6.1	1865	7	US-11-881-406-3556	Sequence 3556, Ap
c1154	139.8	6.1	2001	7	US-11-881-406-3557	Sequence 3557, Ap
c1155	139.6	6.1	917	7	US-11-781-665-2234	Sequence 2234, Ap
1156	139.4	6.1	1050	7	US-11-781-665-2934	Sequence 2934, Ap
1157	139.4	6.1	2166	7	US-11-781-665-1235	Sequence 1235, Ap
1158	139.4	6.1	6000	1	PCT-US07-13803-9	Sequence 9, Appli
c1159	139.2	6.1	6000	1	PCT-US07-13803-117	Sequence 117, App
1160	139	6.1	410	7	US-11-881-406-2400	Sequence 2400, Ap
1161	139	6.1	10240	8	US-60-970-396-5	Sequence 5, Appli
c1162	138.8	6.1	1035	7	US-11-781-665-1590	Sequence 1590, Ap
1163	138.4	6.1	2251	7	US-11-781-665-1072	Sequence 1072, Ap
c1164	138	6.0	1830	7	US-11-781-665-848	Sequence 848, App
c1165	138	6.0	2486	7	US-11-781-665-1081	Sequence 1081, Ap
c1166	137.8	6.0	814	7	US-11-781-665-1567	Sequence 1567, Ap
c1167	137.6	6.0	1827	7	US-11-781-665-1824	Sequence 1824, Ap
c1168	137.6	6.0	2050	7	US-11-781-665-615	Sequence 615, App
c1169	137.4	6.0	2001	7	US-11-881-406-3843	Sequence 3843, Ap
c1170	137.4	6.0	2001	7	US-11-881-406-3844	Sequence 3844, Ap
c1171	137.4	6.0	2203	7	US-11-781-665-2421	Sequence 2421, Ap
c1172	137.2	6.0	1786	7	US-11-781-665-890	Sequence 890, App
1173	137.2	6.0	2105	7	US-11-781-665-1259	Sequence 1259, Ap
c1174	137	6.0	1795	7	US-11-781-665-1080	Sequence 1080, Ap
c1175	137	6.0	1808	7	US-11-781-665-1473	Sequence 1473, Ap
c1176	136.8	6.0	844	7	US-11-781-665-2512	Sequence 2512, Ap
1177	136.8	6.0	1535	7	US-11-781-665-2847	Sequence 2847, Ap
c1178	136.8	6.0	2208	7	US-11-702-018-1	Sequence 1, Appli
1179	136.8	6.0	3600	7	US-11-847-733-6	Sequence 6, Appli
1180	136.8	6.0	4827	7	US-11-816-601-70	Sequence 70, Appl
1181	136.8	6.0	7086	7	US-11-847-733-5	Sequence 5, Appli
c1182	136.6	6.0	713	7	US-11-781-665-2254	Sequence 2254, Ap
c1183	136.6	6.0	2366	7	US-11-781-665-2777	Sequence 2777, Ap
1184	136.4	6.0	1782	7	US-11-781-665-1485	Sequence 1485, Ap
c1185	136.4	6.0	3590	7	US-11-884-496-683	Sequence 683, App
c1186	136.2	6.0	817	7	US-11-781-665-2252	Sequence 2252, Ap
c1187	136.2	6.0	1095	7	US-11-781-665-2772	Sequence 2772, Ap
c1188	136.2	6.0	1633	7	US-11-781-665-2819	Sequence 2819, Ap
c1189	136.2	6.0	2472	7	US-11-884-496-647	Sequence 647, App
c1190	136.2	6.0	3591	7	US-11-490-374A-1815	Sequence 1815, Ap
c1191	136.2	6.0	3591	7	US-11-490-374A-1816	Sequence 1816, Ap
c1192	136.2	6.0	3591	7	US-11-490-374A-1817	Sequence 1817, Ap
c1193	136	6.0	997	7	US-11-881-406-2195	Sequence 2195, Ap
c1194	136	6.0	3080	7	US-11-832-009-45	Sequence 45, Appl

c1195	135.4	5.9	1026	7	US-11-781-665-2846	Sequence 2846, Ap
c1196	135.4	5.9	1055	7	US-11-781-665-1022	Sequence 1022, Ap
1197	135.4	5.9	2180	7	US-11-781-665-2510	Sequence 2510, Ap
c1198	135.2	5.9	2075	7	US-11-781-665-574	Sequence 574, App
c1199	135.2	5.9	6000	1	PCT-US07-13803-171	Sequence 171, App
c1200	135	5.9	2957	7	US-11-781-665-2659	Sequence 2659, Ap
c1201	135	5.9	6000	1	PCT-US07-13803-26	Sequence 26, Appl
c1202	135	5.9	6000	1	PCT-US07-13803-177	Sequence 177, App
c1203	134.6	5.9	2001	7	US-11-881-406-3381	Sequence 3381, Ap
c1204	134.4	5.9	1539	7	US-11-490-374A-1346	Sequence 1346, Ap
c1205	134.4	5.9	1539	7	US-11-490-374A-1351	Sequence 1351, Ap
c1206	134.4	5.9	1539	7	US-11-490-374A-1352	Sequence 1352, Ap
c1207	134.4	5.9	1562	7	US-11-490-374A-1350	Sequence 1350, Ap
c1208	134.4	5.9	1614	7	US-11-781-665-1222	Sequence 1222, Ap
c1209	134.4	5.9	1842	7	US-11-781-665-2921	Sequence 2921, Ap
c1210	134.2	5.9	583	7	US-11-781-665-2653	Sequence 2653, Ap
c1211	134.2	5.9	1552	7	US-11-781-665-341	Sequence 341, App
1212	134	5.9	410	7	US-11-881-406-1984	Sequence 1984, Ap
c1213	134	5.9	18997	7	US-11-835-336-32	Sequence 32, Appl
1214	133.8	5.9	6000	1	PCT-US07-13803-28	Sequence 28, Appl
c1215	133.8	5.9	6000	1	PCT-US07-13803-196	Sequence 196, App
1216	133.8	5.9	6000	1	PCT-US07-13803-268	Sequence 268, App
c1217	133.4	5.8	283	7	US-11-831-404-98	Sequence 98, Appl
c1218	133.4	5.8	1304	7	US-11-781-665-157	Sequence 157, App
c1219	133.4	5.8	6074	7	US-11-835-336-76	Sequence 76, Appl
1220	133.2	5.8	3760	1	PCT-US07-13803-340	Sequence 340, App
c1221	133	5.8	1422	7	US-11-781-665-1083	Sequence 1083, Ap
1222	132.8	5.8	1193	7	US-11-781-665-545	Sequence 545, App
c1223	132.8	5.8	6000	1	PCT-US07-13803-17	Sequence 17, Appl
c1224	132.8	5.8	6000	1	PCT-US07-13803-251	Sequence 251, App
1225	132.6	5.8	1504	7	US-11-781-665-563	Sequence 563, App
1226	132.4	5.8	420	7	US-11-881-406-3355	Sequence 3355, Ap
c1227	132.4	5.8	831	7	US-11-781-665-3068	Sequence 3068, Ap
1228	132.2	5.8	774	7	US-11-781-665-1769	Sequence 1769, Ap
c1229	132	5.8	699	7	US-11-781-665-1137	Sequence 1137, Ap
c1230	131.8	5.8	379	7	US-11-881-406-2141	Sequence 2141, Ap
c1231	131.8	5.8	998	7	US-11-781-665-1715	Sequence 1715, Ap
1232	131.8	5.8	3564	7	US-11-814-954-2	Sequence 2, Appli
c1233	131.6	5.8	7787	7	US-11-490-374A-1234	Sequence 1234, Ap
c1234	131.6	5.8	7787	7	US-11-490-374A-1236	Sequence 1236, Ap
c1235	131.6	5.8	7787	7	US-11-490-374A-1237	Sequence 1237, Ap
c1236	131.6	5.8	7787	7	US-11-490-374A-1238	Sequence 1238, Ap
1237	131.4	5.8	1086	7	US-11-781-665-1218	Sequence 1218, Ap
c1238	131.4	5.8	1560	7	US-11-781-665-2953	Sequence 2953, Ap
1239	131.4	5.8	60401	1	PCT-US06-25800-36	Sequence 36, Appl
c1240	131.2	5.7	1041	7	US-11-781-665-2750	Sequence 2750, Ap
1241	131	5.7	1373	7	US-11-816-601-275	Sequence 275, App
1242	131	5.7	2001	7	US-11-881-406-1328	Sequence 1328, Ap
c1243	131	5.7	5659	7	US-11-835-336-13	Sequence 13, Appl
c1244	130.8	5.7	761	7	US-11-781-665-1411	Sequence 1411, Ap
c1245	130.4	5.7	396	7	US-11-881-406-3972	Sequence 3972, Ap
c1246	130.4	5.7	807	7	US-11-781-665-755	Sequence 755, App
1247	130.2	5.7	1828	7	US-11-781-665-1975	Sequence 1975, Ap
c1248	130	5.7	1061	7	US-11-781-665-388	Sequence 388, App
c1249	130	5.7	6000	1	PCT-US07-13803-238	Sequence 238, App
c1250	129.8	5.7	712	7	US-11-781-665-1885	Sequence 1885, Ap
c1251	129.8	5.7	1234	7	US-11-781-665-763	Sequence 763, App
c1252	129.8	5.7	1234	7	US-11-781-665-1097	Sequence 1097, Ap
1253	129.8	5.7	1801	7	US-11-781-665-229	Sequence 229, App
c1254	129.8	5.7	1874	7	US-11-781-665-584	Sequence 584, App
c1255	129.8	5.7	3775	7	US-11-847-733-71	Sequence 71, Appl
c1256	129.8	5.7	5310	7	US-11-835-336-17	Sequence 17, Appl
c1257	129.6	5.7	3644	7	US-11-847-733-25	Sequence 25, Appl
1258	129.6	5.7	4130	7	US-11-884-496-670	Sequence 670, App
c1259	129.6	5.7	5976	7	US-11-835-336-94	Sequence 94, Appl
c1260	129.4	5.7	9021	7	US-11-835-336-74	Sequence 74, Appl
c1261	129.2	5.7	678	7	US-11-781-665-1776	Sequence 1776, Ap
c1262	129.2	5.7	1067	7	US-11-781-665-1580	Sequence 1580, Ap
1263	129.2	5.7	3536	7	US-11-825-627-354	Sequence 354, App
c1264	128.8	5.6	1114	7	US-11-781-665-2562	Sequence 2562, Ap
1265	128.6	5.6	418	7	US-11-881-406-2807	Sequence 2807, Ap
c1266	128.4	5.6	1445	7	US-11-781-665-1329	Sequence 1329, Ap
c1267	128.4	5.6	6000	1	PCT-US07-13803-143	Sequence 143, App



cl1268	128.2	5.6	623	7	US-11-881-406-1779	Sequence 1779, Ap	cl1341	117.8	5.2	18997	7	US-11-835-336-31	Sequence 31, Appl
cl1269	128.2	5.6	802	7	US-11-781-665-938	Sequence 938, App	cl1342	117.2	5.1	1003	7	US-11-781-665-1330	Sequence 1330, Ap
cl1270	128.2	5.6	1485	7	US-11-781-665-2091	Sequence 2091, Ap	cl1343	117.2	5.1	3647	7	US-11-835-336-42	Sequence 42, Appl
1271	128.2	5.6	1935	7	US-11-883-496-3	Sequence 3, Appli	cl1344	117.2	5.1	5477	7	US-11-835-336-108	Sequence 108, App
cl1272	128.2	5.6	2001	7	US-11-881-406-3769	Sequence 3769, Ap	1345	117	5.1	6000	1	PCT-US07-13803-78	Sequence 78, Appl
cl1273	128	5.6	5659	7	US-11-835-336-14	Sequence 14, Appl	cl1346	116.8	5.1	2249	7	US-11-781-665-285	Sequence 285, App
cl1274	127.8	5.6	429	7	US-11-881-406-2593	Sequence 2593, Ap	cl1347	116.6	5.1	386	7	US-11-881-406-4081	Sequence 4081, Ap
cl1275	127.8	5.6	2001	7	US-11-881-406-2594	Sequence 2594, Ap	1348	116.6	5.1	1576	7	US-11-781-665-1524	Sequence 1524, Ap
cl1276	127.4	5.6	6271	7	US-11-835-336-61	Sequence 61, Appl	cl1349	116.6	5.1	2764	7	US-11-781-665-1547	Sequence 1547, Ap
1277	127.2	5.6	1631	7	US-11-781-665-2650	Sequence 2650, Ap	cl1350	116.4	5.1	619	7	US-11-744-695-17	Sequence 17, Appl
1278	126.8	5.6	3548	7	US-11-884-496-721	Sequence 721, App	1351	116.4	5.1	1936	7	US-11-781-665-2656	Sequence 2656, Ap
cl1279	126.4	5.5	6246	7	US-11-835-336-50	Sequence 50, Appl	cl1352	116	5.1	1391	7	US-11-781-665-1463	Sequence 1463, Ap
1280	126	5.5	637	7	US-11-781-665-2486	Sequence 2486, Ap	cl1353	116	5.1	2001	7	US-11-881-406-2107	Sequence 2107, Ap
1281	125.8	5.5	1293	7	US-11-781-665-2392	Sequence 2392, Ap	cl1354	115.8	5.1	228	6	US-10-587-791-432	Sequence 432, App
1282	125.8	5.5	2345	7	US-11-781-665-786	Sequence 786, App	cl1355	115.8	5.1	4001	7	US-11-835-336-10	Sequence 10, Appl
cl1283	125.8	5.5	6000	1	PCT-US07-13803-7	Sequence 7, Appli	cl1356	115.4	5.1	1112	7	US-11-781-665-1091	Sequence 1091, Ap
cl1284	125.8	5.5	6000	1	PCT-US07-13803-186	Sequence 186, App	cl1357	115.4	5.1	1300	7	US-11-781-665-2911	Sequence 2911, Ap
cl1285	125.8	5.5	7432	7	US-11-835-336-5	Sequence 5, Appli	1358	115.4	5.1	1904	7	US-11-781-665-2905	Sequence 2905, Ap
cl1286	125.8	5.5	14147	7	US-11-835-336-39	Sequence 39, Appl	1359	115.2	5.0	5477	7	US-11-835-336-107	Sequence 107, App
1287	125.6	5.5	2001	7	US-11-881-406-1966	Sequence 1966, Ap	cl1360	114.6	5.0	1453	7	US-11-781-665-1469	Sequence 1469, Ap
cl1288	125.4	5.5	4613	7	US-11-816-601-108	Sequence 108, App	1361	114.6	5.0	2001	7	US-11-881-406-3752	Sequence 3752, Ap
1289	125.2	5.5	402	7	US-11-881-406-1324	Sequence 1324, Ap	1362	114.6	5.0	2001	7	US-11-881-406-3753	Sequence 3753, Ap
cl1290	125.2	5.5	1377	7	US-11-781-665-794	Sequence 794, App	1363	114.2	5.0	2244	7	US-11-847-733-46	Sequence 46, Appl
cl1291	125.2	5.5	1544	7	US-11-781-665-2971	Sequence 2971, Ap	cl1364	113.8	5.0	1879	7	US-11-781-665-800	Sequence 800, App
cl1292	125.2	5.5	1625	7	US-11-781-665-1965	Sequence 1965, Ap	1365	113.6	5.0	1504	7	US-11-781-665-1972	Sequence 1972, Ap
cl1293	125	5.5	1084	7	US-11-781-665-1850	Sequence 1850, Ap	cl1366	113.2	5.0	1317	7	US-11-781-665-2500	Sequence 2500, Ap
cl1294	125	5.5	1610	7	US-11-781-665-1592	Sequence 1592, Ap	cl1367	113.2	5.0	9884	7	US-11-835-336-8	Sequence 8, Appli
cl1295	124.8	5.5	798	7	US-11-881-406-2523	Sequence 2523, Ap	cl1368	113	4.9	413	7	US-11-881-406-1439	Sequence 1439, Ap
1296	124.8	5.5	955	7	US-11-781-665-1424	Sequence 1424, Ap	cl1369	113	4.9	933	7	US-11-831-468-103	Sequence 103, App
1297	124.6	5.5	1345	7	US-11-781-665-2399	Sequence 2399, Ap	cl1370	113	4.9	4001	7	US-11-835-336-9	Sequence 9, Appli
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	235	499.4	21.9	542	14	DB059714	DB059714	DB059714
	236	499	21.8	528	14	DB255096	DB255096	DB255096
	237	499	21.8	539	14	DB256521	DB256521	DB256521
	238	499	21.8	540	14	DB001639	DB001639	DB001639
	239	499	21.8	571	14	DA890033	DA890033	DA890033
	240	498	21.8	540	14	DB244134	DB244134	DB244134
	241	497	21.8	537	14	DA489229	DA489229	DA489229
	242	496	21.7	568	14	DA706892	DA706892	DA706892
	243	495.8	21.7	588	14	DB364984	DB364984	DB364984
C	244	495	21.7	566	14	DB265802	DB265802	DB265802
	245	494	21.6	552	14	DA158656	DA158656	DA158656
	246	493.4	21.6	566	14	DA693173	DA693173	DA693173
	247	492	21.5	507	5	BX100624	BX100624	BX100624
	248	491	21.5	571	14	DA656346	DA656346	DA656346
	249	490	21.5	530	3	BM753270	BM753270	BM753270
	250	489.8	21.4	920	12	DV928382	DV928382	DV928382
	251	489	21.4	560	14	DA022777	DA022777	DA022777
	252	488.8	21.4	566	14	DA453539	DA453539	DA453539
	253	488	21.4	559	14	DB249814	DB249814	DB249814
C	254	487.6	21.3	584	14	DB364075	DB364075	DB364075
	255	487	21.3	528	14	DA761447	DA761447	DA761447
	256	486.8	21.3	561	14	DA884160	DA884160	DA884160
	257	485	21.2	557	14	DA275399	DA275399	DA275399
	258	482.2	21.1	550	7	AU152691	AU152691	AU152691
	259	482	21.1	547	14	DA999982	DA999982	DA999982
	260	480.4	21.0	568	14	DA999605	DA999605	DA999605
	261	479.4	21.0	869	12	DV932206	DV932206	DV932206
	262	479	21.0	521	14	DB248037	DB248037	DB248037
	263	478	20.9	518	14	DB208478	DB208478	DB208478
C	264	478	20.9	543	14	DA688482	DA688482	DA688482
	265	477.4	20.9	520	14	DA6224843	DA6224843	DA6224843
	266	476.4	20.9	526	14	DB207283	DB207283	DB207283
	267	476.4	20.9	569	14	DA149179	DA149179	DA149179
	268	476	20.8	516	14	DA008487	DA008487	DA008487
	269	476	20.8	517	3	BM838896	BM838896	BM838896
	270	470.2	20.6	522	7	AU157477	AU157477	AU157477
	271	469.6	20.6	504	14	DB319107	DB319107	DB319107
	272	469.4	20.6	472	2	BE301806	BE301806	BE301806
	273	468	20.5	496	14	DB195696	DB195696	DB195696
C	274	465	20.4	478	1	AI207832	AI207832	AI207832
	275	461.8	20.2	880	8	CB959572	CB959572	CB959572
	276	460.4	20.2	503	14	DA604196	DA604196	DA604196
	277	458.8	20.1	533	14	DA6224540	DA6224540	DA6224540
	278	452.4	19.8	506	14	DB208508	DB208508	DB208508
	279	451.6	19.8	583	4	BP248346	BP248346	BP248346
	280	451	19.7	564	14	DA014288	DA014288	DA014288
	281	450.6	19.7	697	13	DT891744	DT891744	DT891744
	282	448.6	19.6	528	14	DA698278	DA698278	DA698278
	283	447.6	19.6	692	13	DT895274	DT895274	DT895274

c	307	413	18.1	558	14	DA566772	DA566772	DA566772	DA566772
	308	412.6	18.1	420	14	DB509363	DB509363	DB509363	DB509363
	309	411.2	18.0	580	4	BP291358	BP291358	BP291358	BP291358
	310	411	18.0	441	3	BI031052	BI031052	IL5-MT026	IL5-MT026
	311	410.4	18.0	424	7	AW008237	wv52a11.x	AW008237	wv52a11.x
	312	406.8	17.8	412	3	BM820174	BM820174	K-EST0088	K-EST0088
	313	405	17.7	817	12	DV905318	DV905318	LB0213.C	LB0213.C
	314	405	17.7	853	11	EE234595	EE234595	LB02122.	LB02122.
	315	401	17.6	542	14	DA653625	DA653625	DA653625	DA653625
	316	398.4	17.4	539	14	DA689777	DA689777	DA689777	DA689777
	317	395.4	17.3	766	12	DY497041	DY497041	sh2P0020M	sh2P0020M
	318	393.6	17.2	469	14	DB262059	DB262059	DB262059	DB262059
	319	382	16.7	534	14	DA625746	DA625746	DA625746	DA625746
	320	382	16.7	559	14	DA632196	DA632196	DA632196	DA632196
	321	381.8	16.7	549	14	DA347002	DA347002	DA347002	DA347002
	322	379.8	16.6	555	14	DA710837	DA710837	DA710837	DA710837
	323	375.6	16.4	534	14	DB263443	DB263443	DB263443	DB263443
	324	363.8	15.9	439	11	H50932	H50932	Yo35f03.r1	Yo35f03.r1
	325	362	15.8	362	7	AW057870	AW057870	wv90d06.x	wv90d06.x
	326	361.4	15.8	734	10	CO879641	CO879641	BovGen.0	BovGen.0
	327	360.8	15.8	364	3	BI031814	BI031814	IL5-MT026	IL5-MT026
	328	358.4	15.7	373	4	BQ325584	BQ325584	MR4-CI018	MR4-CI018
	329	358.4	15.7	534	14	DA149350	DA149350	DA149350	DA149350
	330	356.2	15.6	880	10	CR851889	CR851889	CR851889	CR851889
	331	355	15.5	601	4	BP239336	BP239336	BP239336	BP239336
	332	352.8	15.4	464	2	BG899200	BG899200	HOA17-1-F	HOA17-1-F
	333	347.4	15.2	514	14	DA701250	DA701250	DA701250	DA701250
	334	345.4	15.1	707	9	CK974547	CK974547	4105473.B	4105473.B
	335	344.8	15.1	362	1	AI979095	AI979095	wr70d07.x	wr70d07.x
	336	344	15.1	828	13	DN870441	DN870441	nad06g02	nad06g02
c	337	340.4	14.9	342	11	F12992	F12992	HSC3HC051	HSC3HC051
	338	339.8	14.9	1015	5	BY703150	BY703150	BY703150	BY703150
	339	338.8	14.8	961	5	BY720875	BY720875	BY720875	BY720875
	340	335.8	14.7	567	3	BI682666	BI682666	463812.MA	463812.MA
	341	335	14.7	533	3	BM087304	BM087304	500042.MA	500042.MA
	342	334.8	14.7	562	12	DY048683	DY048683	000510BP	000510BP
	343	331.8	14.5	1036	3	BI410030	BI410030	602962510	602962510
	344	330.4	14.4	805	13	DT833902	DT833902	LB00423.	LB00423.
	345	328.2	14.4	764	13	DT848580	DT848580	LB00482.	LB00482.
	346	328.2	14.4	790	13	DT848455	DT848455	LB00482.	LB00482.
	347	327.8	14.4	886	4	BQ922735	BQ922735	AGENCOURT	AGENCOURT
	348	325.2	14.2	1018	3	BI416048	BI416048	602987331	602987331
	349	323	14.1	947	5	BY720818	BY720818	BY720818	BY720818
	350	317	13.9	496	14	DA703232	DA703232	DA703232	DA703232
	351	315.6	13.8	424	11	H51595	H51595	Yo35f03.s1	Yo35f03.s1
	352	309.6	13.6	806	5	BX9202338	BX9202338	BX9202338	BX9202338
	353	309.4	13.5	821	5	BX920277	BX920277	BX920277	BX920277
	354	301.4	13.2	364	3	BI029201	BI029201	IL5-MT026	IL5-MT026
	355	297.4	13.0	631	8	CF746243	CF746243	UI-M-GV0-	UI-M-GV0-
	356	296.2	13.0	439	14	DB4444501	DB4444501	DB4444501	DB4444501
c	357	291	12.7	701	4	BP147701	BP147701	BP147701	BP147701
	358	289.8	12.7	673	7	BB661915	BB661915	BB661915	BB661915
	359	288.6	12.6	784	9	CJ462354	CJ462354	CJ462354	CJ462354
	360	285.8	12.5	727	10	CN793285	CN793285	CN793285	CN793285
	361	281.8	12.3	439	14	DB442366	DB442366	DB442366	DB442366
	362	279.8	12.3	663	7	BB645954	BB645954	BB645954	BB645954
	363	278.6	12.2	323	2	BE710389	BE710389	BE710389	BE710389
	364	274.2	12.0	668	11	EE216707	EE216707	EE216707	EE216707
	365	273.8	12.0	691	14	DN117286	DN117286	DN117286	DN117286
	366	273.8	12.0	691	14	DN117635	DN117635	DN117635	DN117635
c	367	272.2	11.9	641	7	BB624968	BB624968	BB624968	BB624968
	368	269.4	11.8	683	13	DN280755	DN280755	DN280755	DN280755
	369	268.6	11.8	710	2	BG964611	BG964611	BG964611	BG964611
	370	268	11.7	762	13	DN870440	DN870440	DN870440	DN870440
	371	267.2	11.7	862	14	DN132822	DN132822	DN132822	DN132822
	372	266.6	11.7	671	8	CF789259	CF789259	CF789259	CF789259
	373	266.6	11.7	862	9	CN164398	CN164398	CN164398	CN164398
	374	265.2	11.6	314	4	BP224438	BP224438	BP224438	BP224438
	375	262.8	11.5	574	2	BE533293	BE533293	BE533293	BE533293
	376	262	11.5	295	14	DA446001	DA446001	DA446001	DA446001
c	377	261.8	11.5	560	2	BF046016	BF046016	BF046016	BF046016
	378	261.6	11.5	630	9	CK963012	CK963012	CK963012	CK963012
	379	261.6	11.5	630	9	CK971129	CK971129	CK971129	CK971129

380	261.6	11.5	771	10	CO809298	CO809298 AGENCOURT	453	229	10.0	1988	6	HSM802962	AL713640 Homo sapi
381	257	11.3	826	5	BX926783	BX926783 BX926783	454	229	10.0	2194	6	CR610806	CR610806 full-leng
382	255.6	11.2	848	9	CK449279	CK449279 892833 MA	455	229	10.0	2195	6	CR622984	CR622984 full-leng
383	253.2	11.1	388	3	BI024344	BI024344 CM3-MT029	456	228.8	10.0	541	14	DB353009	DB353009 DB353009
C 384	250.2	11.0	587	13	DN279685	DN279685 1160739 M	C 457	228.8	10.0	911	4	BQ676349	BQ676349 AGENCOURT
385	246.2	10.8	447	17	CG620426	CG620426 OST317492	C 458	228.8	10.0	941	4	BQ678783	BQ678783 AGENCOURT
386	245.6	10.8	323	14	D25954	D25954 HUMGS06728	C 459	228.8	10.0	956	4	BQ900958	BQ900958 AGENCOURT
387	245.4	10.7	555	13	DN339203	DN339203 LfB3523-0	460	228.6	10.0	497	7	AW974932	AW974932 EST387037
388	244	10.7	620	5	BX926593	BX926593 BX926593	C 461	228.6	10.0	1023	5	BX356060	BX356060 BX356060
C 389	243	10.6	269	11	F10587	F10587 HSC3HC052 n	462	228.6	10.0	2971	15	AF101960	AF101960 AF101960
390	241.4	10.6	251	10	CR555844	CR555844 DKFZp469A	C 463	228.4	10.0	512	3	BI494531	BI494531 df110h01.
391	239.4	10.5	341	7	AW478661	AW478661 21466 MAR	464	228.4	10.0	641	14	DB117312	DB117312 DB117312
C 392	237.6	10.4	436	3	BI497377	BI497377 df135g02.	465	228.4	10.0	755	4	BU615930	BU615930 UI-H-DF0-
C 393	237	10.4	253	7	AW087232	AW087232 xb97b03.x	466	228.4	10.0	981	4	BQ707985	BQ707985 AGENCOURT
394	236.4	10.4	579	7	AU145055	AU145055 AU145055	C 467	228.2	10.0	598	17	CG696805	CG696805 MUGQ_CH25
C 395	236	10.3	504	14	DA798480	DA798480 DA798480	C 468	228.2	10.0	714	18	CZ459896	CZ459896 MCF748h06
C 396	236	10.3	594	14	DA192037	DA192037 DA192037	C 469	228.2	10.0	1073	16	BZ610713	BZ610713 WHACI55TR
397	236	10.3	614	15	AQ055703	AQ055703 CIT-HSP-2	C 470	228	10.0	618	8	CD369000	CD369000 UI-H-Ft1-
C 398	236	10.3	676	18	AG075207	AG075207 Pan trogl	C 471	228	10.0	1042	5	BX338157	BX338157 BX338157
399	235.2	10.3	735	9	CK963207	CK963207 4077882 B	472	227.8	10.0	486	15	AQ939756	AQ939756 NR5-102R
400	235	10.3	598	7	AW913757	AW913757 uf56g09.y	473	227.6	10.0	556	7	AU152561	AU152561 AU152561
C 401	234.6	10.3	405	7	AW855803	AW855803 RCI-CT027	474	227.6	10.0	562	14	DA283098	DA283098 DA283098
402	234.6	10.3	547	18	CZ464372	CZ464372 MCF755f09	475	227.6	10.0	641	9	CK979245	CK979245 4111113 B
403	234.2	10.3	708	7	AW955693	AW955693 EST367763	C 476	227.6	10.0	658	15	AQ357800	AQ357800 CITBI-EI-
C 404	233.8	10.2	1028	3	BM564754	BM564754 AGENCOURT	C 477	227.6	10.0	680	15	AQ317036	AQ317036 CITBI-EI-
C 405	233.6	10.2	287	2	BF361648	BF361648 CM1-NN000	C 478	227.6	10.0	816	18	CZ450800	CZ450800 MCF731k11
C 406	233.4	10.2	771	12	EB528550	EB528550 303150 Pi	C 479	227.6	10.0	1106	5	BX355356	BX355356 BX355356
C 407	233.2	10.2	318	4	BU531754	BU531754 AGENCOURT	C 480	227.4	10.0	306	2	BF681619	BF681619 602155887
C 408	233.2	10.2	786	4	BU954286	BU954286 AGENCOURT	C 481	227.4	10.0	512	7	AV740009	AV740009 AV740009
C 409	233	10.2	569	14	DA777850	DA777850 DA777850	C 482	227.4	10.0	668	8	CD517214	CD517214 AGENCOURT
C 410	233	10.2	572	14	DA524408	DA524408 DA524408	483	227.2	9.9	358	2	BG236628	BG236628 nai46b07.
C 411	233	10.2	1329	2	BF984807	BF984807 602308054	C 484	227.2	9.9	423	7	AW819125	AW819125 RC3-ST028
C 412	232.8	10.2	376	1	AA579179	AA579179 nf28d09.s	C 485	227.2	9.9	429	15	AQ090219	AQ090219 HS 3009 A
413	232.8	10.2	695	3	BI146784	BI146784 602911863	C 486	227.2	9.9	558	14	DB019422	DB019422 DB019422
C 414	232.4	10.2	472	7	AW855730	AW855730 RCI-CT027	C 487	227.2	9.9	566	14	DA900739	DA900739 DA900739
C 415	232.2	10.2	548	14	DB273413	DB273413 DB273413	C 488	227.2	9.9	591	14	DA303160	DA303160 DA303160
C 416	231.6	10.1	551	14	DB269889	DB269889 DB269889	C 489	227.2	9.9	615	18	AG050659	AG050659 Pan trogl
C 417	231.6	10.1	655	18	DX813762	DX813762 MUGQ_CH25	C 490	227	9.9	552	4	BQ017601	BQ017601 UI-H-DI0-
C 418	231.6	10.1	914	5	BX435087	BX435087 BX435087	C 491	227	9.9	679	9	CN304238	CN304238 170004247
C 419	231.6	10.1	951	5	BX463923	BX463923 BX463923	C 492	227	9.9	4697	6	CR859207	CR859207 Pongo pyg
C 420	231.6	10.1	990	5	BX345245	BX345245 BX345245	493	226.8	9.9	544	14	DB344021	DB344021 DB344021
C 421	231.6	10.1	1207	15	AF102031	AF102031 AF102031	C 494	226.8	9.9	680	2	BG924866	BG924866 HNC38-1-C
C 422	231.6	10.1	1216	15	AF101533	AF101533 AF101533	C 495	226.8	9.9	779	15	AZ517787	AZ517787 RPCI-11-1
423	231.4	10.1	446	13	DN384707	DN384707 LIB3892-0	496	226.6	9.9	339	7	AW270258	AW270258 xp43e01.x
C 424	231.4	10.1	530	14	DN133295	DN133295 997137 MA	497	226.6	9.9	389	2	BF477463	BF477463 nac61e07.
C 425	231.2	10.1	588	14	DA100593	DA100593 DA100593	498	226.6	9.9	546	15	AQ548438	AQ548438 RPCI-11-4
C 426	230.8	10.1	340	7	AW855736	AW855736 RCI-CT027	C 499	226.6	9.9	574	14	DA090879	DA090879 DA090879
C 427	230.8	10.1	1009	5	BX344308	BX344308 BX344308	C 500	226.6	9.9	772	7	AU121695	AU121695 AU121695
C 428	230.6	10.1	317	4	BU602934	BU602934 AGENCOURT	501	226.6	9.9	792	8	CD655541	CD655541 AGENCOURT
C 429	230.6	10.1	518	2	BG577022	BG577022 602599429	502	226.6	9.9	820	8	CD653272	CD653272 AGENCOURT
C 430	230.6	10.1	955	2	BG029224	BG029224 602292436	503	226.6	9.9	894	15	AQ787773	AQ787773 HS 3072_A
C 431	230.6	10.1	1029	16	BZ610725	BZ610725 WHACK01TF	504	226.4	9.9	445	4	BQ008264	BQ008264 UI-H-EI0-
432	230.4	10.1	354	5	BX480821	BX480821 DKFZp686F	505	226.4	9.9	473	15	AQ242916	AQ242916 HS 2061_A
C 433	230.2	10.1	315	9	CN275226	CN275226 170006000	506	226.4	9.9	567	15	AQ546141	AQ546141 CITBI-EI-
C 434	230.2	10.1	534	7	AW500029	AW500029 UI-HF-BN0	507	226.4	9.9	685	18	ED009913	ED009913 MUGQ_CH25
C 435	230.2	10.1	543	14	DB231425	DB231425 DB231425	C 508	226.4	9.9	694	19	AG172896	AG172896 Pan trogl
C 436	230.2	10.1	667	9	CN392067	CN392067 170005998	509	226.4	9.9	761	5	CA426986	CA426986 UI-H-DF0-
C 437	230	10.1	510	2	BF965775	BF965775 602277404	C 510	226.4	9.9	1346	18	DU800579	DU800579 lv01 fp00
C 438	230	10.1	513	3	BI494511	BI494511 df110g02.	511	226.2	9.9	376	15	B78953	B78953 CIT-HSF-456
C 439	230	10.1	900	5	BX407077	BX407077 BX407077	512	226.2	9.9	547	5	BX472351	BX472351 DKFZp686K
440	229.8	10.1	340	7	AW468372	AW468372 he37a08.x	C 513	226.2	9.9	557	3	BM742596	BM742596 K-EST0015
441	229.6	10.1	738	5	AQ547540	AQ547540 RPCI-11-4	514	226.2	9.9	620	1	AL042635	AL042635 DKFZp434M
442	229.4	10.0	394	1	AA613627	AA613627 nol8d06.s	C 515	226.2	9.9	632	5	BX953656	BX953656 DKFZp781O
C 443	229.2	10.0	394	1	AA613627	AA613627 nol8d06.s	C 516	226.2	9.9	642	18	CZ454001	CZ454001 MCF735O22
444	229.2	10.0	487	5	BX954470	BX954470 DKFZp781N	C 517	226	9.9	516	1	AL449689	AL449689 AL449689
445	229.2	10.0	542	14	DB305045	DB305045 DB305045	518	226	9.9	560	14	DB264370	DB264370 DB264370
446	229.2	10.0	585	9	CK825907	CK825907 ik35a09.y	519	226	9.9	566	14	DB349252	DB349252 DB349252
447	229.2	10.0	675	3	BM994911	BM994911 UI-H-DI0-	C 520	226	9.9	635	8	CB216644	CB216644 NISC rq07
448	229.2	10.0	1890	6	CR624170	CR624170 full-leng	521	226	9.9	652	3	BM992081	BM992081 UI-H-DF1-
449	229	10.0	571	3	BM757793	BM757793 K-EST0037	522	226	9.9	741	15	AQ376674	AQ376674 RPCI11-16
450	229	10.0	626	3	BM750039	BM750039 K-EST0025	523	226	9.9	807	13	DR761844	DR761844 HESC4 133
C 451	229	10.0	791	8	CD104542	CD104542 AGENCOURT	C 524	225.8	9.9	451	3	BM853062	BM853062 K-EST0134
452	229	10.0	1925	6	CR602031	CR602031 full-leng	525	225.8	9.9	559	14	DA016896	DA016896 DA016896



c 526	225.8	9.9	665	18	AG049305	AG049305 Pan trogl
c 527	225.8	9.9	765	16	BZ604837	BZ604837 WHABV91TR
c 528	225.8	9.9	769	19	AG123414	AG123414 Pan trogl
c 529	225.6	9.9	427	1	AI821044	AI821044 yb96f10.y
c 530	225.6	9.9	438	1	AA584489	AA584489 nol1f12.s
c 531	225.6	9.9	735	1	AL042756	AL042756 DKFZp434C
c 532	225.6	9.9	780	14	CX866374	CX866374 HESC4_10_
c 533	225.6	9.9	5417	6	HSM803282	AL831975 Homo sapi
c 534	225.4	9.9	477	14	DA621338	DA621338 DA621338
c 535	225.4	9.9	767	16	BZ606672	BZ606672 WHAAO22TR
c 536	225.2	9.9	481	15	AQ244348	AQ244348 HS 2064_B
c 537	225.2	9.9	561	14	DA067793	DA067793 DA067793
c 538	225.2	9.9	700	7	AU253657	AU253657 AU253657
c 539	225.2	9.9	740	8	CB963410	CB963410 AGENCOURT
c 540	225.2	9.9	788	2	BG108021	BG108021 602279942
c 541	225.2	9.9	917	8	CD359746	CD359746 AGENCOURT
c 542	225.2	9.9	2940	6	CR858431	CR858431 Pongo pyg
c 543	225	9.9	499	15	AQ380362	AQ380362 RPCI11-15
c 544	225	9.9	512	10	CR543116	CR543116 DKFZp470I
c 545	225	9.9	623	7	AV762741	AV762741 AV762741
c 546	224.8	9.8	309	4	BU940813	BU940813 AGENCOURT
c 547	224.8	9.8	435	14	DA224227	DA224227 DA224227
c 548	224.8	9.8	440	7	AW408643	AW408643 UI-HF-BM0
c 549	224.8	9.8	565	4	BP264321	BP264321 BP264321
c 550	224.8	9.8	585	15	AQ668477	AQ668477 HS 5422_A
c 551	224.8	9.8	631	5	BX496221	BX496221 DKFZp779N
c 552	224.8	9.8	642	7	AV759557	AV759557 AV759557
c 553	224.8	9.8	680	16	BZ772360	BZ772360 mcv35e11.
c 554	224.8	9.8	979	3	BM468648	BM468648 AGENCOURT
c 555	224.8	9.8	3820	6	HSM803830	AL832522 Homo sapi
c 556	224.8	9.8	3820	6	HSM803831	AL831957 Homo sapi
c 557	224.6	9.8	440	15	AQ593063	AQ593063 HS 5457_A
c 558	224.6	9.8	447	1	AL596543	AL596543 DKFZp451G
c 559	224.6	9.8	456	15	AQ122741	AQ122741 HS 3088_A
c 560	224.6	9.8	504	15	BH001309	BH001309 UP_391-8J
c 561	224.6	9.8	536	15	AQ391735	AQ391735 CITBI-E1-
c 562	224.6	9.8	604	15	AQ262198	AQ262198 CITBI-E1-
c 563	224.6	9.8	795	18	DU797114	DU797114 fv01 fp00
c 564	224.6	9.8	878	5	BX431169	BX431169 BX431169
c 565	224.6	9.8	2320	6	CR860114	CR860114 Pongo pyg
c 566	224.4	9.8	572	7	AU145224	AU145224 AU145224
c 567	224.4	9.8	651	1	AL707137	AL707137 DKFZp686C
c 568	224.4	9.8	660	5	BX484570	BX484570 DKFZp686I
c 569	224.4	9.8	1130	2	BE888786	BE888786 601513704
c 570	224.4	9.8	3577	8	CB617708	CB617708 OX-TES-2
c 571	224.2	9.8	332	1	AA574442	AA574442 nf46g11.s
c 572	224.2	9.8	339	4	BU564846	BU564846 AGENCOURT
c 573	224.2	9.8	456	7	AW021917	AW021917 df30a07.y
c 574	224.2	9.8	491	9	CK902916	CK902916 ip33g03.x
c 575	224.2	9.8	559	14	DA341077	DA341077 DA341077
c 576	224.2	9.8	602	2	BF030641	BF030641 601560021
c 577	224.2	9.8	629	9	CK003458	CK003458 AGENCOURT
c 578	224.2	9.8	671	19	AG164586	AG164586 Pan trogl
c 579	224.2	9.8	685	9	CN274874	CN274874 170006000
c 580	224.2	9.8	694	13	DT892500	DT892500 1474931_M
c 581	224.2	9.8	723	5	BX642407	BX642407 DKFZp686C
c 582	224.2	9.8	942	2	BG287829	BG287829 602384181
c 583	224	9.8	463	1	AA563770	AA563770 nk18c10.s
c 584	224	9.8	529	1	AA680243	AA680243 ac86a01.s
c 585	224	9.8	553	15	AQ246228	AQ246228 HS 2063_B
c 586	224	9.8	561	8	CB549179	CB549179 MMPL0003_
c 587	224	9.8	636	18	ED007091	ED007091 MUGQ_CH25
c 588	224	9.8	960	5	BX407738	BX407738 BX407738
c 589	224	9.8	963	3	BI862349	BI862349 603389135
c 590	224	9.8	4635	6	CR857664	CR857664 Pongo pyg
c 591	223.8	9.8	500	15	AQ194178	AQ194178 RPCI11-65
c 592	223.8	9.8	503	14	DB306267	DB306267 DB306267
c 593	223.8	9.8	665	19	AG107938	AG107938 Pan trogl
c 594	223.8	9.8	750	19	AG184338	AG184338 Pan trogl
c 595	223.8	9.8	841	2	BG256457	BG256457 602370182
c 596	223.6	9.8	310	8	CD518028	CD518028 AGENCOURT
c 597	223.6	9.8	329	8	CD559092	CD559092 AGENCOURT
c 598	223.6	9.8	450	14	DB459908	DB459908 DB459908

c 599	223.6	9.8	514	2	BF814446	BF814446 MR2-CI018
c 600	223.6	9.8	645	10	CR752070	CR752070 DKFZp469F
c 601	223.6	9.8	742	2	BG431052	BG431052 602498667
c 602	223.6	9.8	848	19	CR961389	CR961389 Homo sapi
c 603	223.4	9.8	463	14	DA087633	DA087633 DA087633
c 604	223.4	9.8	477	8	CB067450	CB067450 iq37a09.x
c 605	223.4	9.8	497	15	AQ635538	AQ635538 RPCI-11-4
c 606	223.4	9.8	520	15	AQ877271	AQ877271 HS_2142_B
c 607	223.4	9.8	522	1	AL708846	AL708846 DKFZp686J
c 608	223.4	9.8	528	15	AQ377485	AQ377485 RPCI11-16
c 609	223.4	9.8	543	14	DB348633	DB348633 DB348633
c 610	223.4	9.8	546	14	DB279941	DB279941 DB279941
c 611	223.4	9.8	566	4	BP262254	BP262254 BP262254
c 612	223.4	9.8	578	14	DB371589	DB371589 DB371589
c 613	223.4	9.8	583	4	BP261956	BP261956 BP261956
c 614	223.4	9.8	584	7	AV721886	AV721886 AV721886
c 615	223.4	9.8	635	7	AV711430	AV711430 AV711430
c 616	223.4	9.8	782	1	AL598828	AL598828 DKFZp313L
c 617	223.4	9.8	927	1	AL536665	AL536665 AL536665
c 618	223.4	9.8	1708	6	CR596492	CR596492 full-leng
c 619	223.4	9.8	2334	6	BC018303	BC018303 Homo sapi
c 620	223.2	9.8	431	9	CN413118	CN413118 170005326
c 621	223.2	9.8	457	8	CF788452	CF788452 860404_MA
c 622	223.2	9.8	624	19	AG098912	AG098912 Pan trogl
c 623	223.2	9.8	631	4	BU674105	BU674105 UI-CF-DU0
c 624	223.2	9.8	651	7	AU131834	AU131834 AU131834
c 625	223.2	9.8	669	19	AG182560	AG182560 Pan trogl
c 626	223	9.8	223	2	BF793997	BF793997 602254640
c 627	223	9.8	424	8	CD238242	CD238242 FNPAXG05
c 628	223	9.8	546	14	DA516684	DA516684 DA516684
c 629	223	9.8	576	14	DA615550	DA615550 DA615550
c 630	223	9.8	583	15	AQ391722	AQ391722 CITBI-E1-
c 631	223	9.8	693	19	AG111039	AG111039 Pan trogl
c 632	222.8	9.8	301	12	DW420151	DW420151 HHAGE0198
c 633	222.8	9.8	474	14	DB232036	DB232036 DB232036
c 634	222.8	9.8	495	5	BX956614	BX956614 DKFZp781C
c 635	222.8	9.8	534	15	AQ282060	AQ282060 RPCI11-81
c 636	222.8	9.8	600	15	AQ075668	AQ075668 CIT-HSP-2
c 637	222.8	9.8	643	18	AG052500	AG052500 Pan trogl
c 638	222.8	9.8	649	14	DA326552	DA326552 DA326552
c 639	222.8	9.8	661	14	DA570357	DA570357 DA570357
c 640	222.8	9.8	688	4	BQ447037	BQ447037 UI-H-EU1-
c 641	222.8	9.8	719	18	DX582587	DX582587 MUGQ_CH25
c 642	222.8	9.8	748	18	ED017328	ED017328 MUGQ_CH25
c 643	222.8	9.8	750	18	CZ459718	CZ459718 MCF748c12
c 644	222.8	9.8	909	8	CD299999	CD299999 AGENCOURT
c 645	222.8	9.8	1983	6	CR861149	CR861149 Pongo pyg
c 646	222.6	9.7	337	12	DW409824	DW409824 HHAGE0105
c 647	222.6	9.7	376	1	AI623764	AI623764 ts23a08.x
c 648	222.6	9.7	514	9	CN414996	CN414996 328801351
c 649	222.6	9.7	540	15	AQ415039	AQ415039 RPCI-11-2
c 650	222.6	9.7	556	7	AU152964	AU152964 AU152964
c 651	222.6	9.7	558	4	BU681086	BU681086 UI-CF-EC1
c 652	222.6	9.7	565	14	DA137218	DA137218 DA137218
c 653	222.6	9.7	565	14	DA771719	DA771719 DA771719
c 654	222.6	9.7	642	9	CN483194	CN483194 hw29d11.y
c 655	222.6	9.7	667	2	BG577280	BG577280 602595473
c 656	222.6	9.7	687	5	CA445710	CA445710 UI-H-ED0-
c 657	222.6	9.7	765	18	ED014316	ED014316 MUGQ_CH25
c 658	222.6	9.7	768	5	BX327610	BX327610 BX327610
c 659	222.6	9.7	792	7	AU118852	AU118852 AU118852
c 660	222.6	9.7	818	14	CX871639	CX871639 HESC4_59_
c 661	222.6	9.7	867	4	BQ232704	BQ232704 AGENCOURT
c 662	222.6	9.7	882	8	CD516256	CD516256 AGENCOURT
c 663	222.6	9.7	917	8	CD558585	CD558585 AGENCOURT
c 664	222.6	9.7	941	4	BQ711583	BQ711583 AGENCOURT
c 665	222.6	9.7	1601	6	BC015184	BC015184 Homo sapi
c 666	222.4	9.7	507	18	DX563314	DX563314 MUGQ_CH25
c 667	222.4	9.7	580	2	BE392138	BE392138 601308007
c 668	222.4	9.7	583	4	BP249631	BP249631 BP249631
c 669	222.4	9.7	717	19	AG177220	AG177220 Pan trogl
c 670	222.2	9.7	356	15	B70864	B70864 CIT-HSP-206
c 671	222.2	9.7	389	7	AW271904	AW271904 xr42e04.x

672	222.2	9.7	498	5	BX645799	BX645799 DKFZp781E	C	745	221.2	9.7	703	2	BG429978	BG429978 602495040
673	222.2	9.7	579	18	DX815132	DX815132 MUGQ_CH25	C	746	221.2	9.7	1003	3	BM450614	BM450614 AGENCOURT
674	222.2	9.7	611	15	AQ585842	AQ585842 RPCI-11-4	C	747	221.2	9.7	1077	1	AL524675	AL524675 AL524675
675	222.2	9.7	656	18	AG059506	AG059506 Pan trogl		748	221.2	9.7	1926	6	CR859560	CR859560 Pongo pyg
676	222	9.7	344	12	DW467706	DW467706 HHAGE0089		749	221	9.7	518	5	BX952917	BX952917 DKFZp781C
	222	9.7	461	1	AA225406	AA225406 nc24d02.r		750	221	9.7	526	10	CR556387	CR556387 DKFZp459P
677	222	9.7	513	3	BI494510	BI494510 df110g02.		751	221	9.7	537	15	AZ254548	AZ254548 HSC 00142
678	222	9.7	513	3	BI494530	BI494530 df110h01.		752	221	9.7	547	14	DA696294	DA696294 DA696294
679	222	9.7	556	4	BU658064	BU658064 cl31f08.z	C	753	221	9.7	582	14	DA172599	DA172599 DA172599
680	222	9.7	556	4	BU658064	BU658064 cl31f08.z	C	754	221	9.7	664	2	BE395137	BE395137 601310764
681	222	9.7	566	14	DA330565	DA330565 DA330565	C	755	221	9.7	692	18	AG065442	AG065442 Pan trogl
682	222	9.7	571	4	BQ086265	BQ086265 ij20e04.y		756	221	9.7	748	5	BX501280	BX501280 DKFZp7790
683	222	9.7	570	9	CK822946	CK822946 ij20e04.y		757	221	9.7	754	14	CX870603	CX870603 HESC4_47
684	222	9.7	623	5	BX489100	BX489100 DKFZp686E	C	758	221	9.7	785	18	ED013960	ED013960 MUGQ_CH25
685	222	9.7	629	19	AG139479	AG139479 Pan trogl		759	221	9.7	823	16	BZ608535	BZ608535 WHACA90TR
686	222	9.7	640	8	CF128614	CF128614 UI-HF-ET0		760	221	9.7	827	5	BX414525	BX414525 BX414525
687	222	9.7	659	19	AG148163	AG148163 Pan trogl	C	761	221	9.7	1010	3	BM465334	BM465334 AGENCOURT
688	222	9.7	694	8	CF124970	CF124970 UI-HF-EL0	C	762	221	9.7	4360	6	CR749270	CR749270 Homo sapi
689	222	9.7	727	12	EB388118	EB388118 nbj40b07.	C	763	221	9.7	5957	6	BSM800277	BSM800277 Homo sapi
690	222	9.7	858	15	AQ742838	AQ742838 HS_5482_B	C	764	220.8	9.7	365	2	BF751949	BF751949 RC4-BN053
691	222	9.7	910	4	BU850247	BU850247 AGENCOURT	C	765	220.8	9.7	392	1	AI246796	AI246796 qx72a01.x
692	222	9.7	915	4	BU149187	BU149187 AGENCOURT	C	766	220.8	9.7	470	14	DA107367	DA107367 DA107367
693	222	9.7	924	2	BG697612	BG697612 602660853	C	767	220.8	9.7	547	4	BU600474	BU600474 AGENCOURT
694	222	9.7	1035	4	BQ217751	BQ217751 AGENCOURT	C	768	220.8	9.7	643	19	AG169898	AG169898 Pan trogl
695	221.8	9.7	377	14	DB787367	DB787367 DB787367		769	220.8	9.7	669	14	CX866917	CX866917 HESC4_14
	221.8	9.7	404	7	AW504224	AW504224 UI-HF-BN0		770	220.8	9.7	678	5	CA413435	CA413435 UI-H-EZ0-
696	221.8	9.7	447	15	AQ242689	AQ242689 HS_2058_B		771	220.8	9.7	711	18	AG010148	AG010148 Homo sapi
697	221.8	9.7	452	9	CN275878	CN275878 17006000	C	772	220.8	9.7	729	18	DX822465	DX822465 MUGQ_CH25
698	221.8	9.7	484	1	AI017251	AI017251 ov03g05.x	C	773	220.8	9.7	803	16	BZ601931	BZ601931 WHADO92TR
699	221.8	9.7	554	14	DA105249	DA105249 DA105249		774	220.8	9.7	911	2	BG618992	BG618992 602616510
700	221.8	9.7	554	18	DU638051	DU638051 Ciuffi-HI		775	220.8	9.7	3143	6	BSM805999	BSM805999 Homo sapi
701	221.8	9.7	554	18	DU638051	DU638051 Ciuffi-HI		776	220.6	9.7	401	1	AI358384	AI358384 qw20d04.x
702	221.8	9.7	578	14	DA933755	DA933755 DA933755	C	777	220.6	9.7	416	2	BE062476	BE062476 QV4-BT025
703	221.8	9.7	586	15	AQ196559	AQ196559 CIT-HSP-2	C	778	220.6	9.7	444	4	BU429807	BU429807 UI-HF-BN0
704	221.8	9.7	637	5	CA428427	CA428427 UI-H-DF0-		779	220.6	9.7	454	16	BZ892950	BZ892950 UP_508-19
705	221.8	9.7	709	4	BQ181930	BQ181930 UI-H-EU0-	C	780	220.6	9.7	455	15	AQ167232	AQ167232 HS_3171_A
706	221.8	9.7	5940	6	CR627133	CR627133 Homo sapi	C	781	220.6	9.7	459	1	AI598003	AI598003 ts05d01.x
707	221.6	9.7	432	1	AI003611	AI003611 zF99b04.s		782	220.6	9.7	479	15	AQ225492	AQ225492 HS_2007_B
708	221.6	9.7	447	2	BE147833	BE147833 RC3-HT023		783	220.6	9.7	481	8	CB147163	CB147163 K-EST0202
	221.6	9.7	482	4	BU735500	BU735500 UI-E-DW0-	C	784	220.6	9.7	553	14	DB104990	DB104990 DB104990
709	221.6	9.7	562	5	BX481151	BX481151 DKFZp686N	C	785	220.6	9.7	673	1	AL696209	AL696209 DKFZp686C
710	221.6	9.7	572	14	DB046356	DB046356 DB046356	C	786	220.6	9.7	675	19	AG176894	AG176894 Pan trogl
711	221.6	9.7	596	7	AW962298	AW962298 EST374371	C	787	220.6	9.7	1039	3	BM914519	BM914519 AGENCOURT
712	221.6	9.7	596	7	AW962298	AW962298 EST374371		788	220.6	9.7	305	7	AW732188	AW732188 ba06f05.x
713	221.6	9.7	625	5	CA430874	CA430874 UI-H-FL1-	C	789	220.4	9.6	434	10	CR976138	CR976138 CR976138
714	221.6	9.7	662	18	AG074486	AG074486 Pan trogl	C	790	220.4	9.6	548	14	DA101825	DA101825 DA101825
715	221.6	9.7	689	19	AG092596	AG092596 Pan trogl	C	791	220.4	9.6	583	14	DB153528	DB153528 DB153528
716	221.6	9.7	748	15	AQ426022	AQ426022 CITBI-E1-	C	792	220.4	9.6	592	14	DA102631	DA102631 DA102631
717	221.6	9.7	1071	5	BX402079	BX402079 BX402079		793	220.4	9.6	593	14	DB161277	DB161277 DB161277
	221.6	9.7	5440	6	BSM803133	BSM803133 Homo sapi	C	794	220.4	9.6	599	4	BU676947	BU676947 UI-CF-DU1
718	221.6	9.7	5440	6	BSM803133	BSM803133 Homo sapi	C	795	220.4	9.6	658	15	AQ393450	AQ393450 CITBI-E1-
719	221.4	9.7	389	5	BX484792	BX484792 DKFZp686H	C	796	220.4	9.6	671	12	EB386691	EB386691 nbj19f09.
720	221.4	9.7	434	1	AA610509	AA610509 np93g07.s	C	797	220.4	9.6	682	19	AG148469	AG148469 Pan trogl
721	221.4	9.7	439	2	BF760919	BF760919 CM0-CS004		798	220.4	9.6	797	15	AY758761	AY758761 RP43-99b9
	221.4	9.7	466	4	BU617568	BU617568 UI-H-DF0-	C	799	220.2	9.6	392	2	BG944147	BG944147 ax47a10.x
722	221.4	9.7	492	5	BX280214	BX280214 BX280214	C	800	220.2	9.6	411	9	CK816169	CK816169 AGENCOURT
723	221.4	9.7	492	5	BX280214	BX280214 BX280214	C	801	220.2	9.6	447	14	DB107238	DB107238 DB107238
724	221.4	9.7	515	15	BH634642	BH634642 TAR-CH5-N	C	802	220.2	9.6	458	1	AI733856	AI733856 zol9c03.y
725	221.4	9.7	566	15	AQ274827	AQ274827 RPCI-1-21		803	220.2	9.6	480	15	AQ415807	AQ415807 RPCI-11-2
726	221.4	9.7	575	7	AW574976	AW574976 UI-HF-BN0	C	804	220.2	9.6	500	15	AQ428772	AQ428772 CITBI-E1-
727	221.4	9.7	622	2	BG476240	BG476240 602521795		805	220.2	9.6	508	12	DW525942	DW525942 CYLA_3622
	221.4	9.7	622	2	BG476240	BG476240 602521910	C	806	220.2	9.6	537	10	CR544001	CR544001 DKFZp470G
728	221.4	9.7	697	15	AQ054805	AQ054805 CIT-HSP-2	C	807	220.2	9.6	560	4	BQ287748	BQ287748 ik35a09.x
729	221.4	9.7	697	15	AQ054805	AQ054805 CIT-HSP-2	C	808	220.2	9.6	675	4	BU664420	BU664420 cl116d07.
730	221.4	9.7	698	5	CA431502	CA431502 UI-H-FT0-	C	809	220.2	9.6	695	9	CN277620	CN277620 170006001
731	221.4	9.7	760	18	DX818101	DX818101 MUGQ_CH25	C	810	220.2	9.6	830	18	DX415865	DX415865 MUGQ_CH25
732	221.4	9.7	807	8	CD643859	CD643859 AGENCOURT	C	811	220.2	9.6	835	18	CZ457689	CZ457689 MCF745c16
733	221.4	9.7	967	4	BQ707517	BQ707517 AGENCOURT	C	812	220	9.6	220	11	H60061	H60061 yr19f06.s1
734	221.4	9.7	1016	4	BQ707142	BQ707142 AGENCOURT	C	813	220	9.6	441	1	AI732120	AI732120 ac86a01.x
735	221.4	9.7	1400	6	BC016013	BC016013 Homo sapi	C	814	220	9.6	441	1	AI732180	AI732180 ac85g01.x
736	221.2	9.7	369	1	AA528390	AA528390 ne83g02.s		815	220	9.6	498	1	AA579566	AA579566 nf17d09.s
	221.2	9.7	514	7	AW190505	AW190505 xl63a09.x	C	816	220	9.6	528	1	AA572685	AA572685 nf18h09.s
737	221.2	9.7	515	15	AQ565859	AQ565859 HS_5318_A	C	817	220	9.6	574	14	DA311459	DA311459 DA311459
738	221.2	9.7	515	15	AQ565859	AQ565859 HS_5318_A								
739	221.2	9.7	572	14	DB236781	DB236781 DB236781	C							
740	221.2	9.7	596	15	B95532	B95532 CIT-HSP-216								
741	221.2	9.7	622	4	BU158469	BU158469 AGENCOURT	C							
742	221.2	9.7	663	18	CZ464233	CZ464233 MCF755c03								
743	221.2	9.7	664	19	AG173858	AG173858 Pan trogl	C							
744	221.2	9.7	674	18	AG068517	AG068517 Pan trogl	C							

818 220 9.6 604 12 EC327580 GUTF09168  
819 220 9.6 617 10 CV574570 oe26a09.Y  
820 220 9.6 649 14 DB527805  
C 821 220 9.6 687 10 CR772263 DKF2p468P  
822 220 9.6 858 18 CZ451896  
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867 219.4 9.6 685 5 BX497635  
868 219.4 9.6 733 16 BZ611870  
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899 219 9.6 899 14 DA011940  
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C 901 219 9.6 901 8 CB146604  
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C 903 219 9.6 903 1 AL597814  
C 904 219 9.6 904 8 CB135613  
C 905 219 9.6 905 8 CB141203  
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963 218.4 9.6 963 18 CZ452536

AQ381396 RPCI11-13  
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DA882749 DA882749  
DA209580 DA209580  
DA357821 DA357821  
CZ455724 MCF738F08  
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DA011940 DA011940  
DA387076 DA387076  
CB146604 K-EST0202  
CB148826 K-EST0205  
AL597814 DKF2p313A  
CB135613 K-EST0187  
CB141203 K-EST0194  
AQ538235 RPCI-11-3  
BX457079 BX457079  
AG081865 Pan trogl  
AQ026964 CIT-HSP-2  
BM454752 AGENCOURT  
BX506443 DKF2p779B  
CD365151 UI-H-FT2-  
BM665558 UI-E-CL1-  
CX784339 HESC3 33  
DA568957 DA568957-  
AW504435 UI-HF-BN0  
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BM993628 UI-H-DH0-  
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AQ390912 CITBI-E1-  
B65955 CIT-HSP-202  
AQ490878 RPCI-11-2  
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BM823453 K-EST0094  
BU685838 UI-CF-DU1  
AG183158 Pan trogl  
BZ602401 WHAAR60TR  
CA448487 UI-H-EI0-  
BX404719 BX404719  
BE139267 xr68a06.x  
B91064 CIT-HSP-216  
DA327318 DA327318  
CR774476 DKF2p459G  
DA222896 DA222896  
AV737931 AV737931  
DA803349 DA803349  
DA405230 DA405230  
DA625579 DA625579  
DA436188 DA436188  
DB320019 DB320019  
DN994475 TC110312  
AV761106 AV761106  
BF854308 MR2-EN009  
DX569934 MUGQ\_CH25  
DA647137 DA647137  
AW976010 EST388119  
AQ528690 RPCI-11-3  
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DU710536 aav01\_fp0  
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AW167154 xg71f10.x  
AV710482 AV710482  
AA634837 ab28f04.r  
CA867048 ir56f02.x  
BF814327 MR2-CI012  
DB016498 DB016498  
CA868535 ir81a07.x  
BM876405 ij58d11.y  
DA146497 DA146497  
AQ546229 CITBI-E1-  
AQ387117 RPCI11-15  
CZ452536 MCF733p11



964	218.4	9.6	854	15	AQ747026	AQ747026 HS 5538_A	c1037	217.8	9.5	866	6	CR590505	CR590505 full-leng
c 965	218.4	9.6	1345	7	AV762220	AV762220 AV762220	1038	217.8	9.5	894	4	BUI89287	BUI89287 AGENCOURT
966	218.2	9.6	317	15	AQ035006	AQ035006 CIT-HSP-2	1039	217.8	9.5	964	16	BZ600930	BZ600930 WHACI84TF
c 967	218.2	9.6	322	4	BU928933	BU928933 AGENCOURT	c1040	217.8	9.5	988	8	CD518499	CD518499 AGENCOURT
c 968	218.2	9.6	351	2	BF974756	BF974756 602245404	1041	217.8	9.5	1598	6	CR611538	CR611538 full-leng
c 969	218.2	9.6	351	2	BG684452	BG684452 602636211	1042	217.8	9.5	1973	6	AF289611	AF289611 Homo sapi
c 970	218.2	9.6	351	2	BG685274	BG685274 602637184	c1043	217.8	9.5	360	15	B91708	B91708 CIT-HSP-217
c 971	218.2	9.6	351	2	BG685533	BG685533 602637504	c1044	217.6	9.5	364	12	DW463025	DW463025 HHAGE0057
c 972	218.2	9.6	400	14	DB317789	DB317789 DB317789	c1045	217.6	9.5	445	1	AI570943	AI570943 to24c10.x
c 973	218.2	9.6	412	2	BF809041	BF809041 PM4-CI015	1046	217.6	9.5	466	14	DA222202	DA222202 DA222202
974	218.2	9.6	425	1	AI471691	AI471691 t199e11.x	1047	217.6	9.5	513	14	DA990685	DA990685 DA990685
975	218.2	9.6	464	4	BQ775040	BQ775040 UI-H-FH0-	c1048	217.6	9.5	518	1	AL036282	AL036282 DKFZp564M
c 976	218.2	9.6	464	4	BU589713	BU589713 AGENCOURT	c1049	217.6	9.5	530	10	CR548390	CR548390 DKFZp459E
977	218.2	9.6	509	2	BE294700	BE294700 601173920	1050	217.6	9.5	533	15	AZ517333	AZ517333 RPCI-11-2
978	218.2	9.6	524	14	DB361653	DB361653 DB361653	c1051	217.6	9.5	534	14	DA622364	DA622364 DA622364
979	218.2	9.6	530	5	BX512983	BX512983 BX512983	c1052	217.6	9.5	536	14	DB305212	DB305212 DB305212
c 980	218.2	9.6	622	7	AV761862	AV761862 AV761862	c1053	217.6	9.5	539	14	DA311387	DA311387 DA311387
981	218.2	9.6	647	5	CA428170	CA428170 UI-H-DF0-	c1054	217.6	9.5	570	18	CZ457323	CZ457323 MCF740K16
982	218.2	9.6	690	5	BX484572	BX484572 DKFZp686I	c1055	217.6	9.5	576	14	DB164758	DB164758 DB164758
c 983	218.2	9.6	734	8	CB998641	CB998641 AGENCOURT	c1056	217.6	9.5	602	14	DA334765	DA334765 DA334765
984	218.2	9.6	746	16	DU840729	DU840729 MUGQ CH25	c1057	217.6	9.5	607	7	AV761714	AV761714 AV761714
985	218.2	9.6	771	4	BQ776208	BQ776208 UI-H-FH0-	1058	217.6	9.5	654	14	DB636697	DB636697 DB636697
986	218.2	9.6	818	16	BZ598824	BZ598824 WHABF56TR	c1059	217.6	9.5	656	2	BG546809	BG546809 602574182
c 987	218.2	9.6	868	4	BU933126	BU933126 AGENCOURT	c1060	217.6	9.5	773	18	CZ450219	CZ450219 MCF730n19
c 988	218.2	9.6	889	15	CZ446098	CZ446098 MCF725e16	1061	217.6	9.5	777	2	BG193279	BG193279 RST12407
989	218	9.5	407	5	BX480830	BX480830 DKFZp686F	1062	217.6	9.5	789	18	CZ460194	CZ460194 MCF748015
990	218	9.5	451	4	BQ181691	BQ181691 UI-H-EU0-	1063	217.6	9.5	841	18	ED010990	ED010990 MUGQ CH25
c 991	218	9.5	497	15	AQ569975	AQ569975 HS 5354_A	1064	217.6	9.5	978	8	CD519410	CD519410 AGENCOURT
992	218	9.5	548	14	DB280345	DB280345 DB280345	1065	217.6	9.5	1058	3	BM554734	BM554734 AGENCOURT
993	218	9.5	550	14	DA123991	DA123991 DA123991	c1066	217.4	9.5	438	15	AQ695967	AQ695967 HS 2160_A
994	218	9.5	550	15	AQ020201	AQ020201 CIT-HSP-2	c1067	217.4	9.5	498	15	AQ487770	AQ487770 RPCI-11-2
995	218	9.5	559	14	DA905220	DA905220 DA905220	c1068	217.4	9.5	507	15	AQ169564	AQ169564 HS 3176_B
c 996	218	9.5	570	9	CN346228	CN346228 170006000	c1069	217.4	9.5	538	16	BZ610864	BZ610864 WHADJ62TF
997	218	9.5	570	14	DB290617	DB290617 DB290617	c1070	217.4	9.5	539	8	CD683597	CD683597 EST117_hu
998	218	9.5	572	14	DA995619	DA995619 DA995619	c1071	217.4	9.5	552	4	BQ613908	BQ613908 il01a04.x
999	218	9.5	589	14	DA776632	DA776632 DA776632	1072	217.4	9.5	560	14	DA398384	DA398384 DA398384
1000	218	9.5	634	4	BU069957	BU069957 im19d09.x	1073	217.4	9.5	584	15	B56203	B56203 CIT-HSP-200
1001	218	9.5	655	19	AG119935	AG119935 Pan trogl	1074	217.4	9.5	594	14	DA440810	DA440810 DA440810
c1002	218	9.5	675	5	BX954661	BX954661 DKFZp781P	1075	217.4	9.5	597	15	AQ112406	AQ112406 CIT-HSP-2
c1003	218	9.5	679	19	AG158317	AG158317 Pan trogl	1076	217.4	9.5	607	15	B01406	B01406 CSRL-131c10
1004	218	9.5	696	9	CN417713	CN417713 170004240	c1077	217.4	9.5	635	9	CK820306	CK820306 il01a04.x
1005	218	9.5	698	19	AG183302	AG183302 Pan trogl	c1078	217.4	9.5	656	19	AG158221	AG158221 Pan trogl
1006	218	9.5	773	1	AL040663	AL040663 DKFZp434N	1079	217.4	9.5	686	2	BE888976	BE888976 601513907
1007	218	9.5	791	8	CD652079	CD652079 AGENCOURT	c1080	217.4	9.5	720	18	DX569157	DX569157 MUGQ CH25
c1008	218	9.5	844	15	AQ747032	AQ747032 HS 5538_A	c1081	217.4	9.5	726	19	AG142182	AG142182 Pan trogl
1009	218	9.5	853	4	BU177236	BU177236 AGENCOURT	c1082	217.4	9.5	731	19	AG186212	AG186212 Pan trogl
1010	218	9.5	3057	6	CR749632	CR749632 Homo sapi	c1083	217.4	9.5	739	7	AU117276	AU117276 AU117276
1011	218	9.5	3180	6	HSN800699	AL096734 Homo sapi	c1084	217.4	9.5	739	18	AG031712	AG031712 Pan trogl
1012	217.8	9.5	373	1	AA828047	AA828047 od70g05.s	c1085	217.4	9.5	746	4	BU741907	BU741907 UI-E-EO1-
1013	217.8	9.5	387	1	AI061313	AI061313 an32g07.x	c1086	217.4	9.5	795	2	BG115239	BG115239 602316160
c1014	217.8	9.5	416	2	BG474043	BG474043 602516603	1087	217.4	9.5	815	18	DU797002	DU797002 fv01_fp00
c1015	217.8	9.5	459	14	DA1833796	DA1833796 DA1833796	c1088	217.4	9.5	878	19	CR958416	CR958416 Homo sapi
1016	217.8	9.5	478	15	B67141	B67141 CIT-HSP-201	c1089	217.4	9.5	937	18	DU799058	DU799058 fv01_fp00
c1017	217.8	9.5	500	14	DB276848	DB276848 DB276848	1090	217.2	9.5	341	15	B88989	B88989 CIT-HSP-216
1018	217.8	9.5	501	5	BX485916	BX485916 DKFZp686E	1091	217.2	9.5	347	7	AW768489	AW768489 hk61d03.x
c1019	217.8	9.5	539	3	EM091137	BM091137 ig22g07.y	1092	217.2	9.5	388	15	AQ125184	AQ125184 HS 2163_B
1020	217.8	9.5	565	7	AW979093	AW979093 EST391203	c1093	217.2	9.5	389	2	BG014630	BG014630 IL5-GN023
1021	217.8	9.5	572	14	DA707826	DA707826 DA707826	c1094	217.2	9.5	444	1	AL692023	AL692023 DKFZp313J
1022	217.8	9.5	575	14	DB165721	DB165721 DB165721	1095	217.2	9.5	448	1	AI653515	AI653515 tq95c08.x
c1023	217.8	9.5	578	2	BE252421	BE252421 601108224	c1096	217.2	9.5	467	14	DA818169	DA818169 DA818169
1024	217.8	9.5	582	14	DA755991	DA755991 DA755991	1097	217.2	9.5	501	10	CR546841	CR546841 DKFZp470B
1025	217.8	9.5	593	14	DA115493	DA115493 DA115493	1098	217.2	9.5	547	3	BM831490	BM831490 K-EST0105
1026	217.8	9.5	595	5	BX099082	BX099082 BX099082	c1099	217.2	9.5	554	14	DB350072	DB350072 DB350072
1027	217.8	9.5	600	14	DA237284	DA237284 DA237284	c1100	217.2	9.5	554	14	DB350072	DB350072 DB350072
1028	217.8	9.5	627	10	CV571026	CV571026 oe08a10.y	c1101	217.2	9.5	672	16	BZ610254	BZ610254 WHADR43TR
c1029	217.8	9.5	667	19	AG150197	AG150197 Pan trogl	1102	217.2	9.5	716	19	AG101592	AG101592 Pan trogl
c1030	217.8	9.5	677	18	AG068925	AG068925 Pan trogl	c1103	217.2	9.5	724	19	AG166111	AG166111 Pan trogl
1031	217.8	9.5	715	18	AG010149	AG010149 Homo sapi	c1104	217.2	9.5	770	5	BX953657	BX953657 DKFZp781O
c1032	217.8	9.5	738	2	BF527070	BF527070 602039986	1105	217.2	9.5	783	5	BX093341	BX093341 BX093341
c1033	217.8	9.5	751	15	AQ745128	AQ745128 HS 5501_A	c1106	217.2	9.5	800	10	CX164763	CX164763 HESC2_20-
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c1036	217.8	9.5	864	1	AL574059	AL574059 AL574059	c1109	217	9.5	2273	8	CR933698	CR933698 Homo sapi
										357	2	BE139358	BE139358 xr69d09.x

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CD236861 FNPADE10  
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AU118200 AU118200  
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BM991131 UI-H-DI0-  
BM993430 UI-H-DT0-  
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c1256	216.2	9.5	654	18	AG087678	Pan trogl	1329	215.8	9.4	582	14	DA166100	DA166100
1257	216.2	9.5	681	1	AI561116	tq26e09.x	c1330	215.8	9.4	596	2	BF681607	BF681607
1258	216.2	9.5	682	19	AG165798	Pan trogl	c1331	215.8	9.4	597	8	CF122892	CF122892
c1259	216.2	9.5	730	5	CA417963	UI-H-FH0-	1332	215.8	9.4	600	5	DX951315	DX951315
1260	216.2	9.5	739	18	CZ463661	MCF754e14	c1333	215.8	9.4	602	9	CK430039	CK430039
1261	216.2	9.5	760	15	BH732787	BOMHX25TF	1334	215.8	9.4	611	14	DB372780	DB372780
1262	216.2	9.5	772	5	CA420894	UI-H-FG0-	c1335	215.8	9.4	613	8	CD709038	CD709038
1263	216.2	9.5	799	18	ED006469	MUGQ CH25	1336	215.8	9.4	641	18	DX414988	DX414988
1264	216.2	9.5	802	18	CZ453257	MCF734o17	1337	215.8	9.4	652	3	BM999045	BM999045
c1265	216.2	9.5	811	8	CD511251	AGENCOURT	c1338	215.8	9.4	664	15	AQ343449	AQ343449
c1266	216.2	9.5	826	4	BQ221186	AGENCOURT	c1339	215.8	9.4	666	18	AG084334	AG084334
c1267	216.2	9.5	851	10	CR788530	DKFZp459C	c1340	215.8	9.4	712	8	CD237852	CD237852
1268	216.2	9.5	853	15	AQ747124	HS 5539 A	c1341	215.8	9.4	729	19	AG175633	AG175633
1269	216.2	9.5	895	18	DU797653	fv01_fp01	c1342	215.8	9.4	738	4	BU561758	BU561758
c1270	216.2	9.5	1335	6	BC071992	Homo sapi	c1343	215.8	9.4	740	8	CD512317	CD512317
c1271	216.2	9.5	1808	6	CR858461	Pongo pyg	1344	215.8	9.4	742	8	CF127609	CF127609
1272	216.2	9.5	2177	15	AQ839825	260L13-C3	c1345	215.8	9.4	751	4	BQ772858	BQ772858
1273	216.2	9.5	4042	6	HSM801427	Homo sapi	c1346	215.8	9.4	751	4	BU853245	BU853245
c1274	216	9.5	303	14	DB270104	DB270104	c1347	215.8	9.4	781	4	BU853986	BU853986
1275	216	9.5	309	1	AA720732	nv93d02.r	c1348	215.8	9.4	791	4	BU567220	BU567220
1276	216	9.5	367	1	AA601986	no88g12.s	c1349	215.8	9.4	815	4	BU930469	BU930469
1277	216	9.5	376	7	AW503420	UI-HF-BN0	c1350	215.8	9.4	819	4	BU165654	BU165654
1278	216	9.5	389	7	BE049229	ho02h08.x	c1351	215.8	9.4	838	4	BU570932	BU570932
1279	216	9.5	390	15	B79179	CIT978SK-14	c1352	215.8	9.4	839	4	BQ434443	BQ434443
1280	216	9.5	406	1	AL708766	DKFZp686C	c1353	215.8	9.4	964	15	AQ747314	AQ747314
1281	216	9.5	407	1	AI753113	cr05c11.x	c1354	215.8	9.4	968	2	BG499561	BG499561
c1282	216	9.5	443	9	CN274447	170006000	1355	215.8	9.4	3775	6	CR627381	CR627381
1283	216	9.5	455	1	AA904211	od88e02.s	c1356	215.6	9.4	352	5	BX485943	BX485943
c1284	216	9.5	486	3	BM993751	UI-H-DH0-	c1357	215.6	9.4	376	7	AV735495	AV735495
c1285	216	9.5	497	5	BX480039	DKFZp686F	c1358	215.6	9.4	398	15	AQ122574	AQ122574
c1286	216	9.5	521	8	CF130229	UI-HF-ES0	c1359	215.6	9.4	417	5	BX953071	BX953071
1287	216	9.5	530	14	DB115431	DB115431	1360	215.6	9.4	448	15	AQ634562	AQ634562
1288	216	9.5	549	14	DB302670	DB302670	1361	215.6	9.4	520	2	BE674881	BE674881
c1289	216	9.5	568	14	DA360031	DA360031	c1362	215.6	9.4	549	14	DA399272	DA399272
1290	216	9.5	572	14	DA493918	DA493918	c1363	215.6	9.4	550	10	CR545302	CR545302
1291	216	9.5	580	14	DB051141	DB051141	c1364	215.6	9.4	555	14	DA813919	DA813919
c1292	216	9.5	582	7	AV764329	AV764329	1365	215.6	9.4	563	14	DA083096	DA083096
c1293	216	9.5	596	15	AQ323805	RPCI11-11	c1366	215.6	9.4	564	14	DA547902	DA547902
c1294	216	9.5	630	15	AQ239777	RPCI11-64	c1367	215.6	9.4	576	4	BU078633	BU078633
c1295	216	9.5	657	7	AV701234	AV701234	c1368	215.6	9.4	593	14	DB291492	DB291492
1296	216	9.5	661	13	DR004361	TC110384	1369	215.6	9.4	611	15	AQ554801	AQ554801
1297	216	9.5	665	10	CR750680	DKFZp470B	c1370	215.6	9.4	612	9	CK817709	CK817709
c1298	216	9.5	666	18	DX104772	MUGQ CH25	c1371	215.6	9.4	620	10	CR750555	CR750555
c1299	216	9.5	668	18	AG050903	Pan trogl	1372	215.6	9.4	624	7	AW973777	AW973777
1300	216	9.5	677	18	AG083690	Pan trogl	c1373	215.6	9.4	637	19	AG160849	AG160849
1301	216	9.5	684	15	AQ554303	RPCI-11-4	c1374	215.6	9.4	652	18	AG038075	AG038075
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c1303	216	9.5	714	16	BZ611771	WHAA064TR	c1376	215.6	9.4	692	18	CZ463785	CZ463785
c1304	216	9.5	714	19	AG177522	Pan trogl	c1377	215.6	9.4	720	15	AQ588993	AQ588993
c1305	216	9.5	746	2	BF675678	602083577	1378	215.6	9.4	724	18	AG051798	AG051798
1306	216	9.5	814	5	CA771920	io93a10.x	1379	215.6	9.4	758	4	BQ708090	BQ708090
1307	216	9.5	857	18	CZ464602	MCF755K20	c1380	215.6	9.4	769	15	AQ900076	AQ900076
c1308	216	9.5	932	4	BQ716029	AGENCOURT	c1381	215.6	9.4	799	7	AV755512	AV755512
c1309	216	9.5	967	15	AQ744206	HS 5508 A	c1382	215.6	9.4	803	4	BU570156	BU570156
1310	216	9.5	1428	15	AZ124375	Cg122.25	c1383	215.6	9.4	842	15	AQ748478	AQ748478
1311	216	9.5	2983	6	BC082988	Homo sapi	1384	215.6	9.4	844	16	BZ597986	BZ597986
c1312	215.8	9.4	319	7	AW021116	df19a04.y	c1385	215.6	9.4	873	18	CZ447157	CZ447157
c1313	215.8	9.4	329	4	BU565543	AGENCOURT	c1386	215.6	9.4	900	4	BQ710544	BQ710544
1314	215.8	9.4	330	7	AW189068	xx99d12.x	c1387	215.6	9.4	917	4	BU153359	BU153359
1315	215.8	9.4	357	14	DB325522	DB325522	1388	215.6	9.4	981	3	BM468639	BM468639
c1316	215.8	9.4	421	1	AA631497	np83h03.s	c1389	215.6	9.4	3005	6	BC111052	BC111052
1317	215.8	9.4	427	1	AI338426	qq92a01.x	c1390	215.6	9.4	310	4	BU933518	BU933518
1318	215.8	9.4	452	1	AL041894	DKFZp434I	c1391	215.4	9.4	344	4	BU603545	BU603545
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1320	215.8	9.4	471	4	BQ286229	ik27e06.y	c1393	215.4	9.4	510	15	AQ284649	AQ284649
c1321	215.8	9.4	488	2	BU845939	AGENCOURT	1394	215.4	9.4	522	3	BM993791	BM993791
1322	215.8	9.4	489	2	BG941830	ax17h04.x	1395	215.4	9.4	523	9	CN479672	CN479672
c1323	215.8	9.4	496	7	AW512196	xx71e04.x	1396	215.4	9.4	531	14	DA516868	DA516868
c1324	215.8	9.4	516	8	CB147131	K-EST0202	1397	215.4	9.4	537	1	AL120343	AL120343
c1325	215.8	9.4	541	14	DA496138	DA496138	1398	215.4	9.4	539	14	DB341486	DB341486
c1326	215.8	9.4	544	14	DA801008	DA801008	1399	215.4	9.4	541	15	AQ529925	AQ529925
c1327	215.8	9.4	557	15	B85764	RPCI11-20P1	1400	215.4	9.4	546	7	AW007759	AW007759
1328	215.8	9.4	567	14	DA261198	DA261198	c1401	215.4	9.4				



1402	215.4	9.4	548	3	BI792342	BI792342 ic29d04.x
1403	215.4	9.4	557	14	DA224868	DA224868 DA224868
1404	215.4	9.4	558	14	DB180245	DB180245 DB180245
1405	215.4	9.4	562	8	CF124579	CF124579 UI-HF-CH0
1406	215.4	9.4	575	15	DA2521417	AZ521417 RPCI-11-3
1407	215.4	9.4	589	14	DA043357	DA043357 DA043357
1408	215.4	9.4	646	18	CZ454140	CZ454140 MCF736B22
1409	215.4	9.4	648	14	DA224349	DA224349 DA224349
1410	215.4	9.4	671	2	BG289041	BG289041 602383913
1411	215.4	9.4	678	18	CZ458639	CZ458639 MCF746116
1412	215.4	9.4	694	2	BG900773	BG900773 HOA6-1-E9
1413	215.4	9.4	698	16	BZ601203	BZ601203 WHAAW19TR
1414	215.4	9.4	738	2	BG527374	BG527374 602557360
1415	215.4	9.4	744	7	AU124634	AU124634 AU124634
1416	215.4	9.4	824	18	CZ446272	CZ446272 MCF725i07
1417	215.4	9.4	969	5	BX420927	BX420927 BX420927
1418	215.4	9.4	3238	6	CR861250	CR861250 Pongo pyg
1419	215.4	9.4	4832	6	CR857402	CR857402 Pongo pyg
1420	215.2	9.4	296	4	BQ023663	BQ023663 UI-1-BB0-
1421	215.2	9.4	315	1	AI244356	AI244356 qj76b08.x
1422	215.2	9.4	369	1	AI754037	AI754037 crl8h09.x
1423	215.2	9.4	401	1	AI040051	AI040051 ox28a11.x
1424	215.2	9.4	428	1	AA262752	AA262752 z824b11.s
1425	215.2	9.4	435	1	AI829331	AI829331 wk60f09.x
1426	215.2	9.4	442	15	AQ286079	AQ286079 RPCI11-77
1427	215.2	9.4	447	5	BX489032	BX489032 DKFZp686L
1428	215.2	9.4	497	8	CF140288	CF140288 UI-HF-CB0
1429	215.2	9.4	515	10	CR546036	CR546036 DKFZp470I
1430	215.2	9.4	516	2	BE143634	BE143634 MR0-HT016
1431	215.2	9.4	530	14	DA961685	DA961685 DA961685
1432	215.2	9.4	540	14	DB298137	DB298137 DB298137
1433	215.2	9.4	544	10	CR525105	CR525105 DKFZp459L
1434	215.2	9.4	546	14	DB355648	DB355648 DB355648
1435	215.2	9.4	554	14	DA182971	DA182971 DA182971
1436	215.2	9.4	563	14	DA504439	DA504439 DA504439
1437	215.2	9.4	573	14	DA219710	DA219710 DA219710
1438	215.2	9.4	582	14	DA504434	DA504434 DA504434
1439	215.2	9.4	646	8	CB857198	CB857198 NISC_na05
1440	215.2	9.4	648	18	AG033148	AG033148 Pan_trog1
1441	215.2	9.4	667	2	BG538733	BG538733 602566970
1442	215.2	9.4	678	4	BQ879409	BQ879409 AGENCOURT
1443	215.2	9.4	712	17	CW626343	CW626343 Hsap_11_U
1444	215.2	9.4	721	16	BZ772968	BZ772968 mcv59f11.
1445	215.2	9.4	765	8	CB989518	CB989518 AGENCOURT
1446	215.2	9.4	765	8	CD516602	CD516602 AGENCOURT
1447	215.2	9.4	766	4	BQ000069	BQ000069 UI-H-DP0-
1448	215.2	9.4	793	8	CB988697	CB988697 AGENCOURT
1449	215.2	9.4	838	6	BC039515	BC039515 Homo sapi
1450	215.2	9.4	867	4	BQ441860	BQ441860 AGENCOURT
1451	215.2	9.4	877	4	BQ222830	BQ222830 AGENCOURT
1452	215.2	9.4	1060	3	BM469250	BM469250 AGENCOURT
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1454	215.2	9.4	2731	6	BC013209	BC013209 Homo sapi
1455	215	9.4	321	1	AA526724	AA526724 ni91d06.s
1456	215	9.4	418	15	AQ457164	AQ457164 HS_5162_A
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1458	215	9.4	453	16	BZ609670	BZ609670 WHACG38TF
1459	215	9.4	469	14	DB567068	DB567068 DB567068
1460	215	9.4	477	14	DB572332	DB572332 DB572332
1461	215	9.4	499	3	BM996605	BM996605 UI-H-DT0-
1462	215	9.4	501	10	CR543219	CR543219 DKFZp470N
1463	215	9.4	507	14	DA247673	DA247673 DA247673
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1465	215	9.4	540	14	DB295762	DB295762 DB295762
1466	215	9.4	542	15	B56436	B56436 CIT-HSP-200
1467	215	9.4	544	5	CA396579	CA396579 cs79f06.y
1468	215	9.4	562	5	CA773590	CA773590 im62c06.x
1469	215	9.4	565	14	DA079245	DA079245 DA079245
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1471	215	9.4	594	5	BX504370	BX504370 DKFZp686M
1472	215	9.4	640	18	CZ449815	CZ449815 MCF730f01
1473	215	9.4	659	4	BQ709168	BQ709168 AGENCOURT
1474	215	9.4	665	19	AG092910	AG092910 Pan trogl

1475	215	9.4	670	18	AG084044	AG084044 Pan trogl
1476	215	9.4	680	5	BX507811	BX507811 DKFZp686A
1477	215	9.4	691	3	BM990097	BM990097 UI-H-DI0-
1478	215	9.4	700	7	AU252665	AU252665 AU252665
1479	215	9.4	703	19	AG141722	AG141722 Pan trogl
1480	215	9.4	851	7	AU117777	AU117777 AU117777
1481	215	9.4	7407	6	CR936673	CR936673 Homo sapi
1482	214.8	9.4	320	4	BU959012	BU959012 AGENCOURT
1483	214.8	9.4	345	2	BG223550	BG223550 naj52h02.
1484	214.8	9.4	348	12	DW467041	DW467041 HHAGE0083
1485	214.8	9.4	424	15	AZ515688	AZ515688 UP_430-16
1486	214.8	9.4	458	5	BX508242	BX508242 DKFZp686H
1487	214.8	9.4	460	18	DX585404	DX585404 MUGQ_CH25
1488	214.8	9.4	480	3	BM894065	BM894065 ij63a03.x
1489	214.8	9.4	481	3	BM565475	BM565475 ih25e05.x
1490	214.8	9.4	512	18	CZ464501	CZ464501 MCF755i11
1491	214.8	9.4	520	3	BM894337	BM894337 ij63a03.y
1492	214.8	9.4	521	3	BM507206	BM507206 ih25e05.y
1493	214.8	9.4	538	5	CA425359	CA425359 UI-H-DF0-
1494	214.8	9.4	549	14	DA093799	DA093799 DA093799
1495	214.8	9.4	559	15	AQ534725	AQ534725 RPCI-11-3
1496	214.8	9.4	575	14	DA244825	DA244825 DA244825
1497	214.8	9.4	576	5	CA427630	CA427630 UI-H-DF0-
1498	214.8	9.4	576	14	DA264876	DA264876 DA264876
1499	214.8	9.4	590	15	AQ041377	AQ041377 CIT-HSP-2
1500	214.8	9.4	597	14	DB358385	DB358385 DB358385

ALIGNMENTS

RESULT 1  
CR858919  
LOCUS CR858919 4613 bp mRNA linear HTC 12-NOV-2004  
DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp469A172 (from clone DKFZp469A172).  
ACCESSION CR858919  
VERSION CR858919.1 GI:55728755  
KEYWORDS HTC.

SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Pongo.  
REFERENCE 1 (bases 1 to 4613)  
AUTHORS Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.  
CONSRM The German cDNA Consortium  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY

COMMENT  
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.  
This clone (DKFZp469A172) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469A172  
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES  
source Location/Qualifiers  
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/organism="Pongo pygmaeus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9600"  
/clone="DKFZp469A172"  
/tissue type="kidney"  
/clone\_lib="469 (synonym: pkid1). Vector pSport1\_Sfi; host DH10B; sites SfilA + SfilB"  
/dev stage="adult"  
/note="hypothetical protein (Homo sapiens)"  
1..4613  
gene

CDS		/gene="DKFZp469A172" 280..1575 /gene="DKFZp469A172" /codon_start=1 /product="hypothetical protein" /protein_id="CAH91117.1" /db_xref="GI:55728756" /translation="MFFGGESLTYLVIICFLTRLLSASQDCINKSLEDVWVIDIOSS LSKGIIRNEPIYITSTQEDCINSCSTKNISGDKACNLMI FTRKTRARQPNCYLFFCPD EEACPLRPAGLMSYRIIRDPSLFRNLSSQELPQEDSLLHGQFSPAVTPLAHHTDY SKPTDLSWRDLSQKFSSDHLEKLFKXMDASAQLLAYKEKHSQSQSFSSDQETAHL LPENSAFLATVAVASPHTTSATPKPTLLPSNASVTPSGTSQPQLATPAPVTVTS QPPTLILSTVFTRAMATLQAMATTAVLTTFQAPTDSKGSGLTIPFTETSNLTLNTGN VYNPTALSMSNEESSTMNKTAPWEGREASPGSSSQGRVPENQYGLPEKWLILIGSLLF GVFLFVLIGLILGRILSESLRRKRYSLRDYLINGIYVDI"	
ORIGIN		Query Match 93.3%; Score 2131.2; DB 6; Length 4613; Best Local Similarity 96.1%; Pred. No. 0; Matches 2195; Conservative 0; Mismatches 88; Indels 1; Gaps 1;	
Qy	1	GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCGCGCGGATTTCGCCGCTCCTTCCCGC	60
Db	55	GCGGAACATCCCTGCGGTCCTCGCCGAGACCCCGCGCGGATTTCGCCGCTCCTTCCCGC	114
Qy	61	GGGCGGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGCGCGGGTCTCTCGAC	120
Db	115	GGGCACGACAGAGCTGTCTCGCATCCGGAGGGCAGCAGGGCCCCGGGGTCTCTCGAC	174
Qy	121	GCCAGAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG	180
Db	175	GCCAGAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG	234
Qy	181	GATTATCCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTCGGGGGA	240
Db	235	GATTATCCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTCGGGGGA	294
Qy	241	GAAGGGAGCTTGACTTTACACTTTGGTAATAATTGCTTCCCTGACACTAAGGCTGTCTGCT	300
Db	295	GAAGGGAGCTTGACTTTACACTTTGGTAATAATTGCTTCCCTGACACTAAGGCTGTCTGCT	354
Qy	301	AGTCAGAAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTTCATTGACATCCAGTCACTCTTT	360
Db	355	AGTCAGGAATTGCCTCAACAAGAGTCTAGAAGATGTTGTTCATTGACATCCAGTCACTCTTT	414
Qy	361	TCTAAGGGAATCAGAGGCAATGAGCCCGGTATATACITCAACTCAAGAAGACTGCATTAAT	420
Db	415	TCTAAGGGAATCAGAGGCAATGAGCCCGGTATATATCTTCAACTCAAGAAGACTGCATTAAT	474
Qy	421	TCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC	480
Db	475	TCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC	534
Qy	481	ACTCGAAAAACAGCTAGACAAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCC	540
Db	535	ACTCGAAAAACAGCTAGACAAACCCAACTGCTACCTATTTTCTGTCCCGATGAGGAAGCC	594
Qy	541	TGTCCATTGAAACCCAGCAAAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCT	600
Db	595	TGTCCATTGAGACCAGCAAAAGGACTTATGAGTTACAGGATAATTAGAGATTTTCCATCT	654
Qy	601	TTGACCAGAAATTTGCCAAGCCAAAGATTACCCAGGAAGATTCTCTCTTACATGGCCAA	660
Db	655	TTGACCAGAAATTTGTCAAGCCAAAGATTACCCAGGAAGATTCTCTTACATGGCCAA	714
Qy	661	TTTTCACAAGCAGTCACTCCCTAGCCCATCATCACACAGATTATTCAAAGCCCACCGAT	720
Db	715	TTTTCACCAGCAGTCACTCCCTAGCCCATCATCACACAGATTATTCAAAGCCCACCGAT	774
Qy	721	ATCTCATGGAGAGACACACTTTCTCAGAAAGTTTGGATCCTCAGATCACCTGGAGAAACTA	780
Db	775	ATCTCATGGAGAGACACACTTTCTCAGAAAGTTTGGATCCTCAGATCACCTGGAGAAACTA	834
Qy	781	TTTAAAGATGGATGAAGCAAGTGCCAGCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAG	840
Db	835	TTTAAAGATGGACGAAGCAAGTGCCAGCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAG	894
Qy	841	AGTTCACAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCCCTGAAATGTGAGTGGC	900
Db	895	AGTTCACAGTTTCTCTGATCAAGAAAACGGCTCATCTGCTGCCCTGAAATGTGAGTGCA	954
Qy	901	CTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCTACTCCAAAAGCCCGCC	960
Db	955	TTCTTAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCAGCTACTCCAAAAGCCACAC	1014
Qy	961	ACCCTTCTACCCACCAATGCTTCACTGACACACCTTCTGGGACTTCCCAGCCACAGCTGGCC	1020
Db	1015	ACCCTTTTACCAGCAATGCTTCACTGACACCTTCTGGGACTTCCCAGCCACAGCTGGCC	1074
Qy	1021	ACCACAGCTCCACCTGTAAACCACCTGTCACTTCTCAGCCTCCCACGACCTCAATTTCTACA	1080
Db	1075	ACCACAGCTCCACCTGTAAACCACCTGTCACTTCTCAGCCTCCCACACCTCAATTTCTACA	1134
Qy	1081	GTTTTATACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACAGCAGTTCCTGACTACC	1140
Db	1135	GTTTTATACACGGGCTATGGCTACACTCCAAGCAATGGCTACAACAGCAGTTCCTGACTACC	1194
Qy	1141	ACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATACCGTTTACAGAAATC	1200
Db	1195	ACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATACCGTTTACAGAGACC	1254
Qy	1201	TCCAACTTAACTTTGAACACACAGGGAATGTGTATAACCCCTACTGCACTTTCTATGTCAAAAT	1260
Db	1255	TCCAACTTAACTTTGAACACACAGGGAATGTGTATAACCCCTACTGCACTTTCTATGTCAAAAT	1314
Qy	1261	GTGGAGTCTTCCACTATGAATAAAACTGTCTTCTGGGAAGGTAGGGAGGCCAGTCCAGGC	1320
Db	1315	GAGGAGTCTTCCACTATGAATAAAACTGTCTTCCCTGGGAAGGTAGGGAGGCCAGTCCAGGC	1374
Qy	1321	AGTTCCTCCAGGGCAGTGTTCAGAAAATCAGTACGGCCTTCCATTTGAAAAATGCGCTT	1380
Db	1375	AGTTCCTCCAGGGCAGGGTTCAGAAAATCAGTATGGCCTTCCATTTGAAAAAGTGGCTT	1434
Qy	1381	CTTATCGGGTCCCTGCTCTTTTGGTGTCTGTTCTCTGGTATAGGCCCTCGTCCCTCGTGGT	1440
Db	1435	CTTATCGGGTCCCTGCTCTTTTGGTGTCTGTTCTCTGGTATAGGCCCTCATCCTCCTGGGT	1494
Qy	1441	AGAATCCTTTCGGAATCACTCCGACGGAACGTTACTCAAGACTGGATTATTTGATCAAT	1500
Db	1495	AGAATCCTTTCGGAATCACTCCGACGGAACGTTACTCAAGACTGGATTATTTGATCAAT	1554
Qy	1501	GGGATCTATGTGGACATCTAAGGATGGAACTCGGTGTCTCTTAATTCATTTAGTAACAG	1560
Db	1555	GGGATCTATGTGGACATCTAAGGATGGAACTCGGTGTCTCTTCAATTCATTTAGTAACAG	1614
Qy	1561	AAGCCCAATGCAATGAGTTTCTGCTGACTTTGCTAGTCTTAGCAGGAGGTTGTATTTTGA	1620
Db	1615	AAGCCCAATGCAATGAGTTTCTGCTGACTTTGCTAGTCTTAGCAGGAGGTTGCATTTTGA	1674
Qy	1621	AGACAGGAAAAATGCCCCCTTCTGCTTTCC - TTTT TTTT TTTT TTTT TTTT TTTT TTTT	1679
Db	1675	AGACAGGAAAAATGCCCCCTTCTGCTTTCTCTGCTTTCTTTT TTTT TTTT TTTT TTTT	1734
Qy	1680	GTTGCCCAAGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGCTCTCTG	1739
Db	1735	GTTGTCTAGGCTGGAGTGTAGTGGCACGATCTCGGCTCTCACCGCAGCCTCCATCTCCTG	1794
Qy	1740	GGTTCACAGGATTTCTCTGCCTCAGCCTCCTTAAGTATCTGGATTACAGGCATGTGCCAC	1799
Db	1795	GGTTCAGGCGATTCTCTGCTCGCCTCGGCTCTCTTAAGTAGTGGATTGCGGGCATATGCCAC	1854
Qy	1800	CACACCTGGGTGATTTTGTATTTTATTTAGTAGACAGGGGTTTTCACCATGTTGGTCAGGCT	1859
Db	1855	CATGCTGGGTGATTTTGTGTTTTTGTGTTTTTAGTAGACAGGGGTTTTCGCCATGTTGGTCAGGCT	1914
Qy	1860	GGTCTCAAACTCCTGACCTAGTAGTATCCACCCCTCCTCGGCCCTCCCAAAGTCTGGGATTAC	1919

Db	1915		GGTTTCAAACTCCTGACCTAGTATGATCACCAGCCTTGGCCTCCCGGGGTGCTGGGATTAC	1974
Qy	1920		AGGCATGAGCCACCACAGCTGGCCCCCTTCTGTGTTTTATGTTTGGTTTTTGAGAAAGGAATG	1979
Db	1975		AGCGGTGAGCCACCACATCTGGACCCCTTCTGCTTTATGTTTGGTTTTTGAGAAAGGAGTG	2034
Qy	1980		AAGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACA	2039
Db	2035		AAGTGGGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAAATATTAGCTGAAAAACA	2094
Qy	2040		AAGCTCTATGTAAAGTAATAAAGTATATAATTGCCCATATAAAATTTCAAAATTCAACTGGCTT	2099
Db	2095		AAGCTCTACCTAAAGTAATAAAGTATATAATTGCCCATATAAAATTTCAAAATTCAACTGGCTT	2154
Qy	2100		TTATGCAAGAAACAGGTTAGGACATCTAGGTTCCAAATTCATTCACATCTCTGGTTCAG	2159
Db	2155		TTATGCAAGAAACAGATTAGGACATCTAGGTTCCAAATTCATTGACATCTCTGGTTCAG	2214
Qy	2160		ATAAAATCAACTGTTTATATCAATTTCTAAATGGATTGCTTTTCTTTTATATGGATTCC	2219
Db	2215		ATAAAATCAACTGTTTATATCAATTTCTTATGGATTGCTTTTCTTTTATATGAATTC	2274
Qy	2220		TTTAAAACTTATTCAGATGTAGTTCTTCCCAATTAAATATTTGAATAAATCTTTTGTTA	2279
Db	2275		AATAAACTTATTCAGATGTAGTTCTTCCCAATTAAATATTTGAATAAATCTTTTGTTA	2334
Qy	2280		CTCA	2283
Db	2335		CTCA	2338

RESULT 2					
CR621081					
LOCUS	CR621081	1965 bp	mRNA	linear	HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CSODI054YH07 of Placenta Cot 25-normalized of Homo sapiens (human).				

ACCESSION	CR621081	
VERSION	CR621081.1	GI:50501888
KEYWORDS	HTC; CNSLT_cDNA.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;	
	Catarrhini; Homnidae; Homo.	
REFERENCE	1	(bases 1 to 1965)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished	
REMARK	Contact : Feng Liang Email : <a href="mailto:fliang@lifetech.com">fliang@lifetech.com</a> URL :	
	<a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> Invitrogen Corporation 1600	

REFERENCE	2 (bases 1 to 1965)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004)
	Genoscope - Centre National de Sequencage :

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES	Location/Qualifiers
source	1. .1965
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	/clone="CS0DI054YH07"
	/tissue_type="Placenta Cot 25-normalized"
	/plasmid="pCMVSPORT 6"

## ORIGIN

Query Match		78.9%;	Score 1802.6;	DB 6;	Length 1965;
Best Local Similarity		99.7%;	Pred. No. 5.1e-279;		
Matches 1816;		Conservative	0;	Mismatches	4;
				Indels	1;
				Gaps	1;
Qy	446	CAGGGACAAAGCATGTAACCTTGATGATCTTCGACACCTCGAAAAACAGCTAGACAACCCCA	505		
Db	145	CAGGGACAAAGCATGTAACCTTGATGATCTTCGACACCTCGAAAAACAGCTAGACAACCCCA	204		
Qy	506	ACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAAGCAAAAGGAC	565		
Db	205	ACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAAGCAAAAGGAC	264		
Qy	566	TTATGAGTTACAGGATAAATTACAGATTTTTCATCTTTTGACCAAGAAATTTGCCAAGCCAAG	625		
Db	265	TTATGAGTTACAGGATAAATTACAGATTTTTCATCTTTTGACCAGAAATTTGCCAAGCCAAG	324		
Qy	626	AGTTACCCCAAGGAAGATTCTCTTTACATATGGCCAAATTTTTCACAAGCAGTCACCTCCCCTAG	685		
Db	325	AGTTACCCCAAGGAAGATTCTCTTTACATATGGCCAAATTTTTCACAAGCAGTCACCTCCCCTAG	384		
Qy	686	CCCATCATCACACAGATTATTCAAAGCCCCACCGATATCTCATGGAGAGACACACTTTTCTC	745		
Db	385	CCCATCATCACACAGATTATTCAAAGCCCCACCGATATCTCATGGAGAGACACACTTTTCTC	444		
Qy	746	AGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCC	805		
Db	445	AGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCC	504		
Qy	806	AGCTCCTTGCTTATAAGGAAAAAAGGCCATTCTCAGAGTTTCACAATTTTTCCTCTGATCAAG	865		
Db	505	AGCTCCTTGCTTATAAGGAAAAAAGGCCATTCTCAGAGTTTCACAATTTTTCCTCTGATCAAG	564		
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DEFINITION Homo sapiens HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY401136  
VERSION AY401136.1 GI:39757125  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 1296)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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Best Local Similarity 99.8%; Pred. No. 5.1e-197;  
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DEFINITION Pan troglodytes HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY401137  
VERSION AY401137.1 GI:39757126  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Pan.  
REFERENCE 1 (bases 1 to 1296)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1296)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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AUTHORS			
TITLE			
JOURNAL			
COMMENT			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen. This sequence belongs to sequence cluster			
6656.r			
For more information about this cluster, see			
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AUTHORS			
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JOURNAL			
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;			
Catarrhini; Homidae; Homo.			
1 (bases 1 to 884)			
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen. This sequence belongs to sequence cluster			







Db	861	AAGGCCATTCTCAGAGTTCACAATTTT-CTCTGATCAAG-AANTAGCTCATCTGTGCCTG	918
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Db	919	AMAATGTGAGT--CSCTCCAGCTACGGTGGCAGTTGCTTYTC--ACATACAACTCGGCTA	974
Qy	947	CTCCAAGCCCGCCACCCCTTC	967
Db	975	CWCAAAGCCCGCACCCCTCTTM	995
RESULT 10			
CF593691			
LOCUS			
DEFINITION	CF593691	839 bp mRNA linear EST 26-SEP-2003	
ACCESSION	AGENCOURT 15623843	NIH_MGC_147 Homo sapiens cDNA clone	
VERSION	IMAGE:30531452	5', mRNA sequence.	
KEYWORDS	CF593691		
SOURCE	CF593691.1	GI:36347497	
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;		
	Catarrhini; Homnidae; Homo.		
REFERENCE	1	(bases 1 to 839)	
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgabs-r@mail.nih.gov Tissue Procurement: Dr. Stefan Hansson cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM622 row: d column: 21 High quality sequence stop: 677.		
FEATURES			
source	Location/Qualifiers		
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	/clone="IMAGE:30531452"		
	/tissue type="Human Placenta"		
	/lab_host="DH10B Tona"		
	/clone_lib="NIH_MGC_147"		
	/note="Organ: placenta; Vector: pBluescriptR; Site_1: ali-XhoI; Site_2: BamHI; Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH_MGC library."		
ORIGIN			
Query Match	31.4%	Score 718.2; DB 8; Length 839;	
Best Local Similarity	98.8%;	Pred. No. 3.8e-105;	
Matches 734; Conservative	0; Mismatches 8; Indels 1; Gaps 1;		
QY	1	GCGGAGCATCCGCTCGGTCCTCGCCGAGACCCCCCGCGGATTCGCCGGTCTTCCCGC	60
Db	69	GCGGAGCATCCGCTCGGTCCTCGCCGAGACCCCCCGCGGATTCGCCGGTCTTCCCGC	128
QY	61	GGGCGGACAGAGCTGTCTCGACCTGGATGGCAGCAGGGGCGCGGGTCTCTCTCGAC	120

COMMENT	Contact: Takao Isogai FLJ Project (HRI Team) Helix Research Institute 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: flj-cdna@nifty.com NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.		
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	ORIGIN		
FEATURES	Query Match 31.0%; Score 708.4; DB 14; Length 785; Best Local Similarity 97.7%; Pred. No. 1.4e-103; Matches 737; Conservative 0; Mismatches 15; Indels 2; Gaps 2;		
	source		
	1 GCGAGCATCCGCTGCGTCTCGCCTGCGAGACCCCGCGGGATTGCGCGTCTTCCCGC 60       30 GCGAGCATCCGCTGCGTCTCGCCTGCGAGACCCCGCGGGATTGCGCGTCTTCCCGC 89       61 GGGCGGACAGAGCTGTCTCGCACCTGGATGGCAGAGGGGCGCCGGGTCTCTCGAC 120       90 GGGCGGACAGAGCTGTCTCGCACCTGGATGGCAGAGGGGCGCCGGGTCTCTCGAC 149       121 GCCAGAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG 180       150 GCCAGAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG 209       181 GATTATCCTTGACCTTTGAAGACCACAAACTAAACTGAAATTTAAATGTTCTTCGGGGGA 240       210 GATTATCCTTGACCTTTGAAGACCACAAACTAAACTGAAATTTAAATGTTCTTCGGGGGA 269       241 GAAGGAGCTTGACTTACACTTTGGTAATAATTGCTTCTCTGACACTAAGGCTGTCTGCT 300       270 GAAGGAGCTTGACTTACACTTTGGTAATAATTGCTTCTCTGACACTAAGGCTGTCTGCT 329       301 AGTCAGAAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTTCATTGACATCCAGTCATCTTT 360       330 AGTCAGAAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTTCATTGACATCCAGTCATCTTT 389       361 TCTAAGGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAAT 420       390 TCTAAGGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAAT 449       421 TCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC 480       450 TCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC 509       481 ACTCGAAAAACAGCTAGACAAACCCAACTGCTACCTAATTTTCTGTCCCAACGAGGAAGCC 540       510 ACTCGAAAAACAGCTAGACAAACCCAACTGCTACCTAATTTTCTGTCCCAACGAGGAAGCC 569       541 TGTCCATTGAAACCCAGCAAAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCT 600       570 TGTCCATTGAAACCCAGCAAAAGGACTTATGAGTTACAGGATAATTACAGATTTTNCATCT 629       601 TTGACCAGAAATTTGCCAAGCCCAAGAGTTACCCAGGAAGATTCTCTTTACATGGCCAA 660       630 TTGACCAGAAATTTGCCAAGCCCAAGAGTTACCCAGGAAGATTCTCTTTACATGGGCCAA 689       661 TTTTCAAGCAGTCATCTCCCTAGCCCATCATCATCACAGATTATTCAAAGCCCCACCGAT 720 		
Db	690 -TTTCACAAGCAGTCACTTCCCTAGCCCATCATCACAGATTATTCAAAGCCACCGAT 748 		
	721 ATCTCATGGAGAGACACACTTTTCTCAGAAGTTTG 754 		
	749 NTNT-ATGGAGAGACACCTTTNTTAAAAATTGG 781 		
Qy	RESULT 12 BM480136		
	LOCUS		
	DEFINITION BM480136 728 bp mRNA linear EST 05-FEB-2002 AGENCOURT 6468228 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5574073 5', mRNA sequence.		
Db	ACCESSION BM480136 VERSION BM480136.1 GI:18529178 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.		
	REFERENCE 1 (bases 1 to 728) NIH-MGC http://mgc.nci.nih.gov/ AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC) TITLE Unpublished (1999) JOURNAL Contact: Robert Strausberg, Ph.D. COMMENT Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12322 row: c column: 02 High quality sequence stop: 681.		
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	source		
	ORIGIN		
Qy	Query Match 30.7%; Score 702; DB 3; Length 728; Best Local Similarity 99.9%; Pred. No. 1.6e-102; Matches 713; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		
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	Db 1 CAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTGTATTTTGAAGACAGGAAAA 60 		
Qy	1632 TGCCCCCTTCTGCTTTCC-TTTTTTTTTTGGAGACAGAGTCTTGCTCTGTGCCAGGC 1690 		
	Db 61 TGCCCCCTTCTGCTTTCC-TTTTTTTTTTGGAGACAGAGTCTTGCTCTGTGCCAGGC 120 		
Qy	1691 TGGAGTCAGTAGCAGCATCTCGGCTCTCACCGCAACCTCCGCTCTCTGGGTTCAAGCGA 1750 		
	Db 121 TGGAGTCAGTAGCAGCATCTCGGCTCTCACCGCAACCTCCGCTCTCTGGGTTCAAGCGA 180 		
Qy	1751 TTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCACCACCTGGGT 1810 		
	Db 181 TTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCACCACCTGGGT 240 		
	Qy 1811 GATTTTGTATTTTATAGTAGAGACGGGGTTTCCACCATGTTGGTCAGGCTGCTCTCAAACT 1870 		

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Db 241 GATTTTGTATTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCTCAAACT 300  
  
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Qy 1931 ACCACAGCTGGCCCTTCTGTCTTTATGTTTGGTTTGTGAGGAAGGAATGAAGTGGGAACC 1990  
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Qy 1991 AAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCTATGT 2050  
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Qy 2051 AAAGTAATAAGTATAAATGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAAGA 2110  
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Qy 2111 AACAGGTTAGGACATCTAGGTTCCAATTCAATTCACATTTCTTTTATATGATTCCTTTAAACTTA 2170  
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Qy 2171 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGATTCCTTTAAACTTA 2230  
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Qy 2231 TTCCAGATGTAGTTCTTCCAATTAATAATTTGAATAAATCTTTTGTACTCAA 2284  
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RESULT 13  
DR004375  
LOCUS  
DEFINITION  
DR004375 717 bp mRNA linear EST 17-MAY-2005  
TC105495 Human placenta, large insert, pCMV expression library Homo sapiens cDNA clone TC105495 5' similar to Homo sapiens, hypothetical protein FLJ10298, clone MGC:26021 IMAGE:4824116, complete cds, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 717)  
AUTHORS  
Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.

TITLE  
High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts  
JOURNAL  
COMMENT  
Unpublished (2005)  
Contact: Kovacs, KF  
High Throughput cDNA Cloning  
OriGene Technologies, Inc. ( www.origene.com )  
6 Taft Court, Suite 100, Rockville, MD 20850, USA  
Tel: 301 340 3188  
Fax: 301 340 8606  
Email: CDNA@origene.com

This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc.  
Please contact OriGene for access.  
OriGene Technologies, Inc.  
6 Taft Ct. Suite 100  
Rockville, MD 20850  
Tel: (301) 340-3188  
http://www.origene.com  
Seq primer: pCMV6 5prime forward vector primer, OriGene Technologies Inc.  
Location/Qualifiers  
1. .717

RESULT 14  
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LOCUS  
DEFINITION  
AGENCOURT\_6468229 NIH\_MGC\_88 Homo sapiens cDNA clone IMAGE:5574049 linear EST 05-FEB-2002

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/clone="TC105495"  
/tissue\_type="Placenta"  
/clone\_lib="Human placenta, large insert, pCMV expression library"  
/note="Vector: pCMV6-XL4; Site 1: EcoR1; Site 2: Xho1/Sal1 compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

ORIGIN

Query Match 30.7%; Score 700.4; DB 13; Length 717;  
Best Local Similarity 99.7%; Pred. No. 2.8e-102;  
Matches 701; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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Qy 61 GGGCGGACAGAGCTGTCTCGACCTGGATGGCAGAGGGCGCGGGTCTCTCGAC 120  
Db 75 GGGCGGACAGAGCTGTCTCGACCTGGATGGCAGAGGGCGCGGGTCTCTCGAC 134  
  
Qy 121 GCCAGAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGAG 180  
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BM480099  
BM480099.1 GI:18529141  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
1 (bases 1 to 729)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12322 row: b column: 02  
High quality sequence stop: 673.  
High quality sequence stop: 673.  
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Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally;  
oligo-dT primed. Average insert size 1.767 kb. Library  
enriched for full-length clones and constructed by Life  
Technologies. Note: this is a NIH\_MGC Library."  
ORIGIN  
Query Match 30.7%; Score 700.4; DB 3; Length 729;  
Best Local Similarity 99.7%; Pred. No. 2.8e-102;  
Matches 712; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1572 CAATGAGTTTCTGCTGACTGTGCTAGTCTTAGCAGGAGGTGTATTTGAAGACAGGAAAA 1631  
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QY 1632 TGCCCCCTTCTGCTTTCC-TTTTTTTTTTGGAGACAGAGTCTTGCTCTGTTGCCAGGC 1690  
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ACCESSION BF312571  
VERSION BF312571.1 GI:11260389  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 870)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LLCM1017 row: m column: 12  
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High quality sequence stop: 756.  
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cloned into EcoRI/XhoI sites using the following 5',  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."  
ORIGIN  
Query Match 30.2%; Score 690.6; DB 2; Length 870;  
Best Local Similarity 94.1%; Pred. No. 1e-100;  
Matches 761; Conservative 0; Mismatches 44; Indels 4; Gaps 4;  
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
4 GCGGAGCATCCGCTGCGGTCTCGCGGAGACCCCGCGGATTCCGCGGTCTTCCCGC 63

Qy	61	GGGCGGACAGAGCTGTCTCGCACCTGGATGGCAGAGGGCGCCGGGGTCTCTCGAC	120
Db	64	GGGCGGACAGAGCTGTCTCGCACCTGGATGGCAGAGGGCGCCGGGGTCTCTCGAC	123
Qy	121	GCCAGAGAGAAATCTCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG	180
Db	124	GCCAGAGAGAAATCTCATCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAG	183
Qy	181	GATTATCCTTGACCTTTGAGACCAAAACTAAACTGAAATTTAAAAATGTTCTTCGGGGGA	240
Db	184	GATTATCCTTGACCTTTGAGACCAAAACTAAACTGAAATTTAAAAATGTTCTTCGGGGGA	243
Qy	241	GAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTTGACACATAAGGCTGTCTGCT	300
Db	244	GAAGGGAGCTTGACTTACACTTTGGTAATAA - TTGCTTCCTGACACATAAGGCTGTCTGCT	302
Qy	301	AGTCAGAAATTGCCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTT	360
Db	303	AGTCAGAA - TGCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTT	361
Qy	361	TCTAAGGGAATCAGAGGCAATGAGCCCGTATATATACTTCAACTCAAGAAAGACTGCAATTAAT	420
Db	362	TCTAAGGGAATCAGAGGCAATGAGCCCGTATATATACTTCAACTCAAGAAAGACTGCAATTAAT	421
Qy	421	TCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC	480
Db	422	TCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGAC	481
Qy	481	ACTCGAAAAACAGCTAGACACCCCAACTGCTACCTATTTTCTGTCTCCCAACGAGGAAGCC	540
Db	482	ACTCGAAAAACAGCTAGACACCCCAACTGCTACCTATTTTCTGTCTCCCAACGAGGAAGCC	541
Qy	541	TGTCCATTGAAACCAGCAAAAGACTTATGAGTTACAGGATAAATTACAGATTTTCCATCT	600
Db	542	TGTCCATTGAAACCAGCAAAAGACTTATGAGTTACAGGATAAATTACAGATTTTCCATCT	601
Qy	601	TTGACCAGAAATTTGCCAAGCCCAAGAGTTACCCCGAGGAAGATTCTCTTACATGGCCAA	660
Db	602	TTGACCAGAAATTTGTGCAAGCCCAAGAGTTACCCCGAGGAAGATTCTCTTACATGGCCAA	661
Qy	661	-TTTTCAACAGCAGTCACCTCCCTAGCCCATCATCACACAGATTATTCAAAGCCCACCGA	719
Db	662	TTTTTCACAGCAGTCAACTCCCTAGCCCATCATCACACAGATTATTCAAAGCCCACCGA	721
Qy	720	TATCTCATGGAGAGACACAC - TTTCTCAGAAAGTTTGGATCCTCAGATCACCTGGAGAAAC	778
Db	722	TATCTCATGGAGAGACACACTTTTCTCAGAAAGTTGGGGTTCTCCAGGATACCTGGAGAA	781
Qy	779	TATTTAAGATGGATGAAGCAAGTGCCAG	807
Db	782	ATTTTAGATGGTGAAGCCAGGGGCCAG	810

GenCore version 6.2.1  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 20, 2007, 00:48:04 ; Search time 18533 Seconds  
(without alignments)  
1607.449 Million cell updates/sec

Title: US-09-944-929-83  
Perfect score: 2211  
Sequence: 1 MFFGEGSLTYTLVVICFLT.....LRRKYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15136766

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:  
-THR=4 -MODEL=frame+ p2n.model -DEV=SOFT  
-Q=/abss/ABSSWEB spool/US09944929/runat 19092007 174414 25985/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -SIMRANGE=0.0005 -MINMATCH=0.1 -LOOPCL=0  
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-LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-USER=US09944929@CGN 1 1 8641 @runat 19092007 174414 25985 -NCPU=6 -NO MMAP  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.\*  
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2: gb\_pat:\*  
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7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Match	Length DB ID	Description
1	2211	100.0	2284	2 BD140585
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3	2211	100.0	2284	2 AR252736

4	2211	100.0	2284	2	DD028540	Secreted
5	2211	100.0	2284	2	DD031661	COMPOSITI
6	2211	100.0	2284	2	DD039442	Secreted
7	2211	100.0	2284	2	DD249590	Secreted
8	2211	100.0	2284	2	AR429104	Sequence
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10	2211	100.0	2284	2	AR691142	Sequence
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13	2211	100.0	2284	2	AR706178	Sequence
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19	2211	100.0	2284	2	AR809329	Sequence
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21	2211	100.0	2284	2	AR834082	Sequence
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24	2211	100.0	2284	2	AR862498	Sequence
25	2211	100.0	2284	2	AR869150	Sequence
26	2211	100.0	2284	2	AR891893	Sequence
27	2211	100.0	2284	2	AR897166	Sequence
28	2211	100.0	2284	2	AR902010	Sequence
29	2211	100.0	2284	2	AR914822	Sequence
30	2211	100.0	2284	2	AX403627	Sequence
31	2211	100.0	2284	5	AY358563	Homo sapi
32	2211	100.0	2297	2	AX883044	Sequence
33	2211	100.0	2297	2	BD160088	Primer fo
34	2211	100.0	2297	5	AK023622	Homo sapi
35	2210	99.9	2333	5	BC032998	Homo sapi
36	2072	93.7	2015	2	BD227259	Secreted
37	2039	92.2	2345	5	AB060888	Macaca fa
38	2022	91.5	2221	2	AX876122	Sequence
39	2022	91.5	2221	2	BD155963	Primer fo
40	2022	91.5	2221	2	BD447120	Method fo
41	2022	91.5	2221	2	CQ776818	Sequence
42	2022	91.5	2221	5	AK001160	Homo sapi
43	1573.5	71.2	144000	5	AC007621	Homo sapi
44	1573.5	71.2	188344	12	AC131617	Homo sapi
45	1239	56.0	1907	14	BC120333	Bos tauru
46	1216	55.0	735	2	CQ735543	Sequence
47	1179.5	53.3	2288	6	BC039930	Mus muscu
48	1164.5	52.7	2286	2	BD447563	Method fo
49	1164.5	52.7	2286	2	CQ777667	Sequence
50	865	39.1	517	2	BD458602	NOVEL POL
51	845	38.2	548	2	BD059530	Secreted
52	791	35.8	855	2	AX867136	Sequence
53	791	35.8	855	2	BD147198	Primer fo
54	780.5	35.3	805	2	AX869834	Sequence
55	780.5	35.3	805	2	BD149896	Primer fo
56	707	32.0	196033	12	AC162418	Bos tauru
57	707	32.0	209109	12	AC149660	Bos tauru
58	688.5	31.1	224870	12	AC129657	Rattus no
59	688.5	31.1	250782	12	AC128093	Rattus no
60	678	30.7	188300	6	AC163198	Mus muscu
61	678	30.7	195236	6	AC126692	Mus muscu
62	678	30.7	244911	12	AC159128	Mus muscu
63	633	28.6	422	2	BD071236	Secreted
64	522	23.6	1627	11	AJ719946	Gallus ga
65	503	22.7	1326	6	BC031372	Mus muscu
66	386	17.5	188344	12	AC131617	Homo sapi
67	343.5	15.5	242590	12	AC133722	Rattus no
68	271.5	12.3	244911	12	AC159128	Mus muscu
69	242	10.9	295	2	AX894034	Sequence
70	242	10.9	295	2	BD029567	Sequence
71	242	10.9	295	2	AR729828	Sequence
72	221	10.0	2165	11	AX929877	Gallus ga
73	206.5	9.3	1919	6	BC019471	Mus muscu
74	204.5	9.2	2058	5	AF264781	Homo sapi
75	203	9.2	171026	11	BX572619	Zebrafish
76	197	8.9	112864	12	AC024127	Homo sapi



C	77	197	8.9	187516	5	AP002813	AP002813 Homo sapi	C	150	162.5	7.3	214306	12	CR385054	CR385054 Danio rer
C	78	197	8.9	191589	5	AP002992	AP002992 Homo sapi		151	161.5	7.3	11334	12	AC014605	AC014605 Drosophil
	79	196.5	8.9	1826	2	AR541982	AR541982 Sequence		152	161	7.3	1275	4	AB181301	AB181301 Triticum
	80	196.5	8.9	1826	2	AR699144	AR699144 Sequence		153	161	7.3	2376	10	AY702017	AY702017 Equid her
C	81	196.5	8.9	218688	6	AC132452	AC132452 Mus muscu		154	160.5	7.3	1431	5	HSMUCIN2	Z34277 H.sapiens (
	82	195.5	8.8	1389	2	CQ722760	CQ722760 Sequence		155	160.5	7.3	1638	2	AR578236	AR578236 Sequence
	83	195.5	8.8	1969	5	BC011765	BC011765 Homo sapi		156	160.5	7.3	2365	5	BC025688	BC025688 Homo sapi
	84	194.5	8.8	1642	2	BD223134	BD223134 98 human		157	160.5	7.3	2753	2	CQ612249	CQ612249 Sequence
	85	194.5	8.8	1642	2	AR243832	AR243832 Sequence		158	160.5	7.3	3168	13	AY060815	AY060815 Drosophil
	86	190	8.6	1742	13	AK112387	AK112387 Ciona int		159	160.5	7.3	22622	2	CQ612248	CQ612248 Sequence
	87	188	8.5	1661	2	CS326948	CS326948 Sequence		160	160.5	7.3	94585	12	AC176204	AC176204 Strongylo
	88	188	8.5	1661	2	CS366058	CS366058 Sequence		161	160.5	7.3	167366	13	AC104605	AC104605 Drosophil
	89	188	8.5	1661	2	DD039569	DD039569 SECRETED	C	162	160.5	7.3	290042	13	AE003435	AE003435 Drosophil
	90	188	8.5	1661	2	AR879424	AR879424 Sequence		163	160	7.2	1115	13	AY344834	AY344834 Anopheles
	91	188	8.5	1661	2	AR902828	AR902828 Sequence		164	160	7.2	2148	5	AF253321	AF253321 Homo sapi
	92	188	8.5	1661	2	AR915566	AR915566 Sequence		165	160	7.2	8106	5	AF488829	AF488829 Homo sapi
	93	188	8.5	1661	2	AX464090	AX464090 Sequence		166	160	7.2	10174	2	CS035313	CS035313 Sequence
	94	188	8.5	1661	5	AY358754	AY358754 Homo sapi		167	160	7.2	10174	2	CS044265	CS044265 Sequence
	95	183.5	8.3	4047	5	HSA298318	AY298318 Homo sapi		168	160	7.2	10174	2	CS350720	CS350720 Sequence
	96	183.5	8.3	168002	12	CT583679	CT583679 Danio rer		169	160	7.2	10174	5	HS598F21A	AL096857 Novel hum
	97	176.5	8.0	2091	6	BC098053	BC098053 Rattus no	C	170	160	7.2	110000	10	AJ890364_1	Continuation (2 of
	98	176.5	8.0	271704	12	AC111375	AC111375 Rattus no	C	171	159.5	7.2	171875	12	CR926130	CR926130 Danio rer
C	99	175.5	7.9	179075	12	AC150138	AC150138 Gallus ga		172	159	7.2	1115	13	AY344835	AY344835 Anopheles
	100	175	7.9	131676	5	AC139749	AC139749 Homo sapi		173	159	7.2	37445	13	U51998	U51998 Caenorhabdi
	101	173.5	7.8	155281	12	AC168594	AC168594 Strongylo	C	174	159	7.2	129565	11	CR848731	CR848731 Zebrafish
	102	172.5	7.8	1720	5	HUMMUC2A	M74027 Human mucin	C	175	159	7.2	183614	11	CR735107	CR735107 Zebrafish
	103	172.5	7.8	3811	5	HUMIMUCA	M94131 Human mucin	C	176	159	7.2	196461	6	AL627314	AL627314 Mouse DNA
	104	172.5	7.8	15720	2	AX926462	AX926462 Sequence		177	158.5	7.2	984	5	HSU78550	U78550 Homo sapien
	105	172.5	7.8	15720	2	AX951715	AX951715 Sequence		178	158.5	7.2	1134	2	CQ750558	CQ750558 Sequence
	106	172.5	7.8	15720	2	AX959992	AX959992 Sequence		179	158.5	7.2	1604	2	DD058256	DD058256 EXTRACELL
	107	172.5	7.8	15720	2	AX959993	AX959993 Sequence		180	158.5	7.2	1604	2	AX704762	AX704762 Sequence
	108	172.5	7.8	15720	2	BD3399825	BD3399825 BREAST CA		181	158.5	7.2	2388	2	CS300768	CS300768 Sequence
	109	172.5	7.8	15720	2	BD421463	BD421463 CANCER DI	C	182	158.5	7.2	119883	12	AC181410	AC181410 Strongylo
	110	172.5	7.8	15720	2	CQ834018	CQ834018 Sequence		183	158.5	7.2	120612	5	AC108518	AC108518 Homo sapi
	111	172.5	7.8	15720	2	CS114746	CS114746 Sequence	C	184	158.5	7.2	138320	12	AC181434	AC181434 Strongylo
	112	172.5	7.8	15720	2	CS273953	CS273953 Sequence	C	185	158.5	7.2	243553	12	AC096320	AC096320 Rattus no
	113	172.5	7.8	15720	2	CS353065	CS353065 Sequence		186	158	7.1	245273	12	AC137407	AC137407 Rattus no
	114	172.5	7.8	15720	2	DD018353	DD018353 SELECTION		187	158	7.1	252902	12	AC129164	AC129164 Rattus no
	115	172.5	7.8	15720	2	DD018354	DD018354 SELECTION		188	158	7.1	268213	12	AC103285	AC103285 Rattus no
	116	172.5	7.8	15720	2	AX193491	AX193491 Sequence		189	157.5	7.1	2065	4	BLYHORDCA	M36941 Hordeum vul
	117	172.5	7.8	15720	2	AX330186	AX330186 Sequence		190	157.5	7.1	2350	5	HUMSUBMAND	L13283 Homo sapien
	118	172.5	7.8	15720	5	HUMMUC2X	L21998 Homo sapien		191	157.5	7.1	2429	2	DD139754	DD139754 EXTRACELL
C	119	172	7.8	155358	11	BX323839	BX323839 Zebrafish		192	157.5	7.1	2429	2	AX174734	AX174734 Sequence
	120	171.5	7.8	10371	2	CQ894734	CQ894734 Sequence		193	157.5	7.1	7382	5	HSA298317	AJ298317 Homo sapi
C	121	171	7.7	131199	12	AC180826	AC180826 Strongylo		194	157.5	7.1	174597	12	AC183563	AC183563 Canis fam
	122	169.5	7.7	95933	12	AC178870	AC178870 Strongylo		195	157.5	7.1	232316	12	AC098608	AC098608 Rattus no
C	123	168.5	7.6	82064	12	AC006937	AC006937 Drosophil		196	157	7.1	1367	10	AY034640	AY034640 Equine he
C	124	168.5	7.6	158125	12	CT030000	CT030000 Danio rer		197	157	7.1	110000	4	CR382127_00	CR382127 Yarrowia
C	125	168	7.6	28291	13	CEP56H9	Z74473 Caenorhabdi		198	156.5	7.1	1322	10	AY034644	AY034644 Equine he
C	126	168	7.6	148945	12	CR759744	CR759744 Danio rer		199	156.5	7.1	9964	2	CQ729631	CQ729631 Sequence
	127	167	7.6	215743	11	CR749741	CR749741 Zebrafish	C	200	156	7.1	2300	2	CQ611372	CQ611372 Sequence
	128	166	7.5	1413	4	AB181300	AB181300 Triticum	C	201	156	7.1	3161	2	CQ611375	CQ611375 Sequence
	129	165.5	7.5	6300	6	MMU511869	AJ511869 Mus muscu	C	202	156	7.1	9958	4	SCYJR151C	Z49651 S.cerevisia
	130	165.5	7.5	6616	6	AH012557S4	AJ184388 Mus muscu	C	203	156	7.1	48626	12	AC013119	AC013119 Drosophil
C	131	165.5	7.5	189095	12	AC167551	AC167551 Mus muscu		204	156	7.1	160986	13	AC108481	AC108481 Drosophil
C	132	165.5	7.5	193924	6	AC102524	AC102524 Mus muscu	C	205	156	7.1	252074	12	AC176683	AC176683 Strongylo
C	133	165.5	7.5	200074	6	AC164070	AC164070 Mus muscu	C	206	156	7.1	296227	13	AE003430	AE003430 Drosophil
	134	165	7.5	1866	5	HSMUC5BC	X74955 H.sapiens M		207	156	7.1	333321	13	AC116986	AC116986 Dictyoste
C	135	165	7.5	190110	12	CR854881	CR854881 Danio rer		208	155.5	7.0	1112	13	AY344832	AY344832 Anopheles
	136	164.5	7.4	197012	6	AL669823	AL669823 Mouse DNA		209	155.5	7.0	2806	4	S66938	S66938 C-hordein [
C	137	164.5	7.4	206201	12	AC164757	AC164757 Bos tauru		210	155.5	7.0	5403	2	AR890958	AR890958 Sequence
	138	164	7.4	1115	13	AY344833	AY344833 Anopheles		211	155.5	7.0	5403	13	TRBTCNAA	M61732 T.cruzi neu
	139	164	7.4	14094	2	AR906579	AR906579 Sequence	C	212	155.5	7.0	110000	4	AP008207_205	Continuation (206
	140	164	7.4	14094	5	AJ606308	AJ606308 Homo sapi	C	213	155.5	7.0	157563	12	AC176250	AC176250 Strongylo
	141	164	7.4	14246	2	AR906578	AR906578 Sequence	C	214	155.5	7.0	159509	4	AP004225	AP004225 Oryza sat
	142	164	7.4	14246	5	AJ606307	AJ606307 Homo sapi	C	215	155.5	7.0	172642	4	AP004258	AP004258 Oryza sat
	143	164	7.4	17847	2	CS143783	CS143783 Sequence		216	155	7.0	2194	5	HSM807334	BX647190 Homo sapi
	144	164	7.4	124104	5	AC061979	AC061979 Homo sapi		217	155	7.0	2922	2	AX834322	AX834322 Sequence
C	145	164	7.4	198646	6	AC150683	AC150683 Mus muscu		218	155	7.0	2922	2	CS168201	CS168201 Sequence
	146	163	7.4	153619	12	AC173552	AC173552 Strongylo		219	155	7.0	2922	5	AK096699	AK096699 Homo sapi
C	147	163	7.4	172504	5	AP001999	AP001999 Homo sapi	C	220	155	7.0	143605	12	AC171190	AC171190 Bos tauru
	148	163	7.4	232304	11	BX322616	BX322616 Zebrafish		221	155	7.0	146917	12	AC142043	AC142043 Rattus no
C	149	162.5	7.3	152177	11	AL935114	AL935114 Zebrafish		222	155	7.0	188084	6	AC124523	AC124523 Mus muscu

C	223	155	7.0	209973	12	AC073755	AC073755 Mus muscu	296	151	6.8	228387	12	CR788237	CR788237 Danio rer
	224	154.5	7.0	10713	5	HSMUC5BEX	Z72496 H.sapiens M	297	151	6.8	285860	13	AE003551	AE003551 Drosophil
	225	154.5	7.0	33359	13	CEF55B11	Z83318 Caenorhabdi	298	150.5	6.8	1470	13	LSI132603	AJ132603 Litomosoi
	226	154.5	7.0	195349	12	AC006705	AC006705 Caenorhab	299	150.5	6.8	1630	5	HSMUC5BA	X74370 H.sapiens M
	227	154	7.0	1115	13	AY344830	AY344830 Anopheles	300	150.5	6.8	2057	5	HSM809055	BX648904 Homo sapi
	228	154	7.0	2282	5	AK124374	AK124374 Homo sapi	301	150.5	6.8	3097	4	COICTS2CHI	L41662 Coccidioide
	229	154	7.0	37777	4	SPBC215	AL033534 S.pombe c	302	150.5	6.8	25080	2	CQ737837	CQ737837 Sequence
	230	154	7.0	99886	5	HS598F2	AL021579 Human DNA	303	150.5	6.8	32797	13	CEW01F3	Z92815 Caenorhabdi
	231	154	7.0	110000	12	AC127805_1	Continuation (2 of	304	150.5	6.8	75254	11	BX510925	BX510925 Zebrafish
C	232	154	7.0	110000	13	AC116984_3	Continuation (4 of	C	305	6.8	106121	12	AC179263	AC179263 Strongylo
	233	154	7.0	127643	11	BX321877	BX321877 Zebrafish	306	150.5	6.8	121936	6	AL691513	AL691513 Mouse DNA
	234	154	7.0	317853	12	CR936344	CR936344 Danio rer	307	150.5	6.8	150224	10	AY665713	AY665713 Equine he
C	235	153.5	6.9	4755	2	CQ612725	CQ612725 Sequence	C	308	6.8	182881	12	CT025755	CT025755 Mus muscu
	236	153.5	6.9	65443	12	AC014845	AC014845 Drosophil	309	150.5	6.8	212955	12	AC136676	AC136676 Rattus no
	237	153.5	6.9	149430	10	AY464052	AY464052 Equine he	310	150	6.8	1584	14	SSGMUC2	U10281 Sus scrofa
	238	153.5	6.9	189694	13	AC009848	AC009848 Drosophil	311	150	6.8	15984	15	AF224509	AF224509 Bacteroid
	239	153.5	6.9	192367	12	AC121410	AC121410 Rattus no	C	312	6.8	88203	11	AC097628	AC097628 Takifugu
	240	153.5	6.9	197156	13	AE003760	AE003760 Drosophil	C	313	6.8	132242	12	AC176969	AC176969 Strongylo
	241	153.5	6.9	209201	6	AC139244	AC139244 Mus muscu	C	314	6.8	190628	12	AC176547	AC176547 Strongylo
	242	153.5	6.9	220091	12	AC118835	AC118835 Rattus no	315	150	6.8	198927	6	AC155273	AC155273 Mus muscu
	243	153.5	6.9	237055	12	AC095177	AC095177 Rattus no	316	150	6.8	204611	12	AC171208	AC171208 Mus muscu
	244	153	6.9	2014	5	AK093828	AK093828 Homo sapi	C	317	6.8	252074	12	AC176683	AC176683 Strongylo
	245	153	6.9	2490	2	CS113291	CS113291 Sequence	318	149.5	6.8	47026	13	CBRG41B17	AC084584 Caenorhab
	246	153	6.9	2861	5	AK130557	AK130557 Homo sapi	319	149.5	6.8	82064	12	AC006937	AC006937 Drosophil
	247	153	6.9	3407	11	AY587262	AY587262 Sparus au	320	149.5	6.8	99171	12	AC176529	AC176529 Strongylo
	248	153	6.9	61830	4	AP007157_26	Continuation (27 o	321	149.5	6.8	160208	12	AC184651	AC184651 Strongylo
	249	153	6.9	111824	5	AL160412	AL160412 Human DNA	322	149.5	6.8	163183	13	AC009842	AC009842 Drosophil
C	250	153	6.9	176147	11	AL929105	AL929105 Zebrafish	C	323	6.8	178400	11	BX294376	BX294376 Zebrafish
	251	153	6.9	179429	12	AC120374	AC120374 Mus muscu	324	149.5	6.8	178595	12	AC176386	AC176386 Strongylo
C	252	153	6.9	181999	12	AC162853	AC162853 Mus muscu	325	149.5	6.8	180051	6	AC139223	AC139223 Mus muscu
	253	153	6.9	209579	6	AC124764	AC124764 Mus muscu	C	326	6.8	221935	12	AC176595	AC176595 Strongylo
	254	152.5	6.9	1112	13	AY344831	AY344831 Anopheles	C	327	6.8	289893	13	AE003576	AE003576 Drosophil
	255	152.5	6.9	143605	12	AC171190	AC171190 Bos tauru	328	149	6.7	471	2	CQ486220	CQ486220 Sequence
	256	152.5	6.9	144636	12	AC176815	AC176815 Strongylo	329	149	6.7	515	2	CQ516037	CQ516037 Sequence
	257	152	6.9	1115	13	AY344829	AY344829 Anopheles	330	149	6.7	2903	4	E11860	E11860 Genomic DNA
	258	152	6.9	1297	2	AR448257	AR448257 Sequence	331	149	6.7	2903	4	AB003521	AB003521 Saccharom
C	259	152	6.9	5795	6	RNMUCASGP7	U06752 Rattus norv	332	149	6.7	4830	8	DQ331761	DQ331761 Synthetic
	260	152	6.9	12573	4	SPAPB15E9	AL691401 S.pombe c	333	149	6.7	84902	5	AC021216	AC021216 Homo sapi
	261	152	6.9	110000	15	CR936257_24	Continuation (25 o	C	334	6.7	110000	15	CR936257_17	Continuation (18 o
C	262	152	6.9	110459	5	AC117378	AC117378 Homo sapi	335	149	6.7	110000	15	AE017180_30	Continuation (31 o
	263	152	6.9	141699	12	AC181804	AC181804 Strongylo	336	149	6.7	151160	12	AC151022	AC151022 Callithri
	264	152	6.9	210156	12	AC136829	AC136829 Rattus no	C	337	6.7	166000	13	AC104511	AC104511 Drosophil
	265	152	6.9	236493	12	AC106220	AC106220 Rattus no	338	149	6.7	316613	4	SCCHRII	XS9720 S.cerevisia
C	266	152	6.9	269921	12	AC099286	AC099286 Rattus no	339	149	6.7	332030	13	AE003491	AE003491 Drosophil
	267	151.5	6.9	1403	5	HSA298319	AJ298319 Homo sapi	340	148.5	6.7	1268	10	AY034643	AY034643 Equine he
	268	151.5	6.9	1416	13	AGA010903	AJ010903 Anopheles	341	148.5	6.7	1515	5	HUMGASMUCB	L07518 Homo sapien
	269	151.5	6.9	4458	13	DMU42402	U42402 Drosophila	342	148.5	6.7	38181	6	AC175742	AC175742 Mus muscu
	270	151.5	6.9	4829	2	CQ589581	CQ589581 Sequence	C	343	6.7	41746	6	AC175658	AC175658 Mus muscu
	271	151.5	6.9	5561	6	AK122540	AK122540 Mus muscu	C	344	6.7	66208	5	AL450284	AL450284 Human DNA
	272	151.5	6.9	5754	13	DMU42403	U42403 Drosophila	345	148.5	6.7	110000	4	CR382132_28	Continuation (29 o
C	273	151.5	6.9	110000	4	CR382129_05	Continuation (6 of	346	148.5	6.7	133325	11	AL627423	AL627423 Zebrafish
C	274	151.5	6.9	110000	13	AC116984_0	AC116984 Dictyoste	C	347	6.7	185817	11	BX296521	BX296521 Zebrafish
C	275	151.5	6.9	110000	13	AC116984_1	Continuation (2 of	348	148.5	6.7	219218	12	AC020817	AC020817 Mus muscu
C	276	151.5	6.9	110000	15	AE009442_11	Continuation (12 o	349	148.5	6.7	221879	12	AC096704	AC096704 Rattus no
C	277	151.5	6.9	110000	15	AE009442_14	Continuation (15 o	350	148.5	6.7	222343	12	AC114531	AC114531 Rattus no
C	278	151.5	6.9	121987	12	AC179766	AC179766 Strongylo	351	148.5	6.7	222603	12	AC125755	AC125755 Rattus no
C	279	151.5	6.9	122934	5	AC092898	AC092898 Homo sapi	352	148.5	6.7	234097	12	AC120493	AC120493 Rattus no
C	280	151.5	6.9	132457	5	AC016584	AC016584 Homo sapi	353	148	6.7	1044	2	AX840040	AX840040 Sequence
	281	151.5	6.9	162388	11	BX569794	BX569794 Zebrafish	354	148	6.7	1044	2	AX840626	AX840626 Sequence
	282	151.5	6.9	174142	12	CT583645	CT583645 Danio rer	355	148	6.7	1710	13	GCY299721	AJ299721 Geodia cy
	283	151.5	6.9	175351	12	AC117900	AC117900 Rattus no	356	148	6.7	2032	2	AR195309	AR195309 Sequence
	284	151.5	6.9	177554	12	AC176076	AC176076 Strongylo	357	148	6.7	2032	2	AR222274	AR222274 Sequence
C	285	151.5	6.9	219471	6	CR974473	CR974473 Mouse DNA	358	148	6.7	2032	2	AR907772	AR907772 Sequence
	286	151.5	6.9	247341	12	AC099178	AC099178 Rattus no	359	148	6.7	2032	13	DMU17693	U17693 Drosophila
C	287	151.5	6.9	260558	11	BX950188	BX950188 Zebrafish	C	360	6.7	2570	2	DD154362	DD154362 NOVEL ANT
	288	151	6.8	2161	11	XELFIMC1X	L02115 Frog integu	C	361	6.7	7417	2	CQ594035	CQ594035 Sequence
	289	151	6.8	5929	2	CQ578280	CQ578280 Sequence	C	362	6.7	31095	5	AL391319	AL391319 Human DNA
C	290	151	6.8	11963	2	CQ578279	CQ578279 Sequence	363	148	6.7	31497	2	DD174506	DD174506 Repeat Se
C	291	151	6.8	48836	12	AC020151	AC020151 Drosophil	C	364	6.7	39746	2	CQ589580	CQ589580 Sequence
C	292	151	6.8	139530	11	BX545917	BX545917 Zebrafish	365	148	6.7	42248	12	AC020375	AC020375 Drosophil
C	293	151	6.8	154071	13	AC115598	AC115598 Dictyoste	366	148	6.7	52158	12	AC013185	AC013185 Drosophil
C	294	151	6.8	181063	13	AC010107	AC010107 Drosophil	367	148	6.7	66765	2	CQ874958	CQ874958 Sequence
	295	151	6.8	184657	13	AC010043	AC010043 Drosophil	368	148	6.7	66765	5	AF414442	AF414442 Homo sapi





C 515	145	6.6	276132	13	AE003543	AE003543 Drosophil
516	145	6.6	348551	4	BX649606	BX649606 Aspergill
517	144.5	6.5	1226	6	RNU03407	U03407 Rattus norv
518	144.5	6.5	2156	2	AX536566	AX536566 Sequence
C 519	144.5	6.5	2813	4	CHOOORFS	X64616 Oenothera o
520	144.5	6.5	3378	4	SCYGR022C	Z72807 S.cerevisia
521	144.5	6.5	3423	2	AR527788	AR527788 Sequence
522	144.5	6.5	3776	13	AY865077	AY865077 Drosophil
523	144.5	6.5	3776	13	AY865078	AY865078 Drosophil
524	144.5	6.5	3783	13	AY865076	AY865076 Drosophil
525	144.5	6.5	4327	2	CS047818	CS047818 Sequence
C 526	144.5	6.5	5018	13	AC006797	AC006797 Caenorhab
C 527	144.5	6.5	19802	15	AE009442_25	Continuation (26 o
528	144.5	6.5	30812	4	SC9924	Z54141 S.cerevisia
C 529	144.5	6.5	57395	11	BX927382	BX927382 Zebrafish
C 530	144.5	6.5	110000	15	AE009442_24	Continuation (25 o
531	144.5	6.5	124388	12	AC181015	AC181015 Strongylo
C 532	144.5	6.5	143493	12	AC179429	AC179429 Strongylo
533	144.5	6.5	150747	12	AC177319	AC177319 Strongylo
C 534	144.5	6.5	154530	12	AC179324	AC179324 Strongylo
C 535	144.5	6.5	162296	5	AL161774	AL161774 Human DNA
536	144.5	6.5	167407	12	AC179230	AC179230 Strongylo
C 537	144.5	6.5	179035	6	AL772131	AL772131 Mouse DNA
C 538	144.5	6.5	195420	12	AC128290	AC128290 Rattus no
C 539	144.5	6.5	203401	5	AC015936	AC015936 Homo sapi
540	144.5	6.5	221454	10	AY186194	AY186194 Rhesus cy
541	144	6.5	1720	6	AB094071	AB094071 Rattus no
C 542	144	6.5	2490	2	CS113517	CS113517 Sequence
543	144	6.5	2558	4	AK101838	AK101838 Oryza sat
544	144	6.5	2873	11	BC111516	BC111516 Xenopus l
545	144	6.5	4567	13	AY366511	AY366511 Leishmani
C 546	144	6.5	9416	13	PFAPFS230A	L22219 Plasmodium
547	144	6.5	33270	13	AC116921	AC116921 Dictyoste
548	144	6.5	37604	5	AP006588	AP006588 Homo sapi
C 549	144	6.5	110000	4	AP008212_299	Continuation (300
550	144	6.5	110000	4	AP008214_178	Continuation (179
C 551	144	6.5	122761	12	AC174100	AC174100 Strongylo
552	144	6.5	131273	12	AC168507	AC168507 Strongylo
C 553	144	6.5	143507	4	AC091774	AC091774 Oryza sat
554	144	6.5	146856	4	AP004675	AP004675 Oryza sat
C 555	144	6.5	150660	4	AP003769	AP003769 Oryza sat
C 556	144	6.5	171965	4	AP003614	AP003614 Oryza sat
557	144	6.5	190149	12	AC122097	AC122097 Rattus no
558	144	6.5	207478	11	BX897691	BX897691 Zebrafish
C 559	144	6.5	231341	11	BX004816	BX004816 Zebrafish
560	144	6.5	234452	12	AC137227	AC137227 Rattus no
C 561	144	6.5	258147	12	AC120622	AC120622 Rattus no
562	143.5	6.5	2517	2	CQ610677	CQ610677 Sequence
563	143.5	6.5	2607	2	CQ594036	CQ594036 Sequence
564	143.5	6.5	3770	13	AY865074	AY865074 Drosophil
C 565	143.5	6.5	5146	2	CQ610676	CQ610676 Sequence
566	143.5	6.5	5388	2	CQ608451	CQ608451 Sequence
C 567	143.5	6.5	7782	2	CQ608450	CQ608450 Sequence
C 568	143.5	6.5	8426	12	AC013966	AC013966 Drosophil
C 569	143.5	6.5	24492	13	DMC56G7	AL031028 Drosophil
C 570	143.5	6.5	26160	12	AC019892	AC019892 Drosophil
571	143.5	6.5	35867	13	AC004315	AC004315 Drosophil
572	143.5	6.5	64833	12	AC168732	AC168732 Strongylo
C 573	143.5	6.5	89232	11	AL591175	AL591175 Zebrafish
C 574	143.5	6.5	103691	4	AC189370	AC189370 Brassica
575	143.5	6.5	110000	4	CR382136_03	Continuation (4 of
C 576	143.5	6.5	110000	12	AP006491_0	AP006491 Cyanidios
577	143.5	6.5	139517	5	AC105446	AC105446 Homo sapi
578	143.5	6.5	147369	12	AC147689	AC147689 Chloroceb
579	143.5	6.5	154426	11	AL732515	AL732515 Zebrafish
580	143.5	6.5	164950	11	CR788314	CR788314 Zebrafish
C 581	143.5	6.5	177096	13	AC107326	AC107326 Drosophil
582	143.5	6.5	180311	12	AC140086	AC140086 Chloroceb
583	143.5	6.5	184650	13	AC092186	AC092186 Drosophil
584	143.5	6.5	188374	5	AC005050	AC005050 Homo sapi
C 585	143.5	6.5	210297	12	AC168246	AC168246 Strongylo
586	143.5	6.5	219968	12	AC106650	AC106650 Rattus no
C 587	143.5	6.5	219995	12	AC096351	AC096351 Rattus no

C 588	143.5	6.5	232019	12	AC093939	AC093939 Rattus no
589	143.5	6.5	247509	12	AC099368	AC099368 Rattus no
C 590	143.5	6.5	284024	4	AC183493	AC183493 Brassica
591	143.5	6.5	303641	13	AE003583	AE003583 Drosophil
C 592	143.5	6.5	304204	13	AE003421	AE003421 Drosophil
593	143	6.5	1375	6	MMU54428	U45428 Mus musculu
594	143	6.5	1832	4	SCSECI1B	X60295 S.cereale S
595	143	6.5	1881	2	AX474660	AX474660 Sequence
596	143	6.5	1881	6	MMU14133	U14133 Mus musculu
597	143	6.5	2070	11	BSU43200	U43200 Boreogadus
C 598	143	6.5	2336	2	CQ607976	CQ607976 Sequence
599	143	6.5	3789	2	DD117855	DD117855 Genes Hig
600	143	6.5	3803	5	AF430017	AF430017 Homo sapi
601	143	6.5	24109	12	AC014880	AC014880 Drosophil
C 602	143	6.5	47323	5	AC005937	AC005937 Homo sapi
603	143	6.5	103780	5	AL773541	AL773541 Human DNA
C 604	143	6.5	105320	13	AC116920	AC116920 Dictyoste
C 605	143	6.5	110000	5	BA000025_09	Continuation (10 o
C 606	143	6.5	110000	15	CP000088_26	Continuation (27 o
607	143	6.5	114883	5	CR759747	CR759747 Human DNA
608	143	6.5	130108	12	AC176510	AC176510 Strongylo
C 609	143	6.5	153083	6	CR936849	CR936849 Mouse DNA
C 610	143	6.5	153332	11	BX546485	BX546485 Zebrafish
611	143	6.5	156272	5	AL669830	AL669830 Human DNA
612	143	6.5	159656	11	AL929243	AL929243 Zebrafish
613	143	6.5	161580	12	AC141660	AC141660 Apis mell
614	143	6.5	169511	13	AC007531	AC007531 Drosophil
615	143	6.5	171629	13	AC007691	AC007691 Drosophil
C 616	143	6.5	178688	12	AL713893	AL713893 Homo sapi
617	143	6.5	188701	12	AC102515	AC102515 Mus muscu
C 618	143	6.5	192650	5	AB023048	AB023048 Homo sapi
C 619	143	6.5	207354	6	AL671857	AL671857 Mouse DNA
C 620	143	6.5	214204	12	AC133776	AC133776 Rattus no
621	143	6.5	235164	12	AL672283	AL672283 Mus muscu
622	143	6.5	243490	12	AC131536	AC131536 Rattus no
623	143	6.5	299749	13	AE003606	AE003606 Drosophil
624	143	6.5	349980	2	CS039418	CS039418 Sequence
625	142.5	6.4	926	10	AY847308	AY847308 Bovine he
626	142.5	6.4	1584	14	BOVBRPE1A	M81193 Bovine reti
627	142.5	6.4	1843	4	AK110032	AK110032 Oryza sat
628	142.5	6.4	2315	13	DMU42014	U42014 Drosophila
629	142.5	6.4	2763	10	AY034645	AY034645 Equine he
630	142.5	6.4	2918	4	AK110182	AK110182 Oryza sat
631	142.5	6.4	3700	13	AY865072	AY865072 Drosophil
632	142.5	6.4	7376	15	AB029393	AB029393 Streptoco
633	142.5	6.4	30196	5	AC118759	AC118759 Homo sapi
634	142.5	6.4	110000	4	CR382130_16	Continuation (17 o
635	142.5	6.4	110000	4	AP007150_05	Continuation (6 of
636	142.5	6.4	110000	4	AP008207_042	Continuation (43 o
C 637	142.5	6.4	118250	12	AC168797	AC168797 Strongylo
C 638	142.5	6.4	121149	12	AC179116	AC179116 Strongylo
C 639	142.5	6.4	125026	6	AC091616	AC091616 Rattus no
C 640	142.5	6.4	126745	12	AC181754	AC181754 Strongylo
641	142.5	6.4	128525	4	AP003118	AP003118 Oryza sat
642	142.5	6.4	134865	12	AC177281	AC177281 Strongylo
643	142.5	6.4	141983	4	AP003047	AP003047 Oryza sat
C 644	142.5	6.4	201275	12	AC180749	AC180749 Strongylo
645	142.5	6.4	208615	12	AC079180	AC079180 Mus muscu
C 646	142.5	6.4	239426	12	AC111207	AC111207 Rattus no
647	142.5	6.4	241327	12	AC127126	AC127126 Rattus no
648	142.5	6.4	251075	12	AC132995	AC132995 Rattus no
649	142.5	6.4	251131	12	AC111217	AC111217 Rattus no
650	142	6.4	1271	10	AY034638	AY034638 Equine he
651	142	6.4	1586	6	MMU70653	U70653 Mus musculu
652	142	6.4	1598	6	MMU70654	U70654 Mus musculu
653	142	6.4	1661	6	MMRNAPSGL	X91144 M.musculus
654	142	6.4	2025	13	AY864356	AY864356 Drosophil
C 655	142	6.4	2541	6	MUSIGHMY	M28469 Mouse Ig re
656	142	6.4	2917	5	AK026404	AK026404 Homo sapi
657	142	6.4	9211	13	AB030033	AB030033 Dictyoste
C 658	142	6.4	12685	2	AR527547	AR527547 Sequence
C 659	142	6.4	12685	2	AR634267	AR634267 Sequence
C 660	142	6.4	27982	13	CEZK945	Z48544 Caenorhabdi

661	142	6.4	110000	12	LMFLCHR16_01	Continuation (2 of	c	734	140.5	6.4	13152	2	CS270981	CS270981 Sequence
c 662	142	6.4	165677	12	AC172459	AC172459 Bos tauru	c	735	140.5	6.4	13152	2	AX570447	AX570447 Sequence
663	142	6.4	168311	11	CR792425	CR792425 Zebrafish		736	140.5	6.4	14328	2	CQ897514	CQ897514 Sequence
c 664	142	6.4	196537	12	AC123389	AC123389 Rattus no	c	737	140.5	6.4	14328	2	CS270985	CS270985 Sequence
665	142	6.4	198056	12	AC106280	AC106280 Rattus no		738	140.5	6.4	14328	2	AX570451	AX570451 Sequence
666	142	6.4	282355	12	AC104401	AC104401 Rattus no		739	140.5	6.4	78917	12	AC018146	AC018146 Drosophil
667	141.5	6.4	2293	2	CS047820	CS047820 Sequence		740	140.5	6.4	87124	13	AC004371	AC004371 Drosophil
668	141.5	6.4	2960	13	AY057052	AY057052 Mamestra		741	140.5	6.4	107069	15	DQ116941	DQ116941 Streptomy
669	141.5	6.4	3263	2	CQ585087	CQ585087 Sequence		742	140.5	6.4	110000	4	AP008214_180	Continuation (181
670	141.5	6.4	3296	13	BT003186	BT003186 Drosophil		c 743	140.5	6.4	110000	4	CR382124_05	Continuation (6 of
671	141.5	6.4	3486	2	AR527989	AR527989 Sequence	c	744	140.5	6.4	110000	15	AE005672_16	Continuation (17 o
672	141.5	6.4	3689	13	AY128472	AY128472 Drosophil	c	745	140.5	6.4	110000	15	BA000030_00	BA000030 Streptomy
673	141.5	6.4	3794	13	AY865063	AY865063 Drosophil		746	140.5	6.4	123466	11	CR974440	CR974440 Zebrafish
c 674	141.5	6.4	39215	13	CED1054	Z74030 Caenorhabdi		747	140.5	6.4	125021	4	AC007504	AC007504 Arabidops
c 675	141.5	6.4	55205	4	AY448010S7	AY448016 Ipomoea t		c 748	140.5	6.4	135403	12	AP005423	AP005423 Oryza sat
676	141.5	6.4	110000	12	CT005251_4	Continuation (5 of		749	140.5	6.4	146735	12	AC178122	AC178122 Strongylo
677	141.5	6.4	117199	12	AC176437	AC176437 Strongylo	c	750	140.5	6.4	171686	12	AC186522	AC186522 Zea mays
678	141.5	6.4	146938	11	CR407704	CR407704 Zebrafish	c	751	140.5	6.4	172081	6	AC137124	AC137124 Mus muscu
679	141.5	6.4	150195	12	AC184114	AC184114 Zea mays		752	140.5	6.4	181728	13	AC008003	AC008003 Drosophil
c 680	141.5	6.4	158696	6	AC133581	AC133581 Mus muscu		753	140.5	6.4	192484	6	AC122767	AC122767 Mus muscu
c 681	141.5	6.4	169614	11	BX511115	BX511115 Zebrafish	c	754	140.5	6.4	200542	5	CNS01RG3	AL157736 Human chr
c 682	141.5	6.4	184690	6	AC164304	AC164304 Mus muscu		755	140.5	6.4	200720	4	AP005795	AP005795 Oryza sat
c 683	141.5	6.4	192548	12	AC129738	AC129738 Rattus no		756	140.5	6.4	234684	6	AC133618	AC133618 Rattus no
684	141.5	6.4	209951	6	AC162454	AC162454 Mus muscu	c	757	140.5	6.4	251269	12	AC119030	AC119030 Rattus no
c 685	141.5	6.4	241373	12	AC126747	AC126747 Rattus no		758	140.5	6.4	290034	13	AE003577	AE003577 Drosophil
c 686	141.5	6.4	251872	12	AC125998	AC125998 Rattus no	c	759	140.5	6.4	349980	2	CS272299	CS272299 Sequence
687	141	6.4	1736	15	AB102689	AB102689 Streptoco	c	760	140.5	6.4	349980	2	AX571765	AX571765 Sequence
688	141	6.4	1912	6	AH003203S2	U33442 Rattus norv		761	140	6.3	852	6	RRIMPR	Z11875 R.rattus mR
689	141	6.4	2039	6	BC082555	BC082555 Mus muscu		762	140	6.3	1196	10	AY034641	AY034641 Equine he
690	141	6.4	2130	4	AK103679	AK103679 Oryza sat	c	763	140	6.3	1653	4	TAE276509	AJ276509 Triticum
691	141	6.4	2228	6	AF099018	AF099018 Mus muscu		764	140	6.3	2475	6	AJ715791	AJ715791 Spalax ju
692	141	6.4	2682	4	CAU64206	U64206 Candida alb		765	140	6.3	4500	4	AB182389	AB182389 Oryza sat
693	141	6.4	3925	4	AF280606	AF280606 Triticum		766	140	6.3	6353	2	CQ580242	CQ580242 Sequence
c 694	141	6.4	3953	2	CQ056448	CQ056448 Sequence		767	140	6.3	8429	2	CQ580241	CQ580241 Sequence
c 695	141	6.4	3953	2	CQ145348	CQ145348 Sequence		c 768	140	6.3	13443	12	AC013070	AC013070 Drosophil
c 696	141	6.4	3953	2	CQ180791	CQ180791 Sequence		769	140	6.3	74699	12	AC178623	AC178623 Strongylo
c 697	141	6.4	3953	2	CQ205164	CQ205164 Sequence		770	140	6.3	110000	4	CR382131_34	Continuation (35 o
c 698	141	6.4	3953	2	CQ228543	CQ228543 Sequence		771	140	6.3	110000	13	AM269894_10	Continuation (11 o
c 699	141	6.4	3953	2	CQ266700	CQ266700 Sequence	c	772	140	6.3	113285	6	AL732606	AL732606 Mouse DNA
c 700	141	6.4	3953	2	CQ303653	CQ303653 Sequence	c	773	140	6.3	116782	12	AC178680	AC178680 Strongylo
c 701	141	6.4	3953	2	CQ340982	CQ340982 Sequence		774	140	6.3	126115	12	AC168606	AC168606 Strongylo
c 702	141	6.4	74841	11	AC096997	AC096997 Takifugu	c	775	140	6.3	148394	12	AC178771	AC178771 Strongylo
703	141	6.4	110000	4	CR380947_1	Continuation (2 of		776	140	6.3	148945	12	CR759744	CR759744 Danio rer
c 704	141	6.4	110000	4	CR382139_00	CR382139 Debaryomy	c	777	140	6.3	158257	6	AC158128	AC158128 Mus muscu
c 705	141	6.4	110000	4	CR382139_01	Continuation (2 of	c	778	140	6.3	158478	12	AC181882	AC181882 Strongylo
706	141	6.4	110000	4	AP008207_426	Continuation (427	c	779	140	6.3	163364	12	AC184404	AC184404 Strongylo
707	141	6.4	147210	12	AC179711	AC179711 Strongylo		780	140	6.3	167743	12	BX322580	BX322580 Danio rer
708	141	6.4	148887	4	AP003448	AP003448 Oryza sat	c	781	140	6.3	172674	13	AC007807	AC007807 Drosophil
709	141	6.4	160802	5	AC148477	AC148477 Homo sapi		782	140	6.3	186051	6	AC112957	AC112957 Mus muscu
c 710	141	6.4	173961	12	AC180594	AC180594 Strongylo	c	783	140	6.3	188558	12	AC184574	AC184574 Strongylo
c 711	141	6.4	192670	12	CR456627	CR456627 Danio rer	c	784	140	6.3	190866	13	AC007824	AC007824 Drosophil
c 712	141	6.4	228089	10	AF451898	AF451898 Heliothis	c	785	140	6.3	197507	12	AC140087	AC140087 Pongo pyg
c 713	141	6.4	248871	12	AC094352	AC094352 Rattus no	c	786	140	6.3	215018	12	AC139113	AC139113 Pongo pyg
714	141	6.4	252215	12	AC095632	AC095632 Rattus no	c	787	140	6.3	220035	13	AE003716	AE003716 Drosophil
715	141	6.4	267692	12	AC135138	AC135138 Rattus no		788	140	6.3	224098	12	AC111386	AC111386 Rattus no
716	141	6.4	294212	12	AC129056	AC129056 Rattus no		789	140	6.3	227666	12	AC094474	AC094474 Rattus no
717	140.5	6.4	1133	6	BC111528	BC111528 Mus muscu		790	139.5	6.3	1795	2	BD062750	BD062750 Modulator
718	140.5	6.4	1539	5	AF007190	AF007190 Homo sapi		791	139.5	6.3	1795	2	CS288452	CS288452 Sequence
719	140.5	6.4	1593	13	BT023236	BT023236 Drosophil		792	139.5	6.3	1795	2	AR439671	AR439671 Sequence
720	140.5	6.4	1594	13	BT023208	BT023208 Drosophil		793	139.5	6.3	3463	2	CQ585035	CQ585035 Sequence
721	140.5	6.4	2016	13	AY864361	AY864361 Drosophil	c	794	139.5	6.3	29865	12	AC020047	AC020047 Drosophil
722	140.5	6.4	2032	2	CQ577554	CQ577554 Sequence	c	795	139.5	6.3	72769	15	CP000255_28	Continuation (29 o
723	140.5	6.4	2124	13	LDU78523	U78523 Leishmania	c	796	139.5	6.3	80272	11	AL591180	AL591180 Zebrafish
724	140.5	6.4	2675	13	AY864364	AY864364 Drosophil		797	139.5	6.3	110000	4	AP008213_147	Continuation (148
725	140.5	6.4	2675	13	AY864365	AY864365 Drosophil		798	139.5	6.3	110000	4	AE016818_09	Continuation (10 o
726	140.5	6.4	2675	13	AY864366	AY864366 Drosophil	c	799	139.5	6.3	110000	4	AP007164_18	Continuation (19 o
727	140.5	6.4	2780	13	AK112792	AK112792 Ciona int		800	139.5	6.3	110000	12	AC156266_05	Continuation (6 of
728	140.5	6.4	3428	13	BT024279	BT024279 Drosophil		801	139.5	6.3	111882	13	AC115612	AC115612 Dictyoste
729	140.5	6.4	3794	13	AY865069	AY865069 Drosophil	c	802	139.5	6.3	122559	12	AC179825	AC179825 Strongylo
730	140.5	6.4	3801	13	AY865071	AY865071 Drosophil		803	139.5	6.3	127955	12	AC139907	AC139907 Rattus no
731	140.5	6.4	3873	13	AY428796	AY428796 Dictyoste		804	139.5	6.3	131676	5	AC139749	AC139749 Homo sapi
c 732	140.5	6.4	4282	2	CQ577553	CQ577553 Sequence	c	805	139.5	6.3	132624	12	AC179088	AC179088 Strongylo
733	140.5	6.4	4921	13	AF221506	AF221506 Drosophil	c	806	139.5	6.3	138203	2	DD159574	DD159574 Genes for

C 807	139.5	6.3	138203	15	AY310323	AY310323 Streptomy
808	139.5	6.3	144695	4	AP005451	AP005451 Oryza sat
809	139.5	6.3	150893	12	AC152035	AC152035 Dasypus n
810	139.5	6.3	154000	12	AC152045	AC152045 Dasypus n
811	139.5	6.3	159802	4	AP005447	AP005447 Oryza sat
C 812	139.5	6.3	162356	12	AC181958	AC181958 Strongylo
C 813	139.5	6.3	165619	12	CR847893	CR847893 Danio rer
814	139.5	6.3	166468	11	AC186558	AC186558 Gasterost
C 815	139.5	6.3	177787	12	AC180451	AC180451 Strongylo
C 816	139.5	6.3	194300	12	AC166196	AC166196 Actus nan
C 817	139.5	6.3	223311	12	AC094165	AC094165 Rattus no
C 818	139.5	6.3	243793	12	AC111708	AC111708 Rattus no
C 819	139.5	6.3	276852	12	AC095438	AC095438 Rattus no
C 820	139.5	6.3	283601	12	AC123500	AC123500 Rattus no
C 821	139.5	6.3	286771	12	AC134154	AC134154 Rattus no
C 822	139.5	6.3	290777	12	AC169364	AC169364 Bos tauru
C 823	139.5	6.3	328402	12	AC112887	AC112887 Rattus no
824	139	6.3	867	2	AR279196	AR279196 Sequence
825	139	6.3	867	2	AR279197	AR279197 Sequence
826	139	6.3	867	2	AR884071	AR884071 Sequence
827	139	6.3	867	2	AR884072	AR884072 Sequence
828	139	6.3	1014	2	CQ611376	CQ611376 Sequence
829	139	6.3	1215	6	AB003311	AB003311 Cavia por
830	139	6.3	1226	10	AY034642	AY034642 Equine he
831	139	6.3	1352	4	AK122054	AK122054 Oryza sat
C 832	139	6.3	1397	2	AR279198	AR279198 Sequence
C 833	139	6.3	1397	2	AR279199	AR279199 Sequence
834	139	6.3	1397	2	AR884073	AR884073 Sequence
C 835	139	6.3	1397	2	AR884074	AR884074 Sequence
836	139	6.3	1368	5	AB202102	AB202102 Homo sapi
C 837	139	6.3	9248	4	SCAF000227	AF000227 Secale ce
838	139	6.3	10652	6	AF441786	AF441786 Mus muscu
C 839	139	6.3	21598	4	SPBP19A11	AL512495 S.pombe c
840	139	6.3	32367	6	AF520421S2	AF520422 Mus muscu
841	139	6.3	35265	5	CT009610	CT009610 Human DNA
842	139	6.3	38011	12	AC174159	AC174159 Homo sapi
C 843	139	6.3	70175	4	NCL3E11	AL353820 Neurospor
C 844	139	6.3	92091	11	BX649491	BX649491 Zebrafish
C 845	139	6.3	110000	15	CP000384_28	Continuation (29 o
C 846	139	6.3	139861	12	AC180376	AC180376 Strongylo
847	139	6.3	140822	12	AC179647	AC179647 Strongylo
C 848	139	6.3	174808	12	AC184623	AC184623 Strongylo
C 849	139	6.3	191616	12	AC148723	AC148723 Salmo sal
C 850	139	6.3	197473	12	AC109740	AC109740 Rattus no
C 851	139	6.3	221972	12	CR388218	CR388218 Danio rer
852	139	6.3	227127	6	AC090437	AC090437 Mus muscu
C 853	139	6.3	227677	12	CR388157	CR388157 Danio rer
C 854	139	6.3	232936	12	AC094153	AC094153 Rattus no
C 855	139	6.3	237455	12	AC096815	AC096815 Rattus no
856	139	6.3	240931	12	AC107097	AC107097 Rattus no
857	139	6.3	248614	12	BX548029	BX548029 Danio rer
C 858	139	6.3	248793	12	AC103080	AC103080 Rattus no
C 859	139	6.3	251411	12	AC110407	AC110407 Rattus no
860	139	6.3	274903	12	AC095233	AC095233 Rattus no
861	139	6.3	294769	12	AC098907	AC098907 Rattus no
862	138.5	6.3	1016	5	AF007192	AF007192 Homo sapi
863	138.5	6.3	1612	6	MMU70652	U70652 Mus musculu
864	138.5	6.3	1710	4	YSCS22	M16165 Yeast (S.ce
865	138.5	6.3	2086	4	WHTGGLN	M36999 Wheat gamma
866	138.5	6.3	2202	13	AK114835	AK114835 Ciona int
867	138.5	6.3	2601	14	BC105310	BC105310 Bos tauru
868	138.5	6.3	3183	2	AR261979	AR261979 Sequence
869	138.5	6.3	3183	2	AR487471	AR487471 Sequence
870	138.5	6.3	3183	13	D50685	D50685 trypanosoma
871	138.5	6.3	4104	2	AR527741	AR527741 Sequence
872	138.5	6.3	4104	2	AR778359	AR778359 Sequence
873	138.5	6.3	4116	2	CQ606066	CQ606066 Sequence
874	138.5	6.3	5163	2	AR097042	AR097042 Sequence
875	138.5	6.3	5163	2	AR279261	AR279261 Sequence
876	138.5	6.3	5318	2	AR097041	AR097041 Sequence
877	138.5	6.3	5318	2	AR279260	AR279260 Sequence
C 878	138.5	6.3	6116	2	CQ606065	CQ606065 Sequence
879	138.5	6.3	7295	4	SCU30626	U30626 Saccharomyc
C 880	138.5	6.3	15768	12	AC017147	AC017147 Drosophil
C 881	138.5	6.3	42793	4	SC9168	Z38061 S.cerevisia
C 882	138.5	6.3	110000	15	CP000088_18	Continuation (19 o
883	138.5	6.3	110000	15	CP000379_11	Continuation (12 o
884	138.5	6.3	110000	15	CP000379_12	Continuation (13 o
885	138.5	6.3	120676	12	AC180589	AC180589 Strongylo
C 886	138.5	6.3	122447	12	AC168795	AC168795 Strongylo
C 887	138.5	6.3	128546	12	AC168472	AC168472 Strongylo
C 888	138.5	6.3	138354	6	AC182453	AC182453 Mus muscu
C 889	138.5	6.3	166954	12	AC150676	AC150676 Bos tauru
C 890	138.5	6.3	167390	5	AC007263	AC007263 Homo sapi
891	138.5	6.3	175679	13	AC010025	AC010025 Drosophil
892	138.5	6.3	177590	12	AC005563	AC005563 Drosophil
893	138.5	6.3	179821	12	AC147950	AC147950 Papio anu
894	138.5	6.3	181388	12	AC130062	AC130062 Rattus no
895	138.5	6.3	188864	12	AC135951	AC135951 Macaca mu
C 896	138.5	6.3	190979	12	AC184331	AC184331 Strongylo
C 897	138.5	6.3	200039	12	AC133765	AC133765 Rattus no
C 898	138.5	6.3	208406	12	AC133405	AC133405 Rattus no
C 899	138.5	6.3	212955	12	AC136676	AC136676 Rattus no
C 900	138.5	6.3	235976	12	AC119627	AC119627 Rattus no
C 901	138.5	6.3	245942	12	AC121374	AC121374 Rattus no
902	138.5	6.3	272016	13	AE003539	AE003539 Drosophil
903	138	6.2	1211	10	AY034639	AY034639 Equine he
904	138	6.2	2024	15	AF010469	AF010469 Halofera
905	138	6.2	5985	2	CQ858277	CQ858277 Sequence
906	138	6.2	9308	6	AB093227	AB093227 Mus muscu
907	138	6.2	13134	6	AY929611	AY929611 Mus muscu
908	138	6.2	14032	6	AY772010	AY772010 Mus muscu
909	138	6.2	14049	6	DQ097265	DQ097265 Mus muscu
C 910	138	6.2	33554	4	AC167920	AC167920 Mycosphae
911	138	6.2	48612	12	AC167552	AC167552 Mus muscu
C 912	138	6.2	49265	1	AB201308	AB201308 unculture
913	138	6.2	59720	4	AP004629	AP004629 Lotus jap
C 914	138	6.2	71479	6	BX005170	BX005170 Mouse DNA
C 915	138	6.2	110000	4	CR382131_26	Continuation (27 o
C 916	138	6.2	110000	12	AC120236_0	AC120236 Rattus no
917	138	6.2	117149	5	AC083984	AC083984 Homo sapi
918	138	6.2	126932	12	AC174739	AC174739 Strongylo
C 919	138	6.2	160766	12	AC137686	AC137686 Homo sapi
920	138	6.2	165849	12	AC114251	AC114251 Rattus no
921	138	6.2	170425	12	AC024490	AC024490 Homo sapi
C 922	138	6.2	171096	10	AY037858	AY037858 Cercopith
923	138	6.2	186782	12	AC172425	AC172425 Bos tauru
924	138	6.2	195337	12	AC180126	AC180126 Strongylo
925	138	6.2	196582	12	AC178518	AC178518 Strongylo
926	138	6.2	200439	6	AC160032	AC160032 Mus muscu
927	138	6.2	211149	12	AC133832	AC133832 Rattus no
928	138	6.2	215717	12	AC134484	AC134484 Rattus no
C 929	138	6.2	218838	6	AC153828	AC153828 Mus muscu
C 930	138	6.2	221029	12	AC140292	AC140292 Mus muscu
C 931	138	6.2	231716	6	AC135409	AC135409 Rattus no
932	138	6.2	253094	12	AC113774	AC113774 Rattus no
C 933	138	6.2	253362	12	AC095732	AC095732 Rattus no
934	138	6.2	260662	12	AC180829	AC180829 Strongylo
C 935	138	6.2	268447	12	AC132359	AC132359 Mus muscu
936	137.5	6.2	1216	4	AY667097	AY667097 Aegilops
937	137.5	6.2	2352	11	AY648768	AY648768 Danio rer
938	137.5	6.2	2551	4	YSCAER2	M35861 S.cerevisia
939	137.5	6.2	3150	2	CQ583125	CQ583125 Sequence
940	137.5	6.2	3794	13	AY865073	AY865073 Drosophil
941	137.5	6.2	4452	11	AY507659	AY507659 Danio rer
942	137.5	6.2	4490	11	AY507658	AY507658 Danio rer
943	137.5	6.2	4518	2	DD062470	DD062470 Methods f
944	137.5	6.2	4519	2	DD062469	DD062469 Methods f
945	137.5	6.2	4578	11	AY507660	AY507660 Danio rer
946	137.5	6.2	5718	4	AF234647	AF234647 Triticum
947	137.5	6.2	32986	13	U13646	U13646 Caenorhabdi
948	137.5	6.2	34852	13	AF106582	AF106582 Caenorhab
949	137.5	6.2	37902	4	AC149378	AC149378 Phakopsor
950	137.5	6.2	94341	4	CT954251	CT954251 M.truncat
951	137.5	6.2	99360	4	NCB11N2	AL513444 Neurospor
C 952	137.5	6.2	99802	15	BX571857_27	Continuation (28 o



c 953	137.5	6.2	110000	4	AP008214_278	Continuation (279	c1026	137	6.2	274091	12	CT574544
c 954	137.5	6.2	110000	4	CR380958_12	Continuation (13 o	1027	137	6.2	314743	13	AE003495
c 955	137.5	6.2	110000	4	AE016816_6	Continuation (7 of	1028	136.5	6.2	734	11	DQ120982
c 956	137.5	6.2	110000	4	AP007151_36	Continuation (37 o	1029	136.5	6.2	900	4	DQ146396
c 957	137.5	6.2	110000	15	BA000033_27	Continuation (28 o	1030	136.5	6.2	1512	2	AR778517
c 958	137.5	6.2	110000	15	BA000035_13	Continuation (14 o	1031	136.5	6.2	1512	8	DQ332622
c 959	137.5	6.2	111150	5	CR759772	CR759772 Human DNA	1032	136.5	6.2	1592	6	BC094915
c 960	137.5	6.2	117122	12	AC186577	AC186577 Zea mays	1033	136.5	6.2	1611	6	MMU70651
c 961	137.5	6.2	142010	4	AP003928	AP003928 Oryza sat	1034	136.5	6.2	1795	5	GIBMUC1A
c 962	137.5	6.2	142952	5	AL391495	AL391495 Human DNA	1035	136.5	6.2	1923	2	AX952986
c 963	137.5	6.2	150330	6	AC131186	AC131186 Mus muscu	1036	136.5	6.2	1923	2	DD240139
c 964	137.5	6.2	153108	5	AL355273	AL355273 Human DNA	1037	136.5	6.2	1923	4	AK109569
c 965	137.5	6.2	160618	12	AC181688	AC181688 Strongylo	c1038	136.5	6.2	3584	4	SCYNL283C
c 966	137.5	6.2	165997	12	AC167506	AC167506 Saimiri b	1039	136.5	6.2	3637	2	AX952985
c 967	137.5	6.2	166052	12	AC117008	AC117008 Rattus no	1040	136.5	6.2	3637	2	DD240138
c 968	137.5	6.2	170885	6	AC126933	AC126933 Mus muscu	1041	136.5	6.2	3803	13	AY865075
c 969	137.5	6.2	171307	5	AC104020	AC104020 Homo sapi	1042	136.5	6.2	12412	13	AC006669
c 970	137.5	6.2	177685	12	AC149985	AC149985 Strongylo	1043	136.5	6.2	42596	13	U41263
c 971	137.5	6.2	194709	12	AC132640	AC132640 Rattus no	1044	136.5	6.2	61052	12	AC123513
c 972	137.5	6.2	207210	6	AC162937	AC162937 Mus muscu	1045	136.5	6.2	61187	5	HS83L6
c 973	137.5	6.2	212528	6	AC182761	AC182761 Mus muscu	1046	136.5	6.2	79554	4	NCB11B23
c 974	137.5	6.2	231190	12	AC107096	AC107096 Rattus no	1047	136.5	6.2	84519	12	AC180269
c 975	137.5	6.2	232234	12	AC108634	AC108634 Rattus no	c1048	136.5	6.2	94549	12	AC149512
c 976	137.5	6.2	235471	6	AC124662	AC124662 Mus muscu	c1049	136.5	6.2	96558	5	HS598A24
c 977	137.5	6.2	242309	12	AC098167	AC098167 Rattus no	1050	136.5	6.2	104708	12	AC139336
c 978	137.5	6.2	242516	12	AC106523	AC106523 Rattus no	1051	136.5	6.2	109794	14	AC153156
c 979	137.5	6.2	248568	12	AC115184	AC115184 Rattus no	1052	136.5	6.2	110000	4	AP008214_257
c 980	137.5	6.2	261414	12	AC122960	AC122960 Rattus no	c1053	136.5	6.2	110000	4	AP008217_280
c 981	137.5	6.2	316613	4	SCCHRII	X59720 S.cerevisia	1054	136.5	6.2	110952	12	AP004042
c 982	137.5	6.2	319857	12	AC006782	AC006782 Caenorhab	c1055	136.5	6.2	117199	12	AC176437
c 983	137.5	6.2	329976	12	AC127764	AC127764 Rattus no	c1056	136.5	6.2	117224	12	AC010712
c 984	137	6.2	1124	6	AB003320	AB003320 Mus muscu	1057	136.5	6.2	121440	12	AC178928
c 985	137	6.2	1969	13	AY864508	AY864508 Drosophil	c1058	136.5	6.2	135541	6	AC138108
c 986	137	6.2	2129	13	AY352257	AY352257 Drosophil	c1059	136.5	6.2	136240	13	AC117070
c 987	137	6.2	4616	14	DQ497629	DQ497629 Bos tauru	1060	136.5	6.2	142275	12	AC114996
c 988	137	6.2	5943	2	CQ583124	CQ583124 Sequence	1061	136.5	6.2	145177	4	AP004708
c 989	137	6.2	26356	13	AF077538	AF077538 Caenorhab	1062	136.5	6.2	147516	4	AP004622
c 990	137	6.2	30255	4	AC166541	AC166541 Nectria h	1063	136.5	6.2	152955	6	AC145575
c 991	137	6.2	34828	13	U41994	U41994 Caenorhabdi	1064	136.5	6.2	157564	11	BX537304
c 992	137	6.2	35793	11	AY016024	AY016024 Takifugu	c1065	136.5	6.2	165025	12	AC133393
c 993	137	6.2	39573	13	U80846	U80846 Caenorhabdi	c1066	136.5	6.2	170275	12	AC090446
c 994	137	6.2	42909	13	U53341	U53341 Caenorhabdi	c1067	136.5	6.2	171820	6	AC151281
c 995	137	6.2	86196	5	AL592046	AL592046 Human DNA	c1068	136.5	6.2	174097	5	AC069513
c 996	137	6.2	89216	4	CT867975	CT867975 M.truncat	1069	136.5	6.2	174254	6	AC165443
c 997	137	6.2	95978	13	AY449461	AY449461 Oikopleur	1070	136.5	6.2	177677	12	AC173371
c 998	137	6.2	96573	12	AC136672	AC136672 Rattus no	c1071	136.5	6.2	177935	6	AC129209
c 999	137	6.2	110000	2	AR863642_04	Continuation (5 of	c1072	136.5	6.2	179668	4	AC134045
c1000	137	6.2	110000	15	AE016822_10	Continuation (11 o	c1073	136.5	6.2	183319	6	AC154502
c1001	137	6.2	122007	12	AP007900_	AP007900 Lotus jap	c1074	136.5	6.2	185781	12	AC133071
c1002	137	6.2	123784	12	AC180386	AC180386 Strongylo	1075	136.5	6.2	187080	6	AC154808
c1003	137	6.2	130269	6	AC111067	AC111067 Mus muscu	1076	136.5	6.2	187883	6	AC165141
c1004	137	6.2	130913	12	AC096869	AC096869 Rattus no	c1077	136.5	6.2	198599	5	AC108448
c1005	137	6.2	140216	12	AC177159	AC177159 Strongylo	1078	136.5	6.2	204465	6	AC117232
c1006	137	6.2	142870	6	AL607025	AL607025 Mouse DNA	1079	136.5	6.2	206120	12	AC163879
c1007	137	6.2	147935	6	AC175744	AC175744 Mus muscu	1080	136.5	6.2	208625	12	AC164605
c1008	137	6.2	159448	11	AC147905	AC147905 Xenopus t	1081	136.5	6.2	214060	6	AC131081
c1009	137	6.2	161030	12	AC148042	AC148042 Chloroceb	1082	136.5	6.2	218605	12	AC133816
c1010	137	6.2	165127	12	AC148043	AC148043 Chloroceb	1083	136.5	6.2	232885	12	AC106163
c1011	137	6.2	166564	11	CR376845	CR376845 Zebrafish	c1084	136.5	6.2	237588	12	AC025581
c1012	137	6.2	169913	12	AC031980	AC031980 Homo sapi	1085	136.5	6.2	244434	12	AC111461
c1013	137	6.2	169994	11	BX321875	BX321875 Zebrafish	c1086	136.5	6.2	258319	12	AC127770
c1014	137	6.2	172884	12	AC140084	AC140084 Chloroceb	1087	136.5	6.2	271870	12	AC162814
c1015	137	6.2	174097	5	AC069513	AC069513 Homo sapi	1088	136.5	6.2	298050	15	AL935260
c1016	137	6.2	194815	6	AC121793	AC121793 Mus muscu	1089	136	6.2	989	4	AB027423
c1017	137	6.2	196835	12	AC142538	AC142538 Homo sapi	1090	136	6.2	996	4	AB027422
c1018	137	6.2	197530	6	AC099174	AC099174 Rattus no	1091	136	6.2	1167	4	D55714
c1019	137	6.2	200412	12	AC115666	AC115666 Rattus no	1092	136	6.2	1185	6	AB221697
c1020	137	6.2	203498	13	AC011697	AC011697 Drosophil	1093	136	6.2	1281	4	AK073757
c1021	137	6.2	207685	6	AC132404	AC132404 Mus muscu	1094	136	6.2	1416	4	AB027421
c1022	137	6.2	213347	6	AL831741	AL831741 Mouse DNA	1095	136	6.2	1549	6	MMU70657
c1023	137	6.2	233270	12	AC129038	AC129038 Rattus no	1096	136	6.2	2097	2	CQ733408
c1024	137	6.2	242082	12	AC121699	AC121699 Rattus no	1097	136	6.2	2150	2	AR146449
c1025	137	6.2	268930	12	AC119562	AC119562 Rattus no	1098	136	6.2	2150	2	AR579955

CT574544 Danio rer  
AE003495 Drosophil  
DQ120982 Hucho tai  
DQ146396 Triticum  
AR778517 Sequence  
DQ332622 Synthetic  
BC094915 Mus muscu  
U70651 Mus musculu  
L41589 Hylobates l  
AX952986 Sequence  
DD240139 NOVEL PHO  
AK109569 Oryza sat  
Z71559 S.cerevisia  
AX952985 Sequence  
DD240138 NOVEL PHO  
AY865075 Drosophil  
AC006669 Caenorhab  
U41263 Caenorhabdi  
AC123513 Dictyoste  
Z99130 Human DNA s  
AL669991 Neurospor  
AC180269 Strongylo  
AC149512 Xenopus t  
AL031115 Human DNA  
AC139336 Rattus no  
AC153156 Ornithorh  
Continuation (258  
Continuation (281  
AP004042 Oryza sat  
AC176437 Strongylo  
AC010712 Drosophil  
AC178928 Strongylo  
AC138108 Mus muscu  
AC117070 Dictyoste  
AC141996 Rattus no  
AP004708 Oryza sat  
AP004622 Oryza sat  
AC145575 Mus muscu  
BX537304 Zebrafish  
AC133393 Pan trogl  
AC090446 Baboon cy  
AC151281 Mus muscu  
AC069513 Homo sapi  
AC165443 Mus muscu  
AC173371 Strongylo  
AC129209 Mus muscu  
AC134045 Oryza sat  
AC154502 Mus muscu  
AC133071 Pan trogl  
AC154808 Mus muscu  
AC165141 Mus muscu  
AC108448 Homo sapi  
AC117232 Mus muscu  
AC163879 Bos tauru  
AC164605 Mus muscu  
AC131081 Mus muscu  
AC133816 Rattus no  
AC106163 Rattus no  
AC025581 Mus muscu  
AC111461 Rattus no  
AC127770 Rattus no  
AC162814 Bos tauru  
AL935260 Lactobaci  
AB027423 Oryza sat  
AB027422 Oryza sat  
D55714 Oryza sativ  
AB221697 Mus muscu  
AK073757 Oryza sat  
AB027421 Oryza sat  
U70657 Mus musculu  
CQ733408 Sequence  
AR146449 Sequence  
AR579955 Sequence

1099	136	6.2	2161	4	AK122053	AK122053 Oryza sat	1172	135.5	6.1	117983	12	AC178646
1100	136	6.2	2165	2	CQ733483	CQ733483 Sequence	1173	135.5	6.1	126592	6	AC183374
1101	136	6.2	2188	4	AF001978	AF001978 Candida a	1174	135.5	6.1	150259	12	AC177577
1102	136	6.2	2684	5	BC059356	BC059356 Homo sapi	1175	135.5	6.1	152206	12	AC174251
1103	136	6.2	3015	2	BD129573	BD129573 Polynucle	1176	135.5	6.1	153373	12	AC178242
1104	136	6.2	3015	2	BD277873	BD277873 Meth1 and	1177	135.5	6.1	155683	12	AC180041
1105	136	6.2	3015	13	LMSAP2GN	Z46970 L.mexicana	1178	135.5	6.1	161996	13	AC008284
1106	136	6.2	6783	2	CS252723	CS252723 Sequence	1179	135.5	6.1	167254	5	CNS05TDS
1107	136	6.2	6783	2	CS274060	CS274060 Sequence	1180	135.5	6.1	168122	12	AC146997
1108	136	6.2	6783	2	DD088837	DD088837 A method	1181	135.5	6.1	171849	5	AC010616
1109	136	6.2	6783	2	AX583631	AX583631 Sequence	1182	135.5	6.1	172527	12	AC181183
1110	136	6.2	10792	13	LSU54556	U54556 Litomosoides	1183	135.5	6.1	175506	13	AC008004
1111	136	6.2	26142	4	SC82277	Z46833 S.cerevisia	1184	135.5	6.1	176231	13	AC008367
1112	136	6.2	37487	2	DD158931	DD158931 NOVEL COM	1185	135.5	6.1	177816	12	AC017643
1113	136	6.2	37487	2	AX695389	AX695389 Sequence	1186	135.5	6.1	183915	12	AC141939
1114	136	6.2	74014	4	NCB7A16	AL513445 Neurospor	1187	135.5	6.1	188464	6	AC101660
1115	136	6.2	104629	11	BX323045	BX323045 Zebrafish	1188	135.5	6.1	195729	12	AC178061
1116	136	6.2	104737	11	CR848045	CR848045 Zebrafish	1189	135.5	6.1	198421	6	AC163279
1117	136	6.2	106286	4	AC157758	AC157758 Medicago	1190	135.5	6.1	200011	6	AC153573
1118	136	6.2	109422	15	CP000046_27	Continuation (28 o	1191	135.5	6.1	204850	12	AC184603
1119	136	6.2	110000	4	CR382127_20	Continuation (21 o	1192	135.5	6.1	210061	12	AC181870
1120	136	6.2	110000	15	CP000384_04	Continuation (5 of	1193	135.5	6.1	214204	12	AC133776
1121	136	6.2	114052	12	AC176959	AC176959 Strongylo	1194	135.5	6.1	220242	11	BX664631
1122	136	6.2	117577	4	AC152752	AC152752 Medicago	1195	135.5	6.1	227897	12	AC111962
1123	136	6.2	122884	5	HS1158B12	AL034396 Human DNA	1196	135.5	6.1	229480	11	AL929150
1124	136	6.2	127576	12	AC178144	AC178144 Strongylo	1197	135.5	6.1	231008	12	AC129166
1125	136	6.2	166640	12	AC176417	AC176417 Strongylo	1198	135.5	6.1	234469	12	AC119697
1126	136	6.2	169584	12	AC144463	AC144463 Gorilla g	1199	135.5	6.1	237997	12	AC093989
1127	136	6.2	171495	12	CT030188	CT030188 Danio rer	1200	135.5	6.1	240410	6	AC158617
1128	136	6.2	172764	10	DQ279927	DQ279927 Human rer	1201	135.5	6.1	246913	6	AC109542
1129	136	6.2	172765	11	BX842701	BX842701 Zebrafish	1202	135.5	6.1	264977	12	AC097564
1130	136	6.2	172887	12	BX323011	BX323011 Danio rer	1203	135.5	6.1	279242	12	AC114079
1131	136	6.2	174097	12	AC184616	AC184616 Strongylo	1204	135.5	6.1	290783	13	AE003803
1132	136	6.2	179836	5	AL590822	AL590822 Human DNA	1205	135.5	6.1	307443	13	AE003751
1133	136	6.2	196879	12	AC173077	AC173077 Bos tauru	1206	135.5	6.1	349980	2	AX492783
1134	136	6.2	202214	12	CR848809	CR848809 Danio rer	1207	135.5	6.1	349980	2	AX553950
1135	136	6.2	213432	12	AC068198	AC068198 Homo sapi	1208	135	6.1	730	4	ASQ389679
1136	136	6.2	217735	6	AL596116	AL596116 Mouse DNA	1209	135	6.1	777	4	TAE389668
1137	136	6.2	227026	12	AC136659	AC136659 Rattus no	1210	135	6.1	778	4	TSP389674
1138	136	6.2	229259	12	AC096212	AC096212 Rattus no	1211	135	6.1	792	4	TCO389669
1139	136	6.2	235407	12	AC094280	AC094280 Rattus no	1212	135	6.1	798	4	WHTGLIGP
1140	136	6.2	245967	12	AC112091	AC112091 Rattus no	1213	135	6.1	800	4	TMA389671
1141	136	6.2	254650	12	AC128790	AC128790 Rattus no	1214	135	6.1	801	4	TMA389673
1142	136	6.2	261608	12	AC097158	AC097158 Rattus no	1215	135	6.1	801	4	TSP389676
1143	136	6.2	349391	15	BX572095	BX572095 Prochloro	1216	135	6.1	809	4	TMA389672
1144	135.5	6.1	1350	4	AJ781266	AJ781266 Monascus	1217	135	6.1	850	4	TCO389670
1145	135.5	6.1	1718	4	AK058540	AK058540 Oryza sat	1218	135	6.1	947	4	AF120267
1146	135.5	6.1	1836	4	AB066561	AB066561 Oryza sat	1219	135	6.1	956	4	AF144104
1147	135.5	6.1	1949	13	AY864511	AY864511 Drosophil	1220	135	6.1	1140	2	BD057194
1148	135.5	6.1	2891	4	YSCTUP1A	M31733 S.cerevisia	1221	135	6.1	1232	11	AY852250
1149	135.5	6.1	3045	4	AB236168	AB236168 Pichia mi	1222	135	6.1	1475	4	AK058368
1150	135.5	6.1	3089	2	CQ845920	CQ845920 Sequence	1223	135	6.1	1507	5	BC013325
1151	135.5	6.1	3089	5	AK131434	AK131434 Homo sapi	1224	135	6.1	1701	14	AF411243
1152	135.5	6.1	3794	13	AY865060	AY865060 Drosophil	1225	135	6.1	2127	5	AF043446
1153	135.5	6.1	3949	2	BD160924	BD160924 Galactose	1226	135	6.1	2179	5	AF043447
1154	135.5	6.1	4386	13	DME294538	AJ294538 Drosophil	1227	135	6.1	2385	4	TDU437000
1155	135.5	6.1	5396	2	CQ600026	CQ600026 Sequence	1228	135	6.1	2391	4	DQ073548
1156	135.5	6.1	12664	15	AE005029	AE005029 Halobacte	1229	135	6.1	2425	2	CS047824
1157	135.5	6.1	22398	11	FRU271723	AJ271723 Fugu rubr	1230	135	6.1	2426	12	AC020448
1158	135.5	6.1	77410	12	AC183198	AC183198 Bos tauru	1231	135	6.1	2481	2	AR548073
1159	135.5	6.1	78529	15	BA000017_28	Continuation (29 o	1232	135	6.1	3435	4	AK110185
1160	135.5	6.1	82649	11	CR762486	CR762486 Zebrafish	1233	135	6.1	3832	13	AY865089
1161	135.5	6.1	85918	12	DMBR33H2	AL121812 Drosophil	1234	135	6.1	4138	8	DQ659099
1162	135.5	6.1	93554	12	AC181412	AC181412 Strongylo	1235	135	6.1	4186	13	AY061106
1163	135.5	6.1	95682	5	AC104667	AC104667 Homo sapi	1236	135	6.1	8259	14	AY158087
1164	135.5	6.1	98521	6	AC094507	AC094507 Rattus no	1237	135	6.1	9402	2	CQ574607
1165	135.5	6.1	110000	2	DD086466_07	Continuation (8 of	1238	135	6.1	10789	12	AC017895
1166	135.5	6.1	110000	4	CR382123_09	Continuation (10 o	1239	135	6.1	28709	12	AC160844
1167	135.5	6.1	110000	4	AE016817_10	Continuation (11 o	1240	135	6.1	55963	6	AL663069
1168	135.5	6.1	110000	4	AP007150_07	Continuation (8 of	1241	135	6.1	79554	4	NCB11B23
1169	135.5	6.1	110000	15	CP000431_01	Continuation (2 of	1242	135	6.1	90373	13	AC115680
1170	135.5	6.1	110000	15	AE014295_15	Continuation (16 o	1243	135	6.1	117327	5	AL663093
1171	135.5	6.1	110000	15	BA000018_27	Continuation (28 o	1244	135	6.1	124457	5	AC115115

AC178646 Strongylo  
AC183374 Mus muscu  
AC177577 Strongylo  
AC174251 Strongylo  
AC178242 Strongylo  
AC180041 Strongylo  
AC008284 Drosophil  
AL357093 Human Chr  
AC146997 Arbacia p  
AC010616 Homo sapi  
AC181183 Strongylo  
AC008004 Drosophil  
AC008367 Drosophil  
AC017643 Drosophil  
AC141939 Rattus no  
AC101660 Mus muscu  
AC178061 Strongylo  
AC163279 Mus muscu  
AC153573 Mus muscu  
AC184603 Strongylo  
AC181870 Strongylo  
AC133776 Rattus no  
BX664631 Zebrafish  
AC111962 Rattus no  
AL929150 Zebrafish  
AC129166 Rattus no  
AC119697 Rattus no  
AC093989 Rattus no  
AC158617 Mus muscu  
AC109542 Rattus no  
AC097564 Rattus no  
AC114079 Rattus no  
AE003803 Drosophil  
AE003751 Drosophil  
AX492783 Sequence  
AX553950 Sequence  
AJ389679 Aegilops  
AJ389668 Triticum  
AJ389674 Triticum  
AJ389669 Triticum  
M16060 Wheat (T.ae  
AJ389671 Triticum  
AJ389673 Triticum  
AJ389676 Triticum  
AJ389672 Triticum  
AJ389670 Triticum  
AF120267 Triticum  
AF144104 Triticum  
BD057194 Productio  
AY852250 Meleagris  
AK058368 Oryza sat  
BC013325 Homo sapi  
AF411243 Bos tauru  
AF043446 Cercopith  
AF043447 Cercopith  
AJ437000 Triticum  
DQ073548 Leymus mu  
CS047824 Sequence  
AC020448 Drosophil  
AR548073 Sequence  
AK110185 Oryza sat  
AY865089 Drosophil  
DQ659099 Synthetic  
AY061106 Drosophil  
AY158087 Bos tauru  
CQ574607 Sequence  
AC017895 Drosophil  
AC160844 Homo sapi  
AL663069 Mouse DNA  
AL669991 Neurospor  
AC115680 Dictyoste  
AL663093 Human DNA  
AC115115 Homo sapi

1245	135	6.1	141134	12	AC176729	AC176729 Strongylo	134.5	6.1	165277	12	CR628321	CR628321 Danio rer
1246	135	6.1	144082	12	AC181046	AC181046 Strongylo	134.5	6.1	167889	6	AC175667	AC175667 Mus muscu
1247	135	6.1	157052	11	AL929459	AL929459 Zebrafish	134.5	6.1	168354	4	AP005185	AP005185 Oryza sat
1248	135	6.1	169895	12	AC178023	AC178023 Strongylo	134.5	6.1	168991	12	AC090411	AC090411 Homo sapi
1249	135	6.1	171657	10	AY961628	AY961628 Human her	134.5	6.1	169461	6	AC182486	AC182486 Mus muscu
1250	135	6.1	175302	12	AC020587	AC020587 Homo sapi	134.5	6.1	174673	4	AP005196	AP005196 Oryza sat
1251	135	6.1	187701	6	AC102341	AC102341 Mus muscu	134.5	6.1	179023	12	AC164924	AC164924 Callithri
1252	135	6.1	188872	13	AC099009	AC099009 Drosophil	134.5	6.1	181047	12	AC016765	AC016765 Homo sapi
1253	135	6.1	193341	12	AC134500	AC134500 Rattus no	134.5	6.1	181861	12	AC180715	AC180715 Strongylo
1254	135	6.1	196337	13	AC005894	AC005894 Drosophil	134.5	6.1	183783	11	BX539325	BX539325 Zebrafish
1255	135	6.1	196558	6	AC073946	AC073946 Mus muscu	134.5	6.1	186708	11	BX323873	BX323873 Zebrafish
1256	135	6.1	203127	11	BX322566	BX322566 Zebrafish	134.5	6.1	187303	12	CR318651	CR318651 Danio rer
1257	135	6.1	211585	6	AL626784	AL626784 Mouse DNA	134.5	6.1	190628	12	AC024700	AC024700 Homo sapi
1258	135	6.1	232357	12	AC127133	AC127133 Rattus no	134.5	6.1	192936	6	AC148320	AC148320 Mus muscu
1259	135	6.1	232382	12	AC098991	AC098991 Rattus no	134.5	6.1	205871	12	AC171150	AC171150 Callithri
1260	135	6.1	233760	11	BX681417	BX681417 Zebrafish	134.5	6.1	206116	6	AC132949	AC132949 Mus muscu
1261	135	6.1	234778	12	AC097097	AC097097 Rattus no	134.5	6.1	207267	6	AC145346	AC145346 Mus muscu
1262	135	6.1	238340	12	AC130161	AC130161 Rattus no	134.5	6.1	218334	12	AC162697	AC162697 Bos tauru
1263	135	6.1	239972	12	AC095835	AC095835 Rattus no	134.5	6.1	219754	6	AC175461	AC175461 Mus muscu
1264	135	6.1	242171	13	AE003832	AE003832 Drosophil	134.5	6.1	223662	6	AC170597	AC170597 Mus muscu
1265	135	6.1	245628	12	AC156406	AC156406 Bos tauru	134.5	6.1	227458	12	AC110137	AC110137 Rattus no
1266	135	6.1	250902	12	AC131965	AC131965 Rattus no	134.5	6.1	229615	12	AC095673	AC095673 Rattus no
1267	135	6.1	266726	12	AC112860	AC112860 Rattus no	134.5	6.1	248378	12	AC128989	AC128989 Rattus no
1268	135	6.1	273619	12	AC112062	AC112062 Rattus no	134.5	6.1	349575	15	BX927154	BX927154 Corynebac
1269	135	6.1	278499	12	AC178901	AC178901 Strongylo	134.5	6.1	349980	2	AX127150	AX127150 Sequence
1270	134.5	6.1	1923	2	AR562235	AR562235 Sequence	134.5	6.1	349980	2	AX127151	AX127151 Sequence
1271	134.5	6.1	1923	2	AX112078	AX112078 Sequence	134	6.1	492	5	HUMMMTR	L46721 Homo sapien
1272	134.5	6.1	1949	13	AY864510	AY864510 Drosophil	134	6.1	1261	4	DQ267479	DQ267479 Hordeum v
1273	134.5	6.1	2047	4	AK107645	AK107645 Oryza sat	134	6.1	2075	4	AK111479	AK111479 Oryza sat
1274	134.5	6.1	2058	2	CQ751984	CQ751984 Sequence	134	6.1	2490	2	CS113399	CS113399 Sequence
1275	134.5	6.1	2080	11	AB006322	AB006322 Danio rer	134	6.1	2663	10	EBVBLFL1	X99106 Epstein-Bar
1276	134.5	6.1	2428	11	BC053239	BC053239 Danio rer	134	6.1	3783	2	AX358421	AX358421 Sequence
1277	134.5	6.1	3169	4	AB182388	AB182388 Oryza sat	134	6.1	4287	2	CQ610164	CQ610164 Sequence
1278	134.5	6.1	3170	4	AK111824	AK111824 Oryza sat	134	6.1	5658	2	AX358423	AX358423 Sequence
1279	134.5	6.1	3184	11	CR942683	CR942683 Xenopus t	134	6.1	9113	8	CVPCG1408	U21228 Promoter-pr
1280	134.5	6.1	3220	11	BC117640	BC117640 Danio rer	134	6.1	32768	2	BD003751	BD003751 Polynucle
1281	134.5	6.1	3426	4	AY553933	AY553933 Triticum	134	6.1	32768	2	CQ788980	CQ788980 Sequence
1282	134.5	6.1	5337	2	AX345341	AX345341 Sequence	134	6.1	32768	2	AR218839	AR218839 Sequence
1283	134.5	6.1	9931	2	CS360445	CS360445 Sequence	134	6.1	33706	13	CEC255G4	Z70680 Caenorhabdi
1284	134.5	6.1	13123	4	DQ419514	DQ419514 Aspergill	134	6.1	38773	13	CET06E4	Z70756 Caenorhabdi
1285	134.5	6.1	33998	12	AC145651	AC145651 Homo sapi	134	6.1	79426	6	AL807830	AL807830 Mouse DNA
1286	134.5	6.1	38311	5	AP007215	AP007215 Homo sapi	134	6.1	80060	11	CR936846	CR936846 Zebrafish
1287	134.5	6.1	76995	12	AC168706	AC168706 Strongylo	134	6.1	82895	4	AL732348	AL732348 Oryza sat
1288	134.5	6.1	87093	15	AP006620	AP006620 Nocardia	134	6.1	89019	4	BX842624	BX842624 Neurospor
1289	134.5	6.1	88400	2	CQ924550	CQ924550 Sequence	134	6.1	110000	4	CR382130_13	Continuation (14 o
1290	134.5	6.1	88400	2	DD090936	DD090936 CLONING G	134	6.1	110000	12	AC095248_3	Continuation (4 of
1291	134.5	6.1	110000	4	AP008213_194	Continuation (195	134	6.1	124321	4	OSA245900	Continuation (10 o
1292	134.5	6.1	110000	4	CR382130_08	Continuation (9 of	134	6.1	149052	12	AC179275	AJ245900 Oryza sat
1293	134.5	6.1	110000	4	CR382132_10	Continuation (11 o	134	6.1	160432	11	AL929072	AC179275 Strongylo
1294	134.5	6.1	110000	15	BA000036_23	Continuation (24 o	134	6.1	172918	11	BX323457	AL929072 Zebrafish
1295	134.5	6.1	110000	15	BA000036_24	Continuation (25 o	134	6.1	173714	12	AC147748	BX323457 Zebrafish
1296	134.5	6.1	110254	11	CR7559879	CR7559879 Zebrafish	134	6.1	173714	12	AC147748	AC147748 Pan trogl
1297	134.5	6.1	125354	6	AC175818	AC175818 Mus muscu	134	6.1	179355	6	AC115631	AC115631 Mus muscu
1298	134.5	6.1	129213	12	AC181800	AC181800 Strongylo	134	6.1	180695	12	AC140661	AC140661 Pan trogl
1299	134.5	6.1	133853	12	AC179271	AC179271 Strongylo	134	6.1	185587	6	AC140346	AC140346 Mus muscu
1300	134.5	6.1	137955	12	AC182791	AC182791 Sorex ara	134	6.1	188130	6	AC105976	AC105976 Mus muscu
1301	134.5	6.1	144283	6	AC175385	AC175385 Mus muscu	134	6.1	196783	6	AC137855	AC137855 Mus muscu
1302	134.5	6.1	146080	11	AL953855	AL953855 Zebrafish	134	6.1	203669	12	AC113929	AC113929 Homo sapi
1303	134.5	6.1	149530	12	AC181461	AC181461 Strongylo	134	6.1	210658	5	AC138775	AC138775 Homo sapi
1304	134.5	6.1	150110	12	AC097722	AC097722 Homo sapi	134	6.1	220811	6	AC087795	AC087795 Genomic S
1305	134.5	6.1	150214	5	AP006345	AP006345 Homo sapi	134	6.1	241943	12	AC107476	AC107476 Rattus no
1306	134.5	6.1	151241	6	AC179922	AC179922 Mus muscu	134	6.1	242139	12	AC095431	AC095431 Rattus no
1307	134.5	6.1	153364	12	AC173965	AC173965 Mus muscu	134	6.1	242302	12	AC095431	AC095431 Rattus no
1308	134.5	6.1	154083	12	AC173729	AC173729 Strongylo	134	6.1	242302	12	AC131200	AC131200 Rattus no
1309	134.5	6.1	155057	6	AC136452	AC136452 Mus muscu	134	6.1	242463	12	AC095409	AC095409 Rattus no
1310	134.5	6.1	158080	12	AC176404	AC176404 Strongylo	134	6.1	250467	12	AC094737	AC094737 Rattus no
1311	134.5	6.1	158469	6	AC145586	AC145586 Mus muscu	134	6.1	255562	12	AC095199	AC095199 Rattus no
1312	134.5	6.1	158626	12	AC149853	AC149853 Papio anu	134	6.1	256528	12	AC108270	AC108270 Rattus no
1313	134.5	6.1	159336	12	AC182228	AC182228 Mus muscu	134	6.1	257028	12	AC129248	AC129248 Rattus no
1314	134.5	6.1	159689	12	AC176566	AC176566 Strongylo	134	6.1	261093	6	AC027740	AC027740 Mus muscu
1315	134.5	6.1	162684	12	AC145741	AC145741 Mus muscu	133.5	6.0	403	11	DQ121048	AC180940 Strongylo
1316	134.5	6.1	162856	12	CT027820	CT027820 Danio rer	133.5	6.0	840	4	WHTGMPA	DQ121048 Hucho tai
1317	134.5	6.1	163379	6	AC140394	AC140394 Mus muscu	133.5	6.0	1098	2	DD132881	DD132881 T Cell Re



1391	133.5	6.0	1397	4	WHTGLIGY	M16064 Wheat (T.ae	1464	133	6.0	2125	5	AB220498	AB220498 Macaca fa
1392	133.5	6.0	1858	4	AB059812	AB059812 Triticum	1465	133	6.0	2139	5	AF043448	AF043448 Cercopith
1393	133.5	6.0	1938	13	AY864491	AY864491 Drosophil	1466	133	6.0	2191	5	AF043449	AF043449 Cercopith
1394	133.5	6.0	1938	13	AY864509	AY864509 Drosophil	1467	133	6.0	2297	5	BC004140	BC004140 Homo sapi
1395	133.5	6.0	2531	14	CFU19489	U19489 Canis famil	1468	133	6.0	2399	5	AB000095	AB000095 Homo sapi
1396	133.5	6.0	3406	4	AY848709	AY848709 Triticum	1469	133	6.0	2400	2	CQ726503	CQ726503 Sequence
1397	133.5	6.0	3574	6	MUSPRMPB	M12099 Mouse PRP g	1470	133	6.0	2486	5	BC018702	BC018702 Homo sapi
1398	133.5	6.0	6412	11	BC076786	BC076786 Xenopus 1	1471	133	6.0	2594	5	AY144615	AY144615 Homo sapi
1399	133.5	6.0	11048	5	HS889J22B	AL049851 Human DNA	1472	133	6.0	2636	6	RNU89744	U89744 Rattus norv
1400	133.5	6.0	16521	5	PHAL8001	Y18001 Papio hamad	c1473	133	6.0	2785	4	SCYNL176C	Z71452 S.cerevisia
c1401	133.5	6.0	33998	12	AC145651	AC145651 Homo sapi	1474	133	6.0	3083	13	AY314775	AY314775 Caenorhab
c1402	133.5	6.0	39246	13	CBRG45E13	AC084630 Caenorhab	c1475	133	6.0	3102	4	SCYOL105C	Z74847 S.cerevisia
c1403	133.5	6.0	110000	6	AJ851868_12	Continuation (13 o	1476	133	6.0	3228	2	AR778360	AR778360 Sequence
1404	133.5	6.0	120646	12	AC176957	AC176957 Strongylo	1477	133	6.0	3228	8	DQ331924	DQ331924 Synthetic
c1405	133.5	6.0	145651	12	AC180418	AC180418 Strongylo	1478	133	6.0	3228	8	DQ331924	DQ331924 Synthetic
c1406	133.5	6.0	146624	12	AC182840	AC182840 Mus muscu	1479	133	6.0	3676	6	BC091647	BC091647 Mus muscu
1407	133.5	6.0	147596	12	AC186148	AC186148 Mus muscu	1480	133	6.0	3906	14	BTNACAKEX	X66481 B.taurus mR
1408	133.5	6.0	150886	6	AC142409	AC142409 Mus muscu	1481	133	6.0	4162	13	AY865058	AY865058 Drosophil
1409	133.5	6.0	152486	12	AC172871	AC172871 Brassica	1482	133	6.0	4777	2	CQ612432	CQ612432 Sequence
c1410	133.5	6.0	155750	12	AC186276	AC186276 Loxodonta	1483	133	6.0	22259	12	AC160519	AC160519 Lytechinu
c1411	133.5	6.0	156459	6	AC147155	AC147155 Mus muscu	1484	133	6.0	26154	13	CEF33E2	Z84574 Caenorhabdi
1412	133.5	6.0	169136	6	AC185132	AC185132 Mus muscu	c1485	133	6.0	27543	5	AB126081	Z48149 S.cerevisia
c1413	133.5	6.0	171987	5	AC100757	AC100757 Homo sapi	1486	133	6.0	44019	4	SCCHRKV44	U00029 Saccharomyc
c1414	133.5	6.0	173783	12	AC151381	AC151381 Callithiri	1487	133	6.0	56097	4	YSC9177	AL353822 Neurospor
1415	133.5	6.0	174101	11	CR925784	CR925784 Zebrafish	c1488	133	6.0	72305	4	NCB13A5	AL513465 Neurospor
c1416	133.5	6.0	174935	6	AC148984	AC148984 Mus muscu	c1489	133	6.0	84793	11	AC096684	AC096684 Takifugu
1417	133.5	6.0	177061	12	AC142479	AC142479 Rattus no	c1490	133	6.0	98505	4	AP006692	AP006692 Lotus jap
1418	133.5	6.0	178530	5	AC018738	AC018738 Homo sapi	c1491	133	6.0	102606	12	AC176436	AC176436 Strongylo
c1419	133.5	6.0	182193	12	AC147692	AC147692 Gorilla g	c1492	133	6.0	110000	4	AP008214_003	Continuation (4 of
1420	133.5	6.0	184427	10	EHVU20824	U20824 Equine herp	1493	133	6.0	110000	4	CR380947_3	Continuation (4 of
1421	133.5	6.0	185195	6	AC134565	AC134565 Mus muscu	1494	133	6.0	110000	4	CR382128_13	Continuation (14 o
1422	133.5	6.0	187101	5	AL589862	AL589862 Human DNA	c1495	133	6.0	110000	4	CR382132_20	Continuation (21 o
c1423	133.5	6.0	188412	12	AC119098	AC119098 Rattus no	c1496	133	6.0	110000	4	CR382132_21	Continuation (22 o
1424	133.5	6.0	192187	13	AC117072	AC117072 Dictyoste	c1497	133	6.0	110000	4	AE016818_05	Continuation (6 of
c1425	133.5	6.0	196544	5	AC185241	AC185241 Pan trogl	1498	133	6.0	112893	11	CR356224	CR356224 Zebrafish
c1426	133.5	6.0	202943	5	AC010134	AC010134 Homo sapi	1499	133	6.0	117679	13	AC167662	AC167662 Culex pip
c1427	133.5	6.0	204142	5	AC010976	AC010976 Homo sapi	c1500	133	6.0	117683	13	AC167718	AC167718 Culex pip
c1428	133.5	6.0	204839	12	AC144882	AC144882 Gorilla g							
1429	133.5	6.0	208378	12	AC126293	AC126293 Rattus no							
1430	133.5	6.0	212885	6	RN139I21	CR937048 Rattus no							
1431	133.5	6.0	219484	12	AC096353	AC096353 Rattus no							
c1432	133.5	6.0	222797	12	AC126213	AC126213 Rattus no							
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1434	133.5	6.0	234964	12	AC128786	AC128786 Rattus no							
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c1437	133.5	6.0	238071	12	AC133970	AC133970 Rattus no							
1438	133.5	6.0	240261	12	AC183445	AC183445 Gorilla g							
1439	133.5	6.0	254733	13	AC117075	AC117075 Dictyoste							
c1440	133.5	6.0	256879	13	AC116982	AC116982 Dictyoste							
1441	133.5	6.0	258818	12	AC135265	AC135265 Rattus no							
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1443	133	6.0	840	4	TAE416336	AJ416336 Triticum							
1444	133	6.0	840	4	TAE416338	AJ416338 Triticum							
1445	133	6.0	840	4	TAE416339	AJ416339 Triticum							
1446	133	6.0	1257	4	DQ148297	DQ148297 Hordeum v							
1447	133	6.0	1542	2	AR148260	AR148260 Sequence							
1448	133	6.0	1542	2	AR237449	AR237449 Sequence							
1449	133	6.0	1542	2	E12898	E12898 Human cDNA							
1450	133	6.0	1542	2	E21838	E21838 Preventive							
1451	133	6.0	1542	5	BT007425	BT007425 Homo sapi							
1452	133	6.0	1542	8	AY888714	AY888714 Synthetic							
1453	133	6.0	1542	8	AY888715	AY888715 Synthetic							
1454	133	6.0	1542	8	AY891371	AY891371 Synthetic							
1455	133	6.0	1542	8	BT009882	BT009882 Synthetic							
1456	133	6.0	1671	2	AR528251	AR528251 Sequence							
1457	133	6.0	1671	2	AR778518	AR778518 Sequence							
1458	133	6.0	1671	8	DQ333123	DQ333123 Synthetic							
1459	133	6.0	1767	5	AF007191	AF007191 Homo sapi							
1460	133	6.0	1775	4	HVB1HOR2	X87232 H.vulgare B							
1461	133	6.0	1813	2	CQ774958	CQ774958 Sequence							
1462	133	6.0	1944	4	AF497720	AF497720 Aspergill							
1463	133	6.0	2052	13	LDU78522	U78522 Leishmania							

RESULT 1

BD140585

LOCUS

BD140585

Polypeptides and nucleic acids encoding the same.

BD140585

BD140585.1 GI:23235530

JP 2002505850-A/68.

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2284)

Wood,W.I., Goddard,A., Gurney,A.L., Yuan,J., Baker,K.P. and Zheng,J.

REFERENCE

AUTHORS

Polyptides and nucleic acids encoding the same

TITLE

JOURNAL

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COMMENT

OS Homo sapiens (human)

PN JP 2002505850-A/68

PD 26-FEB-2002

PP 01-DEC-1998 JP 2000523338

PR 03-DEC-1997 US 60/067411,11-DEC-1997 US 60/069334 PR

11-DEC-1997 US 60/069335,11-DEC-1997 US 60/069278 PR

12-DEC-1997 US 60/069425,16-DEC-1997 US 60/069696 PR

16-DEC-1997 US 60/069694,16-DEC-1997 US 60/069702 PR

17-DEC-1997 US 60/069870,17-DEC-1997 US 60/069873 PR

18-DEC-1997 US 60/068017,05-JAN-1998 US 60/070440 PR

09-FEB-1998 US 60/074086,09-FEB-1998 US 60/074092 PR

25-FEB-1998 US 60/075945

PI WILLIAM I WOOD,AUDREY GODDARD,AUSTIN L GURNEY,JEAN YUAN,KEVIN P BAKER,

ALIGNMENTS

2284 bp

DNA

linear

PAT 18-SEP-2002



PI godowski, PI audrey goddard,mary e gerritsen,ellen filvaroff,dan pi 1 eaton,david botstein, PI kevin p baker,napoleone ferrara,william i wood CC FH Key Location/Qualifiers 1. .2284 /organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"									
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Db	586	ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCCAAGAGTTACCCCGAGGAAATTCT	645						
QY	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160						
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QY	161	SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp	180						
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QY	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240						
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QY	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260						
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Db	1006	CAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACCTGTCACTTCTCAGCCTCCCACG	1065						
QY	281	ThrLeuIleSerThrValPheThrArgAlaAlaAalaThrLeuGlnAlaMetAlaThrThr	300						
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QY	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260						
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Alignment Scores:	2.72e-139	Length:	2284
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Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAGACTGCATTAAATCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465  
Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
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Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
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Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
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Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
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Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
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DEFINITION the Same.  
ACCESSION DD028540  
VERSION DD028540.1 GI:92561177  
KEYWORDS JP 2004203742-A/369.  
SOURCE unidentified  
ORGANISM unidentified  
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AUTHORS 1 (bases 1 to 2284)  
Grimaldi,C.J., Ashkenazi,A.J., Desnoyers,L., Baker,K.P.,  
Godowski,P.J., Goddard,A., Gerritsen,M.E., Gerber,H., Fong,S.,  
Ferrara,N., Eaton,D.L., Botstein,D., Gurney,A.L., Kljavin,I.J.,  
Napier,M.A., Zhang,Z., Wood,W.I., Williams,M.P., Tumas,D.,  
Watanabe,C.K., Stewart,T.A., Roy,M.A., Paoni,N.F. and Pan,J.  
TITLE Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding  
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JOURNAL Patent: JP 2004203742-A 369 22-JUL-2004;  
Genentech Inc,Kevin Baker,Jian Chen,Audrey Goddard,Austin Gurney,  
Victoria Smith,Colin K Watanabe,William I Wood,Jean Yuan  
COMMENT OS Homo Sapien  
PN JP 2004203742-A/369  
PD 22-JUL-2004  
PF 25-SEP-2002 JP 2002341509  
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06-JAN-2000 US US0000376,11-FEB-2000 US US00003565, PR  
18-FEB-2000 US US0004341,22-FEB-2000 US US0004414, PR  
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02-MAR-2000 US US0005841,15-MAR-2000 US US0006884, PR  
05-JAN-2000 US US0000219,20-DEC-1999 US US9930911, PR  
16-DEC-1999 US US9930095,28-JUL-1999 US 60/146222, PR  
17-AUG-1999 US 60/149396,15-SEP-1999 US US9921090, PR  
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christopher j grimaldi,avi j ashkenazi,luc desnoyers,kevin p pi  
baker,  
PI paul j godowski,audrey goddard,mary e gerritsen,hanspeter pi  
gerber,  
PI sherman fong,napoleone ferrara,dan l eaton,david botstein, pi  
austin l gurney,  
PI ivar j kljavin,mary a napier,zemin zhang,william pi i  
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US-09-944-929-83 (1-431) x DD028540 (1-2284)

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ACCESSION DD031661  
VERSION DD031661.1 GI:92605001  
KEYWORDS JP 2004516227-A/57.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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1 (bases 1 to 2284)  
Watanabe,C.K., Yan,M., Shelton,D.L., Smith,V., Stewart,T.A., Wood,W.I., Tumas,D., Gurney,A.L., Pennica,D., Ashkenazi,A.J., Baker,K.P., Lu,Y., Pan,J., Kabakoff,R.C., Henzel,W., Hebert,C. and Goddard,A.  
COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE RELATED  
Patent: JP 2004516227-A 57 03-JUN-2004;  
Genentech Inc et al  
OS Homo sapiens  
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PD 03-JUN-2004  
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PI colin k watanabe,minhong yan,david l shelton,victoria smith,  
PI timothy a stewart,william i wood,daniel tumas,austin l gurney,  
PI diane pennica,avi j ashkenazi,kevin p baker,yanmei lu,james  
PI pan,  
PI rhona c kabakoff,william henzel,carolyn hebert,audrey goddard  
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Db	346	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATATACTTCAACTCAA	405		
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Db	406	GAAGACTGCATTAAATCTTGTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC	465		
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Db	466	TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCCAACTGCTACCTATTTTCTGT	525		
QY	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120		
Db	526	CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT	585		
QY	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140		
Db	586	ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCCAAGAGTTACCCCCAGGAAGATTCT	645		
QY	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160		
Db	646	CTCTTACATGGCCAAATTTTCAAGCAGTCACTCCCCTAGCCCATCATCACAGATTAT	705		
QY	161	SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp	180		
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QY	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200		
Db	766	CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAAGTCTCTTGCTTATAAGGAA	825		
QY	201	LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220		
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QY	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240		
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QY	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260		
Db	946	ACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC	1005		
QY	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280		
Db	1006	CAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCCACG	1065		

Qy	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
Db	1066	ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGTACACTCCAAGCAATGGCTACAACA	1125
Qy	301	AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320
Db	1126	GCAGTTCTGACTACCACTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATATA	1185
Qy	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
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Qy	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg	360
Db	1246	CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGTAGG	1305
Qy	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1306	GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTCCAGAAAATCAGTACGGCCTTCCA	1365
Qy	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
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Qy	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu	420
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Qy	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
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RESULT 6			
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LOCUS			linear
DEFINITION			PAT 04-NOV-2005
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ACCESSION	DD039442		
VERSION	DD039442.1	GI:92629391	
KEYWORDS	JP 2004522402-A/369.		
SOURCE	unidentified		
ORGANISM	unidentified		
REFERENCE	unclassified sequences.		
AUTHORS	1 (bases 1 to 2284)		
	Zhang, Z., Wood, W.I., Ashkenazi, A.J., Botstein, D., Napier, M.A., Kljavin, I.J., Gurney, A.L., Grimaldi, C.J., Godowski, P.J., Goddard, A., Paoni, N.F., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, M.P., Baker, K.P., Pan, J., Roy, M.A., Gerritsen, M.E., Gerber, H., Fong, S., Ferrara, N., Eaton, D.L. and Desnoyers, L.		
TITLE	Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding		
	the Same		
JOURNAL	Patent: JP 2004522402-A 369 29-JUL-2004;		
	Genentech Inc, Kevin Baker, Jian Chen, Audrey Goddard, Austin Gurney, Victoria Smith, Colin K Watanabe, William I Wood, Jean Yuan		
COMMENT	OS Homo Sapien		
	PN JP 2004522402-A/369		
	PD 29-JUL-2004		
	PF 30-MAR-2000 JP 2001500766		
	PR 06-JAN-2000 US US0000376,11-FEB-2000 US	US00003565,	PR
	18-FEB-2000 US	US0004341,22-FEB-2000 US	US0004414, PR
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	05-JAN-2000 US	US0000219,17-AUG-1999 US	60/149396, PR
	15-SEP-1999 US	US9921547,15-MAR-2000 US	US0006884, PR
	23-JUN-1999 US	60/141037,07-JUL-1999 US	60/143048, PR
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	20-DEC-1999 US	US9930911,16-DEC-1999 US	US9930095, PR
	01-DEC-1999 US	US9928301,30-NOV-1999 US	US9928313, PR
	08-OCT-1999 US	60/158663,02-MAR-2000 US	US0005841, PR
	20-MAR-2000 US	US0007377,02-JUN-1999 US	US9912252 PI
	zhang,william i wood,avi j ashkenazi,david pi		botstein,mary
	PI a napier,		



PI ivar j kljavin,austin l gurney,christopher j grimaldi,paul j  
PI godowski,  
PI audrey goddard,nicholas f paoni,timothy  
PI a stewart,daniel tumas,  
PI colin k watanabe,mickey p williams,kevin p baker,james pan, PI  
margaret ann roy,mary e gerritsen,hanspeter gerber,sherman PI  
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ORIGIN

Alignment Scores:  
Pred. No.: 2.72e-139 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
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DB: 2 Gaps: 0

US-09-944-929-83 (1-431) x DD039442 (1-2284)

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Db 1006 CAGCCACAGCTGGCCACCACAGCTCCACTGTAACTGTCTCTCAGCTCCACG 1065  
  
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
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Db 1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGTACACTCCAAGCAATGGGTACAACA 1125  
  
QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
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Db 1126 GCAGTTCTGACTACCACCTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185  
  
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Db 1186 CCGTTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCTTACTGCA 1245  
  
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QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
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Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518

RESULT 7

DD249590 2284 bp DNA linear PAT 18-MAY-2006  
LOCUS Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding  
DEFINITION the Same.

ACCESSION DD249590  
VERSION DD249590.1 GI:99025485  
KEYWORDS JP 2005304500-A/369.

SOURCE unidentified  
ORGANISM unidentified

REFERENCE unclassified sequences.

AUTHORS 1 (bases 1 to 2284)

Napier,M.A., Kljavin,I.J., Gurney,A.L., Grimaldi,C.J.,  
Watanabe,C.K., Stewart,T.A., Zhang,Z., Wood,W.I., Williams,P.M.,  
Tumas,D., Godowski,P.J., Goddard,A., Gerritsen,M.E., Gerber,H.,  
Fong,S., Paoni,N.F., Pan,J., Roy,M.A., Ferrara,N., Baton,D.L.,  
Desnovers,L., Botstein,D., Baker,K.P. and Ashkenazi,A.J.

Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding  
the Same

JOURNAL Patent: JP 2005304500-A 369 04-NOV-2005;  
Genentech Inc,Kevin Baker,Jian Chen,Audrey Goddard,Austin Gurney,  
Victoria Smith,Colin K Watanabe,William I Wood,Jean Yuan

COMMENT OS Homo Sapien  
PN JP 2005304500-A/369  
PD 04-NOV-2005

PF 14-MAR-2005 JP 2005117472  
PR 11-FEB-2000 US T/US00/03565,06-JAN-2000 US T/US00/00376, PR  
05-JAN-2000 US T/US00/00219,20-DEC-1999 US T/US99/30911, PR  
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23-JUN-1999 US 60/141037,07-JUL-1999 US 60/143048, PR  
02-JUN-1999 US T/US99/12252,20-JUL-1999 US 60/144758 PI mary a  
napier,ivar j kljavin,austin l gurney,christopher j PI grimaldi,  
PI colin k watanabe,timothy a steward,zemin zhang,william i wood,  
PI p mickey williams,daniel tumas,paul j godowski,audrey goddard,  
PI mary e gerritsen,hanspeter gerber,sherman fong,nicholas f PI  
paoni,james pan,  
PI margaret ann roy,napoleone ferrara,dan l eaton,luc desnoyers,  
PI david botstein,kevin p baker,avi j ashkenazi  
CC

FH Key Location/Qualifiers.

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source

1. .2284  
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ORIGIN

Alignment Scores:

Pred. No.: 2.72e-139 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 2 Gaps: 0

US-09-944-929-83 (1-431) x DD249590 (1-2284)

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RESULT 8

AR429104

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

AR429104  
Sequence 82 from patent US 6642360.

AR429104  
GI:40189199

Unknown.  
Unclassified.

1 (bases 1 to 2284)  
Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L.  
and Wood,W.I.

Secreted polypeptides that stimulate release of proteoglycans from  
cartilage

Patent: US 6642360-A 82 04-NOV-2003;  
Genentech, Inc.; South San Francisco, CA

Location/Qualifiers  
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Alignment Scores: 2.72e-139 Length: 2284

Pred. No.:

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Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0
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Db	226	ATGTTCTTCGGGGGAGAAGGAGCTTGACTTACACTTGGTAATAATTGCTTCCTGACA	285
Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp	40
Db	286	CTAAGGCTGCTGCTAGTCAGAAATTGCCTCAAAAAGAGCTAGAGATGTTGTCAATTGAC	345
Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60
Db	346	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA	405
Qy	61	GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80
Db	406	GAAGACTGCATTAAATCTTGCTGTTCAACAAAAACATATACAGGGACAAAGCATGTAAC	465
Qy	81	LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys	100
Db	466	TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTCTGT	525
Qy	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120
Db	526	CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT	585
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Db	586	ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCAAGAGTTACCCAGGAAGATTCT	645
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Qy	161	SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp	180
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Db	766	CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCCTTGCTTATAAGGAA	825
Qy	201	LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220
Db	826	AAAGGCCATTCTCAGAGTTCACAATTTTCCCTCTGTATCAAGAAATAGCTCATCTGCTGCCT	885
Qy	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240
Db	886	GAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT	945
Qy	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260
Db	946	ACTCAAAGCCCCGACCCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC	1005
Qy	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280
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Qy	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
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Qy	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340

Db	1186	CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCTACTGCA	1245
Qy	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg	360
Db	1246	CTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGTAGG	1305
Qy	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
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Qy	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1366	TTTGAAAAAATGGCTTCTTATCGGTCCTGCTCTTTGGTGTCTGTCTCTGGTGATAGGC	1425
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DEFINITION	AR534995		
ACCESSION	AR534995.1	GI:53925785	
VERSION	Unknown.		
KEYWORDS	Unknown.		
SOURCE	Unclassified.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 2284)		
AUTHORS	Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L. and Wood,W.I.		
TITLE	Antibodies against a secreted polypeptide that stimulates release of proteoglycans from cartilage		
JOURNAL	Patent: US 6734288-A 82 11-MAY-2004;		
Genentech, Inc.; San Francisco, CA			
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LOCUS AR691142 2284 bp DNA linear PAT 13-SEP-2005
DEFINITION Sequence 82 from patent US 6908993.
ACCESSION AR691142
VERSION AR691142.1 GI:74478541
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2284)
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L.,
Hillan,K.J., Roy,M.A. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6908993-A 82 21-JUN-2005;
Genentech, Inc.; South San Francisco, CA
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DEFINITION Sequence 514 from patent US 6913919.  
ACCESSION AR693626  
VERSION AR693626.1 GI:75184121  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2284)  
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Gurney,A.L., Roy,M.A. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: US 6913919-A 514 05-JUL-2005;  
Genetech, Inc.; South San Francisco, CA  
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Alignment Scores: 2.72e-139 Length: 2284  
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Score: 100.0% Conservative: 0  
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DEFINITION Sequence 82 from patent US 6929947.  
ACCESSION AR705580  
VERSION AR705580.1 GI:75924126  
KEYWORDS  
SOURCE Unknown.  
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REFERENCE 1 (bases 1 to 2284)  
AUTHORS Botstein,D., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Roy,M.A. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: US 6929947-A 82 16-AUG-2005;  
Genentech, Inc.; South San Francisco, CA  
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Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAATGTGTAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945  
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
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Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACACACAGCTCCACCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCACG 1065  
Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1066 ACCCTCATTTCTACAGTTTACACGGGCTGGGCTACACTCCAAGCAATGGCTACAACA 1125  
Qy 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1126 GCAGTTCTGACTACCACTTTTCAGGCACCTACGACTCGAAGGCAGCTTAGAAACCATATA 1185  
Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db 1186 CCGTTTACAGAAATCTCCAACCTTAACCTTTGACACACAGGGAATGTGTATAACCCCTACTGCA 1245  
Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGTAGG 1305  
Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
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Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
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Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
Db 1426 CTCGTCTCTCTGGGTAGAAATCCTTTCGGAATCACTCCGCAAGAAACGTTACTCAAGACTG 1485  
Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518  
RESULT 13  
AR706178  
LOCUS AR706178 2284 bp DNA linear PAT 20-SEP-2005  
DEFINITION Sequence 514 from patent US 6930170.



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ACCESSION   AR706178
VERSION     AR706178.1  GI:75924899
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 2284)
AUTHORS     Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.
TITLE       PRO1184 polypeptides
JOURNAL     Patent: US 6930170-A 514 16-AUG-2005;
            Genentech, Inc.; South San Francisco, CA;
            WOX;

FEATURES
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Alignment Scores:
Pred. No.:      2.72e-139      Length:      2284
Score:          2211.00        Matches:      431
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match:    100.0%          Indels:      0
DB:             2              Gaps:         0

us-09-944-929-83 (1-431) x AR706178 (1-2284)

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Qy      121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
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Qy      141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
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Qy      161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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Qy      201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
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Db      826 AAAGGCCATTCTCAGAGTTCAAAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

Qy      221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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Qy      261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
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Qy      321 PropheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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Db      1186 CCGTTTACAGAAATCTCCAACCTTAACCTTGAACACACAGGGAATGTGTATAACCCCTACTGCA 1245

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Qy      421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
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RESULT 14
AR708652
LOCUS      AR708652      2284 bp      DNA      linear      PAT 21-SEP-2005
DEFINITION Sequence 82 from patent US 6936254.
ACCESSION AR708652
VERSION    AR708652.1  GI:75998546
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 2284)
AUTHORS    Baker,K.P., Botstein,D., Eaton,D.L., Ferrara,N., Filvaroff,E.,
            Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C.,
            Gurney,A.L., Hillan,K.J., Kljavin,I.J., Napier,M.A., Roy,M.A.,
            Tumas,D. and Wood,W.I.
TITLE      Method of inducing fetal hemoglobin synthesis
JOURNAL    Patent: US 6936254-A 82 30-AUG-2005;
            Genentech, Inc.; South San Francisco, CA
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.:      2.72e-139      Length:      2284
Score:          2211.00        Matches:      431
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches: 0
Query Match:    100.0%          Indels:      0
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US-09-944-929-83 (1-431) x AR708652 (1-2284)

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AR757551

LOCUS AR757551 2284 bp DNA linear PAT 08-DEC-2005

DEFINITION Sequence 514 from patent US 6953836.

ACCESSION AR757551

VERSION AR757551.1 GI:83322728

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2284)

AUTHORS Desnoyers,L., Goddard,A., Godowski,P.J., Gurney,A.L. and Wood,W.I.

TITLE PRO844 polypeptides

JOURNAL Patent: US 6953836-A 514 11-OCT-2005;

Genentech, Inc.; South San Francisco, CA

FEATURES

Location/Qualifiers

source

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/organism="unknown"

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Score: 2211.00 Matches: 431

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Best Local Similarity: 100.0% Mismatches: 0

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Db 346 ATCCAGTCATCTCTTCTAAGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

QY 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
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Db 406 GAAGACTGCATTAAATCTTGTGCTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465

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Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTCTGT 525

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Db 526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

QY	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140
Db	586	ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAAGAGTTACCCAGGAAGATTCT	645
QY	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160
Db	646	CTCTTACATGGCCAAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT	705
QY	161	SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp	180
Db	706	TCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT	765
QY	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200
Db	766	CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCGAGCTCCTTGCTTATAAGGAA	825
QY	201	LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220
Db	826	AAAGGCCATTCTCAGAGTTTCAAAATTTTCTGTGATCAAGAAATAGCTCATCTGCTGCCT	885
QY	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240
Db	886	GAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT	945
QY	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260
Db	946	ACTCCAAAGCCCGCCACCCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC	1005
QY	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280
Db	1006	CAGCCACAGCTGGCCACCACAGTCCACCTGTAACTGTACCTTCTCAGCCTCCACAG	1065
QY	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
Db	1066	ACCCTCATTTCTACAGTTTTTACACGGGCTCGGGTACACTCCAAGCAATGGCTACAACA	1125
QY	301	AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320
Db	1126	GCAGTTCTGACTACCACTTTTCCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCAT	1185
QY	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
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QY	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg	360
Db	1246	CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAGGTAGG	1305
QY	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1306	GAGGCAGTCCAGGCAGTTCCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCCA	1365
QY	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1366	TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTTGGTGTCTGTCTCTGGTGATAGGC	1425
QY	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgGlyLysArgTyrSerArgLeu	420
Db	1426	CTCGTCTCTCTGGGTAGAACTCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG	1485
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GenCore version 6.2.1  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PD	10-JUN-1999.					
PA	(GETH ) GENENTECH INC.					
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Percent Similarity:	100.0%	Conservative:	0			
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Query Match:	100.0%	Indels:	0			
RESULT 4						
ID	ACA64519	standard;	cdna;	2284	BP.	
DE	Novel	human	secreted	and	transmembrane	protein
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			
RESULT 5						
ID	ABX96832	standard;	cdna;	2284	BP.	
DE	Human	cdna	encoding	secreted	/transmembrane	protein
PN	US2002173463-A1.					
PD	21-NOV-2002.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			
RESULT 6						
ID	ABX78486	standard;	cdna;	2284	BP.	
DE	DNA	encoding	Novel	human	secreted	protein
PN	US2002150976-A1.					
PD	17-OCT-2002.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			
RESULT 7						
ID	ABX77120	standard;	cdna;	2284	BP.	
DE	CDNA	encoding	human	PRO361	protein.	
PN	US2002142958-A1.					
PD	03-OCT-2002.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			
RESULT 8						
ID	ABX80978	standard;	cdna;	2284	BP.	
DE	Human	secreted	/transmembrane	protein	cdna, #182.	
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			
RESULT 9						
ID	ACD44487	standard;	cdna;	2284	BP.	
DE	CDNA	encoding	human	PRO361	polypeptide.	
PN	US2002127576-A1.					
PD	12-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			
RESULT 10						
ID	ABX75951	standard;	cdna;	2284	BP.	
DE	Human	cdna	encoding	secreted	/transmembrane	protein,
PN	US2002132981-A1.					
PD	19-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			
RESULT 11						
ID	ABX89662	standard;	cdna;	2284	BP.	
DE	CDNA	encoding	novel	secreted	and	transmembrane
PN	US2002168715-A1.					
PD	14-NOV-2002.					

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 12  
ID ABX79658 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane protein cDNA, #182.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 13  
ID ACA93679 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 14  
ID ABX81361 standard; DNA; 2284 BP.  
DE Novel human secreted or transmembrane protein PRO846 DNA.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 15  
ID ACA93177 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 16  
ID ABX17261 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 17  
ID ABX34148 standard; cDNA; 2284 BP.  
DE cDNA encoding human pro361 protein.  
PN US2002127643-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 18  
ID ACA04368 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #15.  
PN US2002165143-A1.  
PD 07-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 19  
ID ACA68116 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0

RESULT 20  
ID ACA8565 standard; cDNA; 2284 BP.  
DE Human secreted and transmembrane polypeptide PRO361 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 21  
ID ACD82072 standard; cDNA; 2284 BP.  
DE cDNA encoding human PRO361 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 22  
ID ADA38025 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003008297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 23  
ID ADA21711 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO361.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 24  
ID ADA10498 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO361.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 25  
ID ADA18042 standard; cDNA; 2284 BP.  
DE cDNA encoding human PRO361 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 26  
ID ADA28150 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 27  
ID ADA94730 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0  
RESULT 28  
ID ADA38955 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Percent Similarity: 100.0%      Conservative: 0  
Best Local Similarity: 100.0%      Mismatches: 0  
Query Match: 100.0%      Indels: 0

Query Match: 100.0% Indels: 0  
RESULT 29  
ID ADA93076 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 30  
ID ACH65633 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 31  
ID ADA22637 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO361.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 32  
ID ACD39623 standard; cDNA; 2284 BP.  
DE Human cDNA encoding PRO846.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 33  
ID ADA06803 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #146.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 34  
ID ADA39496 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 35  
ID ADB96522 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 36  
ID ADC57994 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 37  
ID ADC25838 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2002142419-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0

Query Match: 100.0% Indels: 0  
RESULT 38  
ID ADC25596 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2002156004-A1.  
PD 24-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 39  
ID ADC55358 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 40  
ID ADC12225 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 41  
ID ADC56647 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 42  
ID ADC11692 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 43  
ID ADC25717 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003077698-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 44  
ID ADC14814 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 45  
ID ADD08346 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 46  
ID ADC82171 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0



Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 47  
ID ADD07813 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 48  
ID ADC82704 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 49  
ID ADD08884 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 50  
ID ADD07133 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 51  
ID ADC83380 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 52  
ID ADD55487 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 53  
ID ADD56445 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 54  
ID ADD54883 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2002132253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 55  
ID ADE31902 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003068647-A1.

PD 10-APR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 56  
ID ADE27037 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 57  
ID ADE26504 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 58  
ID ADF67441 standard; cDNA; 2284 BP.  
DE Human PRO361 nucleotide sequence SEQ ID NO:514.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 59  
ID ADH27502 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003083479-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 60  
ID ADI35695 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 61  
ID ADI00188 standard; cDNA; 2284 BP.  
DE Novel human secreted and transmembrane protein PRO361 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 62  
ID ABX75504 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane protein PRO361 cDNA.  
PN US2002142959-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 63  
ID ABX78062 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #146.  
PN US2003027163-A1.  
PD 06-FEB-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 64  
ID ABX80474 standard; DNA; 2284 BP.

DE Novel human secreted or transmembrane protein PRO846 DNA.  
PN US2002132252-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 65  
ID ACA69380 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003032023-A1.  
PD 13-FEB-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 66  
ID ABX90451 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane protein cDNA, #182.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 67  
ID ABX64297 standard; cDNA; 2284 BP.  
DE cDNA encoding human PRO361 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 68  
ID ABX89495 standard; cDNA; 2284 BP.  
DE Human PRO polynucleotide #15.  
PN US2002132768-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 69  
ID ADE71551 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003096742-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 70  
ID ADF35640 standard; cDNA; 2284 BP.  
DE cDNA encoding human PRO361 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 71  
ID ADG11890 standard; cDNA; 2284 BP.  
DE cDNA encoding human PRO361 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 72  
ID ADG63494 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003211570-A1.  
PD 13-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 73  
ID ADH19760 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 74  
ID ADH21253 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 75  
ID ADH20293 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO361.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 76  
ID ADH43223 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2003207401-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 77  
ID ADN00461 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2004091972-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 78  
ID ADU25385 standard; cDNA; 2284 BP.  
DE Human cDNA encoding secreted/transmembrane PRO polypeptide #15.  
PN US2004220385-A1.  
PD 04-NOV-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 79  
ID ADY39548 standard; cDNA; 2284 BP.  
DE Human mucin/chitinase homolog PRO361 precursor cDNA.  
PN US2005048613-A1.  
PD 03-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 80  
ID ADY73829 standard; cDNA; 2284 BP.  
DE Human PRO361 cDNA, SEQ ID NO: 82.  
PN US2005059115-A1.  
PD 17-MAR-2005.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 81  
ID AEA38662 standard; cDNA; 2284 BP.  
DE Human secreted/transmembrane protein cDNA, #215.  
PN US2005112725-A1.  
PD 26-MAY-2005.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 82  
ID AEH50178 standard; cDNA; 2284 BP.  
DE Human cDNA clone DNA45410-1250 SEQ ID NO: 82.  
PN US2006105427-A1.  
PD 18-MAY-2006.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 83  
ID AEI36386 standard; cDNA; 2284 BP.  
DE Human PRO protein coding sequence - SEQ ID 82.  
PN US2006127983-A1.  
PD 15-JUN-2006.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 84  
ID AAH18096 standard; cDNA; 2297 BP.  
DE Human cDNA sequence SEQ ID NO:17949.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 85  
ID AAC59840 standard; DNA; 2342 BP.  
DE Human secreted protein encoding DNA clone vo27 1.  
PN WO200053375-A1.  
PD 21-SEP-2000.  
PA (ALPH-) ALPHAGENE INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 86  
ID AAC58593 standard; cDNA; 2418 BP.  
DE Human PRO361 protein UNQ316 encoding cDNA SEQ ID NO:71.  
PN WO200053758-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
RESULT 87  
ID AAA16637 standard; cDNA; 2015 BP.  
DE Human secreted protein clone cf85\_1 nucleotide sequence SEQ ID NO:39.  
PN WO200009552-A1.  
PD 24-FEB-2000.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 99.5% Conservative: 0  
Best Local Similarity: 99.5% Mismatches: 1  
Query Match: 93.7% Indels: 2  
RESULT 88  
ID AAH13971 standard; cDNA; 2221 BP.  
DE Human cDNA sequence SEQ ID NO:11027.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 92.1% Conservative: 0  
Best Local Similarity: 92.1% Mismatches: 0

Query Match: 91.5% Indels: 34  
RESULT 89  
ID ADJ75252 standard; DNA; 2221 BP.  
DE Marker gene SEQ ID NO:504.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Percent Similarity: 92.1% Conservative: 0  
Best Local Similarity: 92.1% Mismatches: 0  
Query Match: 91.5% Indels: 34  
RESULT 90  
ID ADN05895 standard; cDNA; 2221 BP.  
DE Antipsoriatic cDNA sequence #1179.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 92.1% Conservative: 0  
Best Local Similarity: 92.1% Mismatches: 0  
Query Match: 91.5% Indels: 34  
RESULT 91  
ID AAH99840 standard; cDNA; 1423 BP.  
DE Human protein encoding cDNA sequence SEQ ID NO:675.  
PN WO200153455-A2.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 99.5% Conservative: 0  
Best Local Similarity: 99.5% Mismatches: 0  
Query Match: 83.7% Indels: 2  
RESULT 92  
ID AAS78315 standard; cDNA; 2487 BP.  
DE DNA encoding novel human diagnostic protein #14119.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 82.8% Indels: 0  
RESULT 93  
ID ABL89648 standard; cDNA; 842 BP.  
DE Human polynucleotide SEQ ID NO 210.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 97.2% Conservative: 0  
Best Local Similarity: 97.2% Mismatches: 6  
Query Match: 60.7% Indels: 3  
RESULT 94  
ID ADJ76101 standard; DNA; 2286 BP.  
DE Marker gene SEQ ID NO:1353.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Percent Similarity: 68.4% Conservative: 37  
Best Local Similarity: 59.9% Mismatches: 119  
Query Match: 52.7% Indels: 17  
RESULT 95  
ID AAC76591 standard; cDNA; 517 BP.  
DE Human ORFX ORF2146 polynucleotide sequence SEQ ID NO:4291.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 99.4% Conservative: 0  
Best Local Similarity: 99.4% Mismatches: 1  
Query Match: 39.1% Indels: 0  
RESULT 96  
ID AAV87407 standard; cDNA; 548 BP.  
DE EST clone CF85.  
PN WO9845435-A2.  
PD 15-OCT-1998.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 98.8% Conservative: 2  
Best Local Similarity: 97.6% Mismatches: 1  
Query Match: 38.2% Indels: 2



RESULT 97  
ID AAH05206 standard; cDNA; 855 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:2041.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 73.9%  
Best Local Similarity: 72.2%  
Query Match: 35.8%  
Conservative: 4  
Mismatches: 24  
Indels: 40  
RESULT 98  
ID AAH07904 standard; cDNA; 805 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:4739.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 94.1%  
Best Local Similarity: 92.9%  
Query Match: 35.3%  
Conservative: 2  
Mismatches: 5  
Indels: 5  
RESULT 99  
ID AAV89087 standard; cDNA; 422 BP.  
DE EST clone CC335.  
PN WO9845436-A2.  
PD 15-OCT-1998.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 100.0%  
Best Local Similarity: 98.5%  
Query Match: 28.6%  
Conservative: 2  
Mismatches: 0  
Indels: 0  
RESULT 100  
ID ABX53012 standard; cDNA; 402 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #2941.  
PN US2002137160-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Percent Similarity: 82.6%  
Best Local Similarity: 72.0%  
Query Match: 22.5%  
Conservative: 14  
Mismatches: 22  
Indels: 1  
RESULT 101  
ID ADP28197 standard; DNA; 141 BP.  
DE Human secreted protein encoding sequence SEQ ID #195.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 11.8%  
Conservative: 0  
Mismatches: 0  
Indels: 0  
RESULT 102  
ID AAC05822 standard; cDNA; 295 BP.  
DE Human secreted protein 5' EST, SEQ ID NO: 9897.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GENSET.  
Percent Similarity: 91.5%  
Best Local Similarity: 91.5%  
Query Match: 10.9%  
Conservative: 0  
Mismatches: 3  
Indels: 2  
RESULT 103  
ID AAA45200 standard; cDNA; 242 BP.  
DE Human secreted expressed sequence tag SEQ ID NO:1775.  
PN WO200021991-A1.  
PD 20-APR-2000.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 95.9%  
Best Local Similarity: 93.9%  
Query Match: 10.3%  
Conservative: 1  
Mismatches: 2  
Indels: 0  
RESULT 104  
ID AAD33828 standard; cDNA; 1766 BP.  
DE Human secreted protein-encoding gene 17 cDNA clone HLDQZ72, SEQ ID NO:27.  
PN WO200224719-A1.  
PD 28-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 40.6%  
Conservative: 66

Best Local Similarity: 25.9%  
Query Match: 9.3%  
Mismatches: 162  
Indels: 106  
RESULT 105  
ID ADQ86436 standard; cDNA; 2050 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3308.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 34.5%  
Best Local Similarity: 23.4%  
Query Match: 9.2%  
Conservative: 60  
Mismatches: 170  
Indels: 187  
RESULT 106  
ID ADQ83349 standard; cDNA; 2050 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #163.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 34.5%  
Best Local Similarity: 23.4%  
Query Match: 9.2%  
Conservative: 60  
Mismatches: 170  
Indels: 187  
RESULT 107  
ID ADL91882 standard; cDNA; 2058 BP.  
DE Human PRO60929 encoding cDNA SEQ ID NO:103.  
PN WO2004024076-A2.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 34.5%  
Best Local Similarity: 23.4%  
Query Match: 9.2%  
Conservative: 60  
Mismatches: 170  
Indels: 187  
RESULT 108  
ID ADQ22215 standard; DNA; 2535 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5035.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 34.5%  
Best Local Similarity: 23.4%  
Query Match: 9.2%  
Conservative: 60  
Mismatches: 170  
Indels: 187  
RESULT 109  
ID AAA96478 standard; cDNA; 1716 BP.  
DE CDNA encoding a human transmembrane protein.  
PN WO200056891-A2.  
PD 28-SEP-2000.  
PA (INCY-) INCYTE PHARM INC.  
Percent Similarity: 32.6%  
Best Local Similarity: 22.2%  
Query Match: 8.9%  
Conservative: 55  
Mismatches: 143  
Indels: 215  
RESULT 110  
ID ABX71003 standard; cDNA; 1826 BP.  
DE Novel human cDNA sequence #228.  
PN WO200281731-A2.  
PD 17-OCT-2002.  
PA (HYSE-) HYSEQ INC.  
PA (GOOD/) GOODRICH R W.  
Percent Similarity: 34.5%  
Best Local Similarity: 23.2%  
Query Match: 8.9%  
Conservative: 61  
Mismatches: 170  
Indels: 187  
RESULT 111  
ID ADL25760 standard; cDNA; 1987 BP.  
DE Human cancer suppressing protein cDNA #13.  
PN CN1403478-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV CO LTD.  
Percent Similarity: 34.3%  
Best Local Similarity: 23.2%  
Query Match: 8.8%  
Conservative: 60  
Mismatches: 171  
Indels: 187  
RESULT 112  
ID ADL25762 standard; cDNA; 1987 BP.  
DE Human cancer suppressing protein cDNA #14.

PN	CN1403478-A.
PD	19-MAR-2003.
PA	(SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.
Percent Similarity:	34.3%
Conservative:	60
Mismatches:	171
Indels:	187
Query Match:	8.8%
RESULT 113	
ID	ABA08275 standard; cDNA; 2095 BP.
DE	Human secreted protein homologue-encoding cdNA, SEQ ID NO:51.
PN	WO200157188-A2.
PD	09-AUG-2001.
PA	(HYSE-) HYSEQ INC.
Percent Similarity:	34.3%
Conservative:	60
Mismatches:	171
Indels:	187
Query Match:	8.8%
RESULT 114	
ID	AAA26405 standard; cDNA; 1642 BP.
DE	Human secreted protein gene 60 SEQ ID NO:70.
PN	WO200006698-A1.
PD	10-FEB-2000.
PA	(HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:	37.1%
Conservative:	64
Mismatches:	166
Indels:	121
Query Match:	8.8%
RESULT 115	
ID	ADA56613 standard; DNA; 1642 BP.
DE	Gene encoding human secreted protein #424.
PN	WO2002102994-A2.
PD	27-DEC-2002.
PA	(HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:	37.1%
Conservative:	64
Mismatches:	166
Indels:	121
Query Match:	8.8%
RESULT 116	
ID	ADL71466 standard; cDNA; 1642 BP.
DE	Novel human secreted protein cdNA seqid 70.
PN	US2004034196-A1.
PD	19-FEB-2004.
PA	(KOMA/) KOMATSOULIS G A.
PA	(ROSE/) ROSEN C A.
PA	(RUBE/) RUBEN S M.
PA	(DUAN/) DUAN D R.
PA	(MOOR/) MOORE P A.
PA	(SHIY/) SHI Y.
PA	(LAFL/) LAFLEUR D W.
PA	(WEIY/) WEI Y.
Percent Similarity:	37.1%
Conservative:	64
Mismatches:	166
Indels:	121
Query Match:	8.8%
RESULT 117	
ID	AEL28822 standard; cDNA; 1642 BP.
DE	Human secreted protein coding sequence, SEQ ID 802.
PN	US2006223088-A1.
PD	05-OCT-2006.
Percent Similarity:	37.1%
Conservative:	64
Mismatches:	166
Indels:	121
Query Match:	8.8%
RESULT 118	
ID	ADA56245 standard; DNA; 1895 BP.
DE	Gene encoding human secreted protein #424.
PN	WO2002102994-A2.
PD	27-DEC-2002.
PA	(HUMA-) HUMAN GENOME SCI INC.
Percent Similarity:	34.4%
Conservative:	59
Mismatches:	169
Indels:	189
Query Match:	8.8%
RESULT 119	
ID	AEL28454 standard; cDNA; 1895 BP.
DE	Human secreted protein coding sequence, SEQ ID 434.
PN	US2006223088-A1.
PD	05-OCT-2006.
Percent Similarity:	34.4%
Conservative:	59
Mismatches:	169
Indels:	189
Query Match:	8.8%

Query Match:	8.8%	Indels:	189
RESULT 120			
ID ACH44978 standard; cDNA; 478 BP.			
DE Human foetal brain cDNA #5703.			
PN US2003073623-A1.			
PD 17-APR-2003.			
PA (DRMA/) DRMANAC R T.			
PA (LABA/) LABAT I.			
PA (STAC/) STACHE-CRAIN B.			
PA (DICK/) DICKSON M C.			
PA (JONE/) JONES L W.			
Percent Similarity: 51.2%		Conservative: 0	
Best Local Similarity: 51.2%		Mismatches: 5	
Query Match: 8.5%		Indels: 35	
RESULT 121			
ID AAS21355 standard; cDNA; 1661 BP.			
DE Human cDNA sequence encoding for PRO4315 polypeptide.			
PN WO200140466-A2.			
PD 07-JUN-2001.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 31.2%		Conservative: 49	
Best Local Similarity: 22.0%		Mismatches: 167	
Query Match: 8.5%		Indels: 196	
RESULT 122			
ID ACA03714 standard; cDNA; 1661 BP.			
DE cDNA encoding human PRO polypeptide #112.			
PN US2003036180-A1.			
PD 20-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 31.2%		Conservative: 49	
Best Local Similarity: 22.0%		Mismatches: 167	
Query Match: 8.5%		Indels: 196	
RESULT 123			
ID ABX89252 standard; cDNA; 1661 BP.			
DE DNA encoding novel secreted and transmembrane protein PRO4315.			
PN US2003017563-A1.			
PD 23-JAN-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 31.2%		Conservative: 49	
Best Local Similarity: 22.0%		Mismatches: 167	
Query Match: 8.5%		Indels: 196	
RESULT 124			
ID ACD41906 standard; cDNA; 1661 BP.			
DE Human secreted/transmembrane protein (PRO) cDNA #112.			
PN US2003036179-A1.			
PD 20-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 31.2%		Conservative: 49	
Best Local Similarity: 22.0%		Mismatches: 167	
Query Match: 8.5%		Indels: 196	
RESULT 125			
ID ACA04135 standard; cDNA; 1661 BP.			
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 223.			
PN US2003032155-A1.			
PD 13-FEB-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 31.2%		Conservative: 49	
Best Local Similarity: 22.0%		Mismatches: 167	
Query Match: 8.5%		Indels: 196	
RESULT 126			
ID ADA5742 standard; cDNA; 1661 BP.			
DE Novel human secreted and transmembrane protein PRO4315 cDNA.			
PN US2003023228-A1.			
PD 30-JAN-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 31.2%		Conservative: 49	
Best Local Similarity: 22.0%		Mismatches: 167	
Query Match: 8.5%		Indels: 196	
RESULT 127			
ID ADA76173 standard; cDNA; 1661 BP.			
DE Human PRO polynucleotide #112.			
PN US2003073212-A1.			
PD 17-APR-2003.			
PA (GETH ) GENENTECH INC.			
Percent Similarity: 31.2%		Conservative: 49	
Best Local Similarity: 22.0%		Mismatches: 167	
Query Match: 8.5%		Indels: 196	

PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 128  
ID ADA18823 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 129  
ID ADA61446 standard; cDNA; 1661 BP.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 130  
ID ADB19231 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 131  
ID ADB27772 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 132  
ID ADA86251 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 133  
ID ADB15815 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 134  
ID ADA47601 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 135  
ID ADA67396 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 136  
ID ADB30403 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 137  
ID ADA85699 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 138  
ID ADA96911 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 139  
ID ADA79215 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 140  
ID ADA87354 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 141  
ID ADB16556 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 142  
ID ADA91648 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 143  
ID ADB14711 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 144  
ID ADA67396 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Conservative: 49  
Mismatches: 167  
Indels: 196



Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 144  
ID ADB18672 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 145  
ID ADA93887 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 146  
ID ADB19783 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 147  
ID ADB13095 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 148  
ID ACD98535 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 149  
ID ADA74349 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 150  
ID ADB24582 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 151  
ID ADA82106 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196

Query Match: 8.5% Indels: 196  
RESULT 152  
ID ADA75069 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 153  
ID ADA85147 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 154  
ID ADA84595 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 155  
ID ADB29851 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 156  
ID ADA80379 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 157  
ID ADA75621 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 158  
ID ADA46846 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 159  
ID ADB25142 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196

RESULT 160  
ID ADA93318 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US200307721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 161  
ID ADB26668 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 162  
ID ADB30955 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 163  
ID ADA60883 standard; cDNA; 1661 BP.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 164  
ID ADB24030 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US200307714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 165  
ID ADA96359 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 166  
ID ADA80931 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 167  
ID ADA95807 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 168  
ID ADA95807 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196

ID ADB26116 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 169  
ID ADB21601 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 170  
ID ADA77380 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 171  
ID ADB18120 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 172  
ID ADA86803 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 173  
ID ADA87906 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 174  
ID ADA46294 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 175  
ID ADB28324 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 176  
ID ADB28876 standard; cDNA; 1661 BP.

DE CDNA encoding human PRO polypeptide #112.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 177  
ID ADA76828 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 178  
ID ADA88458 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 179  
ID ADA97463 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 180  
ID ADB27220 standard; cDNA; 1661 BP.  
DE CDNA encoding human PRO polypeptide #112.  
PN US2003022339-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 181  
ID ADB22153 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 182  
ID ADA66844 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 183  
ID ADB22705 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 184  
ID ADB23478 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US2003077712-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 185  
ID ADA92200 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 186  
ID ADB15263 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 187  
ID ADB38515 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 188  
ID ADB37963 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 189  
ID ADB66435 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 190  
ID ADB89515 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 191  
ID ADB90247 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 192  
ID ADB39348 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.



Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 193  
ID ADB46971 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 194  
ID ADB86578 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 195  
ID ADB77183 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 196  
ID ADB34340 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US200307717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 197  
ID ADB35444 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US200307719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 198  
ID ADB33788 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US200307716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 199  
ID ADB34892 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US200307718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 200  
ID ADB35996 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US200307720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196

Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 201  
ID ADB46391 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 202  
ID ADC50264 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 203  
ID ADC71811 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 204  
ID ADC59790 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 205  
ID ADC52797 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID223.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 206  
ID ADC57151 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID223.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 207  
ID ADC60342 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 208  
ID ADC50817 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 209  
ID ADB35996 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide SEQ ID NO 223.  
PN US200307720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196

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Query Match: 8.5% Indels: 196
RESULT 209
ID ADC5344 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 210
ID ADC54442 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 211
ID ADC53403 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 212
ID ADC58926 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 213
ID ADC55804 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 214
ID ADC58374 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID223.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 215
ID ADD03048 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 216
ID ADC90040 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 217
ID ADC69459 standard; cDNA; 1661 BP.
DE cDNA encoding human PRO polypeptide #112.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 218
ID ADC48348 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 219
ID ADD09877 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 220
ID ADD04452 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 221
ID ADC80408 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 222
ID ADD10915 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 223
ID ADC47796 standard; cDNA; 1661 BP.
DE Human PRO polynucleotide #112.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 224
ID ADC79856 standard; cDNA; 1661 BP.
DE Novel human secreted and transmembrane protein PRO4315 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 31.2%
Best Local Similarity: 22.0%
Query Match: 8.5%
Conservative: 49
Mismatches: 167
Indels: 196
RESULT 225
```

ID ADD09325 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 226  
ID ADD41038 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 227  
ID ADD52177 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 228  
ID ADD52917 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 229  
ID ADD53469 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 230  
ID ADD51625 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 231  
ID ADD02424 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 232  
ID ADD01858 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 233  
ID ADD54040 standard; cDNA; 1661 BP.

DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 234  
ID ADD92357 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 235  
ID ADD91253 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 236  
ID ADE03867 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 237  
ID ADE32164 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 238  
ID ADE22096 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 239  
ID ADD79320 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 240  
ID ADE41856 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatches: 167  
Indels: 196  
RESULT 241  
ID ADE17673 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.





PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 258  
ID ADE04535 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 259  
ID ADE92664 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 260  
ID ADG21373 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 261  
ID ADG23014 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 262  
ID ADF97349 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 263  
ID ADG80413 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 264  
ID ADG79861 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 265  
ID ADH55153 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Conservative: 49  
Mismatch: 167  
Indel: 196

Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 266  
ID ADH55705 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 267  
ID ADI63924 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 268  
ID ADI64873 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 269  
ID ADI63372 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 270  
ID ADH81786 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 271  
ID ADH81234 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 272  
ID ACD23964 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 273  
ID ACA67105 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
Conservative: 49  
Mismatch: 167  
Indel: 196

Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 274  
ID ADM82403 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 275  
ID ADN15802 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 276  
ID ADN16431 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 277  
ID ADN15250 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 278  
ID ADN14698 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 279  
ID ADC80960 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 280  
ID ADD76408 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 281  
ID ADD87772 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196

Query Match: 8.5% Indels: 196  
RESULT 282  
ID ADD86176 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 283  
ID ADE75624 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 284  
ID ADE23200 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 285  
ID ADE23752 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 286  
ID ADE24395 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 287  
ID ADD87220 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 288  
ID ADE89086 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 289  
ID ADE18225 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196



RESULT 290  
ID ADE88534 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 291  
ID ADE94554 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 292  
ID ADE90965 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 293  
ID ADE95106 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 294  
ID ADE93216 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 295  
ID ADF34797 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 296  
ID ADE92112 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 297  
ID ADE90413 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 298  
ID ADF99024 standard; cDNA; 1661 BP.

ID ADE91560 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 299  
ID ADG02139 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 300  
ID ADG21925 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 301  
ID ADG1995 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 302  
ID ADF97901 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 303  
ID ADG24118 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 304  
ID ADF98472 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 305  
ID ADG03303 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%      Conservative: 49  
Best Local Similarity: 22.0%      Mismatches: 167  
Query Match: 8.5%      Indels: 196  
RESULT 306  
ID ADF99024 standard; cDNA; 1661 BP.

DE Human PRO polynucleotide #112.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 307  
ID ADG16609 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 308  
ID ADG05068 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 309  
ID ADG19335 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 310  
ID ADG13172 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 311  
ID ADG08229 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 312  
ID ADG15399 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 313  
ID ADF96797 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 314  
ID ADG05982 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.

PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 315  
ID ADG23566 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 316  
ID ADG03855 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 317  
ID ADG24756 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 318  
ID ADG07053 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 319  
ID ADG07605 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 320  
ID ADG55100 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 321  
ID ADG60764 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 322  
ID ADG61868 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207428-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 323  
ID ADG82069 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 324  
ID ADG57308 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 325  
ID ADG56756 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 326  
ID ADG55652 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 327  
ID ADG58412 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 328  
ID ADG70778 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 329  
ID ADG57860 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 330  
ID ADG53444 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207415-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 331  
ID ADG71330 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 332  
ID ADG81517 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 333  
ID ADH30479 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 334  
ID ADH11846 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 335  
ID ADG52268 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 336  
ID ADG53996 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 337  
ID ADG80965 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 338  
ID ADG56204 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2%  
Best Local Similarity: 22.0%  
Query Match: 8.5%  
RESULT 339  
ID ADG53444 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207415-A1.  
PD 06-NOV-2003.

Conservative: 49  
Mismatches: 167  
Indels: 196



Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 339  
ID ADH12470 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 340  
ID ADG61316 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 341  
ID ADH28403 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 342  
ID ADG54548 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 343  
ID ADG59588 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 344  
ID ADI81012 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003207361-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 345  
ID ADG09755 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 346  
ID ADI15226 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196

Query Match: 8.5% Indels: 196  
RESULT 347  
ID ADG09103 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 348  
ID ADI14558 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 349  
ID ADI18153 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 350  
ID ADJ63434 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 351  
ID ADJ77329 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 352  
ID ADJ65451 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 353  
ID ADM27587 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 354  
ID ADM42311 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196

RESULT 355  
ID ADM28173 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 356  
ID ADI95655 standard; cDNA; 1661 BP.  
DE cDNA encoding human PRO polypeptide #112.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 357  
ID ADI96207 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 358  
ID ADS32159 standard; cDNA; 1661 BP.  
DE Novel human secreted and transmembrane protein PRO4315 cDNA.  
PN US2004203125-A1.  
PD 14-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 359  
ID ADT03143 standard; cDNA; 1661 BP.  
DE Human PRO polynucleotide #112.  
PN US2004214269-A1.  
PD 28-OCT-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 360  
ID ADZ03194 standard; cDNA; 1661 BP.  
DE Human secreted/transmembrane PRO4315 cDNA.  
PN US2005074837-A1.  
PD 07-APR-2005.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 361  
ID AEB13940 standard; cDNA; 1661 BP.  
DE Cancer cell diagnosis method-related human cDNA sequence - SEQ ID 223.  
PN US2005153396-A1.  
PD 14-JUL-2005.  
PA (BAKE/) BAKER K P.  
PA (BERE/) BERESINI M.  
PA (DEFO/) DEFORGE L.  
PA (DESN/) DESNOYERS L.  
PA (FILV/) FILVAROFF E.  
PA (GAOW/) GAO W.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (SHER/) SHERWOOD S.  
PA (SMIT/) SMITH V.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.

PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
PA (ZHAN/) ZHANG Z.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 362  
ID AED86138 standard; cDNA; 1661 BP.  
DE Human PRO cDNA, seq id 223.  
PN US2005245730-A1.  
PD 03-NOV-2005.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 363  
ID AEG58085 standard; cDNA; 1661 BP.  
DE Human PRO4315 cDNA SEQ ID NO: 223.  
PN US2006073568-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 364  
ID AEI43730 standard; cDNA; 1661 BP.  
DE Human cancer-related PRO protein coding sequence - SEQ ID 223.  
PN US2006040351-A1.  
PD 23-FEB-2006.  
PA (BAKE/) BAKER K P.  
PA (BERE/) BERESINI M.  
PA (DEFO/) DEFORGE L.  
PA (DESN/) DESNOYERS L.  
PA (FILV/) FILVAROFF E.  
PA (GAOW/) GAO W.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (SHER/) SHERWOOD S.  
PA (SMIT/) SMITH V.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WATA/) WATANABE C K.  
PA (WOOD/) WOOD W I.  
PA (ZHAN/) ZHANG Z.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 365  
ID AEI23813 standard; cDNA; 1661 BP.  
DE Human secreted/transmembrane protein PRO4315 cDNA, SEQ ID NO:223.  
PN EP1672070-A2.  
PD 21-JUN-2006.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 31.2% Conservative: 49  
Best Local Similarity: 22.0% Mismatches: 167  
Query Match: 8.5% Indels: 196  
RESULT 366  
ID AEA61164 standard; DNA; 30542 BP.  
DE Human MUC2 gene genomic sequence SEQ ID NO:74.  
PN US2005130172-A1.  
PD 16-JUN-2005.  
PA (FARB ) BAYER CORP.  
Percent Similarity: 34.1% Conservative: 35  
Best Local Similarity: 25.5% Mismatches: 176  
Query Match: 7.9% Indels: 95  
RESULT 367  
ID AAI29504 standard; cDNA; 15720 BP.  
DE C899P determined cDNA sequence.  
PN WO200149716-A2.  
PD 12-JUL-2001.  
PA (CORI-) CORIXA CORP.

Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 368  
ID ABL62358 standard; DNA; 15720 BP.  
DE Colon adenocarcinoma related gene sequence SEQ ID NO:695.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 369  
ID ABZ33690 standard; cDNA; 15720 BP.  
DE Human colon tumour cDNA for clone C899P SEQ ID NO:1058.  
PN WO200283070-A2.  
PD 24-OCT-2002.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 370  
ID ACD13431 standard; cDNA; 15720 BP.  
DE Human DNA encoding a p53 modifier, SEQ ID 103.  
PN WO200299122-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 371  
ID AAD63141 standard; DNA; 15720 BP.  
DE Human mucin 2 (MUC2) DNA.  
PN US2003190656-A1.  
PD 09-OCT-2003.  
PA (WANG/) WANG Y.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 372  
ID AAD62742 standard; DNA; 15720 BP.  
DE Human mucin 2 (MUC2) DNA.  
PN US2003194733-A1.  
PD 16-OCT-2003.  
PA (WANG/) WANG Y.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 373  
ID ADP88237 standard; cDNA; 15720 BP.  
DE Colon cancer marker gene MUC2, SEQ ID NO:14.  
PN EP1349104-A2.  
PD 01-OCT-2003.  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 374  
ID ADP88236 standard; cDNA; 15720 BP.  
DE Colon cancer marker gene NOX1, SEQ ID NO:13.  
PN EP1349104-A2.  
PD 01-OCT-2003.  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 375  
ID ADQ29628 standard; DNA; 15720 BP.  
DE Human colorectal cancer-associated protein coding sequence #50.  
PN EP1439393-A2.  
PD 21-JUL-2004.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 376  
ID ADQ80264 standard; cDNA; 15720 BP.  
DE Intestinal/tracheal mucin 2 cDNA.  
PN WO2004063709-A2.  
PD 29-JUL-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 377  
ID ADZ49011 standard; DNA; 15720 BP.  
DE Insulin signaling pathway related gene, SEQ ID 340.  
PN US2005085436-A1.  
PD 21-APR-2005.  
PA (LIHH/) LI H.  
PA (MAJJ/) MA J.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 378  
ID AEA04440 standard; cDNA; 15720 BP.  
DE Human cDNA from gene under-expressed in cancer, MUC2.  
PN WO2005044990-A2.  
PD 19-MAY-2005.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 379  
ID AEA27625 standard; cDNA; 15720 BP.  
DE Human intestinal mucin cDNA.  
PN WO2005047321-A2.  
PD 26-MAY-2005.  
PA (UYCR-) UNIV CREIGHTON.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 380  
ID AEF69940 standard; DNA; 15720 BP.  
DE Colorectal cancer-associated marker DNA SEQ ID NO:118.  
PN WO2006015047-A2.  
PD 09-FEB-2006.  
PA (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 381  
ID AEF96654 standard; DNA; 15720 BP.  
DE Colorectal carcinoma (CRC) detection method-related human gene SeqID82.  
PN WO2006015742-A2.  
PD 16-FEB-2006.  
PA (UYER-) UNIV ERLANGEN-NUERNBURG.  
Percent Similarity: 35.0% Conservative: 31  
Best Local Similarity: 24.8% Mismatches: 102  
Query Match: 7.8% Indels: 98  
RESULT 382  
ID ADX97496 standard; DNA; 10371 BP.  
DE Pancreatic cancer associated human protein encoding DNA, SEQ ID 44.  
PN EP1471075-A2.  
PD 27-OCT-2004.  
PA (HINZ/) HINZMANN B.  
PA (ROSE/) ROSENTHAL A.  
PA (PILA/) PILARSKY C.  
PA (DAHL/) DAHL E.  
PA (SPEC/) SPECHT T.  
PA (LICH/) LICHTNER R.  
Percent Similarity: 35.9% Conservative: 55  
Best Local Similarity: 22.4% Mismatches: 172



Query Match: 7.8% Indels: 91  
RESULT 383  
ID AEA08147 standard; DNA; 14094 BP.  
DE Human mucin 17 (MUC17SEC) coding sequence - SEQ ID 2.  
PN US2005100925-A1.  
PD 12-MAY-2005.  
PA (BATR/) BATRA S.  
PA (MONI/) MONIAUX N.  
Percent Similarity: 39.0% Conservative: 68  
Best Local Similarity: 22.9% Mismatches: 164  
Query Match: 7.4% Indels: 95  
RESULT 384  
ID AEA08146 standard; DNA; 14246 BP.  
DE Human mucin 17 coding sequence - SEQ ID 1.  
PN US2005100925-A1.  
PD 12-MAY-2005.  
PA (BATR/) BATRA S.  
PA (MONI/) MONIAUX N.  
Percent Similarity: 39.0% Conservative: 68  
Best Local Similarity: 22.9% Mismatches: 164  
Query Match: 7.4% Indels: 95  
RESULT 385  
ID AEB56450 standard; cDNA; 17847 BP.  
DE Radiochemotherapy response detection associated cDNA SEQ ID NO 25.  
PN WO2005073411-A1.  
PD 11-AUG-2005.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Percent Similarity: 37.0% Conservative: 31  
Best Local Similarity: 27.6% Mismatches: 101  
Query Match: 7.4% Indels: 107  
RESULT 386  
ID ABZ11530 standard; cDNA; 1638 BP.  
DE Human polynucleotide SEQ ID NO 412.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 39.9% Conservative: 42  
Best Local Similarity: 24.4% Mismatches: 114  
Query Match: 7.3% Indels: 49  
RESULT 387  
ID ADM44048 standard; cDNA; 1638 BP.  
DE Novel human arginine-rich protein cDNA #412.  
PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Percent Similarity: 39.9% Conservative: 42  
Best Local Similarity: 24.4% Mismatches: 114  
Query Match: 7.3% Indels: 49  
RESULT 388  
ID ABL28511 standard; DNA; 2753 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37006.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 37.5% Conservative: 60  
Best Local Similarity: 22.9% Mismatches: 149  
Query Match: 7.3% Indels: 110  
RESULT 389  
ID ABL28510 standard; DNA; 22622 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37003.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 37.5% Conservative: 60  
Best Local Similarity: 22.9% Mismatches: 149  
Query Match: 7.3% Indels: 110  
RESULT 390  
ID ADQ22365 standard; DNA; 6564 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5185.  
PN WO2004048938-A2.  
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 391  
ID AEL84674 standard; cDNA; 8106 BP.  
DE Tumor marker gene BAT2D1 cDNA SEQ ID NO 41.  
PN WO2006110593-A2.  
PD 19-OCT-2006.  
PA (MACR-) MACROGENICS INC.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 392  
ID ACF12869 standard; cDNA; 10174 BP.  
DE Human cervical cancer cell marker protein SEQ ID NO:82.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 393  
ID ADQ59188 standard; cDNA; 10174 BP.  
DE MSI-H carcinoma cDNA sequence SEQ ID NO:25.  
PN KR2004008012-A.  
PD 28-JAN-2004.  
PA (KIMH/) KIM H G.  
PA (KIMN/) KIM N G.  
PA (LEEJ/) LEE J S.  
PA (RHEE/) RHEE H S.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 394  
ID ADX05906 standard; DNA; 10174 BP.  
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 471.  
PN WO2005012875-A2.  
PD 10-FEB-2005.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 395  
ID ADY19013 standard; DNA; 10174 BP.  
DE DNA encoding a PRO polypeptide, SEQ ID NO 4819.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 396  
ID AEF74590 standard; DNA; 10174 BP.  
DE Human polynucleotide #104.  
PN WO2006013561-A2.  
PD 09-FEB-2006.  
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV LTD.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 397  
ID AAF28060 standard; cDNA; 10347 BP.  
DE Human 07CG27 gene cDNA.  
PN WO200116291-A2.  
PD 08-MAR-2001.  
PA (MYRI-) MYRIAD GENETICS INC.  
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 398  
ID AAF28060 standard; cDNA; 10347 BP.  
DE Human 07CG27 gene cDNA.  
PN WO200116291-A2.  
PD 08-MAR-2001.  
PA (MYRI-) MYRIAD GENETICS INC.  
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
Percent Similarity: 39.5% Conservative: 39  
Best Local Similarity: 26.8% Mismatches: 127  
Query Match: 7.2% Indels: 59  
RESULT 399

ID ADQ97652 standard; DNA; 10361 BP.  
DE Human Cancer associated sequence HR10-021, SEQ ID 629.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 39.5%  
Best Local Similarity: 26.8%  
Query Match: 7.2%  
Indels: 59  
Conservative: 39  
Mismatches: 127  
RESULT 399  
ID AEL84675 standard; DNA; 10383 BP.  
DE Tumor marker gene BAT2D1 DNA SEQ ID NO 42.  
PN WO2006110593-A2.  
PD 19-OCT-2006.  
PA (MACR-) MACROGENICS INC.  
Percent Similarity: 39.5%  
Best Local Similarity: 26.8%  
Query Match: 7.2%  
Indels: 59  
Conservative: 39  
Mismatches: 127  
RESULT 400  
ID ADT07432 standard; DNA; 7140 BP.  
DE Human colon specific nucleic acid (CSNA) #19.  
PN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 33.2%  
Best Local Similarity: 23.8%  
Query Match: 7.2%  
Indels: 139  
Conservative: 37  
Mismatches: 125  
RESULT 401  
ID ADT07433 standard; DNA; 7925 BP.  
DE Human colon specific nucleic acid (CSNA) #20.  
PN WO2004089301-A2.  
PD 21-OCT-2004.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 33.2%  
Best Local Similarity: 23.8%  
Query Match: 7.2%  
Indels: 139  
Conservative: 37  
Mismatches: 125  
RESULT 402  
ID ADI28074 standard; cDNA; 1604 BP.  
DE ECMCAD gene clone 1825473CB1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 34.0%  
Best Local Similarity: 24.4%  
Query Match: 7.2%  
Indels: 98  
Conservative: 36  
Mismatches: 153  
RESULT 403  
ID ABQ99543 standard; cDNA; 2388 BP.  
DE Human coding sequence SEQ ID 276.  
PN WO200259260-A2.  
PD 01-AUG-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 34.0%  
Best Local Similarity: 24.4%  
Query Match: 7.2%  
Indels: 98  
Conservative: 36  
Mismatches: 153  
RESULT 404  
ID ADP81023 standard; DNA; 1779 BP.  
DE Human ovarian specific gene, SEQ ID No 57.  
PN WO2004053079-A2.  
PD 24-JUN-2004.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 33.1%  
Best Local Similarity: 22.1%  
Query Match: 7.1%  
Indels: 203  
Conservative: 60  
Mismatches: 162  
RESULT 405  
ID AAD08051 standard; cDNA; 2429 BP.  
DE Human extracellular matrix and cell adhesion molecule-7 (XMAD-7) cDNA.  
PN WO200142285-A2.  
PD 14-JUN-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 34.0%  
Best Local Similarity: 24.4%  
Query Match: 7.1%  
Indels: 98  
Conservative: 36  
Mismatches: 153  
RESULT 406  
ID AEB29656 standard; cDNA; 7382 BP.

DE Human Mucin 5 (subtypes A and C), cDNA SEQ ID 7.  
PN WO2005067667-A2.  
PD 28-JUL-2005.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Percent Similarity: 33.2%  
Best Local Similarity: 23.1%  
Query Match: 7.1%  
Indels: 109  
Conservative: 38  
Mismatches: 142  
RESULT 407  
ID ABL27926 standard; DNA; 2300 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35251.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 34.6%  
Best Local Similarity: 24.8%  
Query Match: 7.1%  
Indels: 68  
Conservative: 34  
Mismatches: 160  
RESULT 408  
ID ABL27928 standard; DNA; 3161 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35257.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 34.6%  
Best Local Similarity: 24.8%  
Query Match: 7.1%  
Indels: 68  
Conservative: 34  
Mismatches: 160  
RESULT 409  
ID AAT80043 standard; DNA; 40875 BP.  
DE Insert from cosmid 109.  
PN WO9704106-A2.  
PD 06-FEB-1997.  
PA (INNO-) INNOGENETICS NV.  
Percent Similarity: 35.9%  
Best Local Similarity: 23.3%  
Query Match: 7.1%  
Indels: 120  
Conservative: 53  
Mismatches: 151  
RESULT 410  
ID ADC21532 standard; DNA; 5403 BP.  
DE T. cruzi trans-sialidase gene, TS, clone 7F.  
PN US2002137667-A1.  
PD 26-SEP-2002.  
PA (TUFT) UNIV TUFTS.  
Percent Similarity: 36.1%  
Best Local Similarity: 26.9%  
Query Match: 7.0%  
Indels: 74  
Conservative: 30  
Mismatches: 137  
RESULT 411  
ID AEL43167 standard; DNA; 5403 BP.  
DE T. cruzi neuraminidase (TCNA) gene.  
PN US2006229247-A1.  
PD 12-OCT-2006.  
PA (CHUE/) CHUENKOVA M.  
PA (PERE/) PEREIRA M A.  
Percent Similarity: 36.1%  
Best Local Similarity: 26.9%  
Query Match: 7.0%  
Indels: 74  
Conservative: 30  
Mismatches: 137  
RESULT 412  
ID AEF22095 standard; DNA; 2380 BP.  
DE Human non-basal transcription modulator splice variant DNA #237.  
PN WO2006005042-A2.  
PD 12-JAN-2006.  
PA (CEMI-) CEMINES INC.  
Percent Similarity: 34.0%  
Best Local Similarity: 22.2%  
Query Match: 7.0%  
Indels: 137  
Conservative: 56  
Mismatches: 176  
RESULT 413  
ID ADM02761 standard; cDNA; 2922 BP.  
DE Human cDNA of the invention SEQ ID NO:1446.  
PN EPI347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 34.0%  
Best Local Similarity: 22.2%  
Query Match: 7.0%  
Indels: 137  
Conservative: 56  
Mismatches: 176  
RESULT 414  
ID AEC85691 standard; cDNA; 2922 BP.

DE Human cDNA clone PERIC20003870, SEQ ID 1446.  
PN EP1580263-A1.  
PD 28-SEP-2005.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 34.0% Conservative: 56  
Best Local Similarity: 22.2% Mismatches: 176  
Query Match: 7.0% Indels: 137  
RESULT 415  
ID ABQ61152 standard; cDNA; 13715 BP.  
DE MUC5B partial gene protein encoding sequence.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 35.9% Conservative: 37  
Best Local Similarity: 25.4% Mismatches: 133  
Query Match: 7.0% Indels: 94  
RESULT 416  
ID ACH89790 standard; DNA; 904 BP.  
DE Human genome derived single exon probe #22985.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 45.3% Conservative: 29  
Best Local Similarity: 30.0% Mismatches: 87  
Query Match: 7.0% Indels: 18  
RESULT 417  
ID ADQ59189 standard; DNA; 81679 BP.  
DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:26.  
PN KR2004008012-A.  
PD 28-JAN-2004.  
PA (KIMH/) KIM H G.  
PA (KIMN/) KIM N G.  
PA (LEEJ/) LEE J S.  
PA (RHEE/) RHEE H S.  
Percent Similarity: 45.3% Conservative: 29  
Best Local Similarity: 30.0% Mismatches: 87  
Query Match: 7.0% Indels: 18  
RESULT 418  
ID ADQ97651 standard; DNA; 127943 BP.  
DE Human cancer associated sequence HD10-021, SEQ ID 628.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 45.3% Conservative: 29  
Best Local Similarity: 30.0% Mismatches: 87  
Query Match: 7.0% Indels: 18  
RESULT 419  
ID ABL28828 standard; DNA; 4755 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37957.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.9% Conservative: 55  
Best Local Similarity: 24.0% Mismatches: 160  
Query Match: 6.9% Indels: 108  
RESULT 420  
ID ADU01598 standard; cDNA; 3711 BP.  
DE Novel human polynucleotide seqid 65.  
PN WO2004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 38.7% Conservative: 57  
Best Local Similarity: 22.9% Mismatches: 154  
Query Match: 6.9% Indels: 70  
RESULT 421  
ID ADL13221 standard; cDNA; 1297 BP.  
DE Human steroid-induced C3A liver cell cDNA #950.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 35.9% Conservative: 38

Best Local Similarity: 23.8% Mismatches: 129  
Query Match: 6.9% Indels: 73  
RESULT 422  
ID AAL04593 standard; DNA; 13555 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 7281.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 33.3% Conservative: 54  
Best Local Similarity: 21.9% Mismatches: 179  
Query Match: 6.9% Indels: 137  
RESULT 423  
ID ABL97516 standard; DNA; 13555 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2168.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC..  
Percent Similarity: 33.3% Conservative: 54  
Best Local Similarity: 21.9% Mismatches: 179  
Query Match: 6.9% Indels: 137  
RESULT 424  
ID AAS34526 standard; DNA; 13555 BP.  
DE Human DNA for a novel foetal antigen, SEQ ID No 1950.  
PN WO200155312-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 33.3% Conservative: 54  
Best Local Similarity: 21.9% Mismatches: 179  
Query Match: 6.9% Indels: 137  
RESULT 425  
ID ABL13399 standard; cDNA; 4829 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34679.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 38.2% Conservative: 64  
Best Local Similarity: 23.1% Mismatches: 155  
Query Match: 6.9% Indels: 109  
RESULT 426  
ID AEL00856 standard; DNA; 6526 BP.  
DE Mucin-like protein associated polynucleotide SEQ ID NO 172.  
PN WO2006082851-A1.  
PD 10-AUG-2006.  
PA (UITY ) UNIV TOKYO.  
Percent Similarity: 33.1% Conservative: 28  
Best Local Similarity: 25.1% Mismatches: 129  
Query Match: 6.9% Indels: 105  
RESULT 427  
ID ADP84151 standard; DNA; 57082 BP.  
DE Human CA125 genomic DNA amino terminal sequence SeqID 1.  
PN WO2004045553-A2.  
PD 03-JUN-2004.  
PA (UYAR-) UNIV ARKANSAS.  
Percent Similarity: 33.5% Conservative: 53  
Best Local Similarity: 21.8% Mismatches: 145  
Query Match: 6.9% Indels: 157  
RESULT 428  
ID ABL05865 standard; cDNA; 5929 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12077.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 40.2% Conservative: 25  
Best Local Similarity: 29.7% Mismatches: 100  
Query Match: 6.8% Indels: 43  
RESULT 429  
ID ABL05864 standard; cDNA; 11963 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 12074.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 40.2% Conservative: 25  
Best Local Similarity: 29.7% Mismatches: 100



Query Match: 6.8% Indels: 43  
RESULT 430  
ID AEI04880 standard; DNA; 2583 BP.  
DE Coccidioides posadasii strain C735 chitinase 2 open reading frame.  
PN US2006121061-A1.  
PD 08-JUN-2006.  
PA (UYOH-) UNIV OHIO MEDICAL.  
Percent Similarity: 38.8% Conservative: 49  
Best Local Similarity: 23.9% Mismatches: 141  
Query Match: 6.8% Indels: 59  
RESULT 431  
ID AEI04879 standard; DNA; 3090 BP.  
DE Coccidioides posadasii strain C735 chitinase 2 (CTS2) gene.  
PN US2006121061-A1.  
PD 08-JUN-2006.  
PA (UYOH-) UNIV OHIO MEDICAL.  
Percent Similarity: 38.8% Conservative: 49  
Best Local Similarity: 23.9% Mismatches: 141  
Query Match: 6.8% Indels: 59  
RESULT 432  
ID ADP74211 standard; DNA; 149158 BP.  
DE Equine herpesvirus 1 genome gm deletion mutant #2.  
PN US2004109873-A1.  
PD 10-JUN-2004.  
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
Percent Similarity: 34.7% Conservative: 25  
Best Local Similarity: 24.3% Mismatches: 131  
Query Match: 6.8% Indels: 25  
RESULT 433  
ID ADP74212 standard; DNA; 149261 BP.  
DE Equine herpesvirus 1 genome gm deletion mutant #3.  
PN US2004109873-A1.  
PD 10-JUN-2004.  
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
Percent Similarity: 34.7% Conservative: 25  
Best Local Similarity: 24.3% Mismatches: 131  
Query Match: 6.8% Indels: 25  
RESULT 434  
ID ADP74216 standard; DNA; 150071 BP.  
DE Equine herpesvirus 1 genome gm deletion mutant #1.  
PN US2004109873-A1.  
PD 10-JUN-2004.  
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
Percent Similarity: 34.7% Conservative: 25  
Best Local Similarity: 24.3% Mismatches: 131  
Query Match: 6.8% Indels: 25  
RESULT 435  
ID ADP74201 standard; DNA; 150223 BP.  
DE Equine herpesvirus 1 genome seqid 1.  
PN US2004109873-A1.  
PD 10-JUN-2004.  
PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
Percent Similarity: 34.7% Conservative: 25  
Best Local Similarity: 24.3% Mismatches: 131  
Query Match: 6.8% Indels: 25  
RESULT 436  
ID ABV88065 standard; cDNA; 513 BP.  
DE Human colon cancer related cDNA SEQ ID NO 1376.  
PN WO200258534-A2.  
PD 01-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 6.8% Indels: 0  
RESULT 437  
ID ABV87510 standard; cDNA; 513 BP.  
DE Human colon cancer related cDNA SEQ ID NO 821.  
PN WO200258534-A2.  
PD 01-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 6.8% Indels: 0

RESULT 438  
ID ABV18096 standard; cDNA; 471 BP.  
DE Human prostate expression marker cDNA 18087.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 6.7% Indels: 0  
RESULT 439  
ID ABV47885 standard; cDNA; 515 BP.  
DE Human prostate expression marker cDNA 47876.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 6.7% Indels: 0  
RESULT 440  
ID AAT45666 standard; DNA; 2903 BP.  
DE Partial yeast gene, Ig-FLO1, involved in flocculation.  
PN JP08205900-A.  
PD 13-AUG-1996.  
PA (KIRI) KIRIN BREWERY KK.  
Percent Similarity: 38.4% Conservative: 68  
Best Local Similarity: 23.0% Mismatches: 198  
Query Match: 6.7% Indels: 76  
RESULT 441  
ID ADS46792 standard; cDNA; 4830 BP.  
DE Bacterial polynucleotide #1535.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 39.2% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 142  
Query Match: 6.7% Indels: 69  
RESULT 442  
ID ADH89334 standard; DNA; 1044 BP.  
DE H. vulgare C-hordein DNA.  
PN WO2003078629-A1.  
PD 25-SEP-2003.  
PA (BADI) BASF PLANT SCI GMBH.  
Percent Similarity: 44.8% Conservative: 24  
Best Local Similarity: 30.1% Mismatches: 76  
Query Match: 6.7% Indels: 14  
RESULT 443  
ID ADG44130 standard; DNA; 1044 BP.  
DE H. vulgare C-hordein DNA.  
PN WO2003077643-A2.  
PD 25-SEP-2003.  
PA (BADI) BASF PLANT SCI GMBH.  
Percent Similarity: 44.8% Conservative: 24  
Best Local Similarity: 30.1% Mismatches: 76  
Query Match: 6.7% Indels: 14  
RESULT 444  
ID AAT10117 standard; cDNA; 2032 BP.  
DE Drosophila scavenger receptor class CI cDNA.  
PN WO9600288-A2.  
PD 04-JAN-1996.  
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.  
Percent Similarity: 36.1% Conservative: 37  
Best Local Similarity: 23.5% Mismatches: 108  
Query Match: 6.7% Indels: 80  
RESULT 445  
ID ABS53745 standard; cDNA; 2032 BP.  
DE cDNA encoding fruit fly scavenger receptor type CI (dsr-CI).  
PN US6429289-B1.  
PD 06-AUG-2002.  
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

Percent Similarity: 36.1%      Conservative: 37  
Best Local Similarity: 23.5%      Mismatches: 108  
Query Match: 6.7%      Indels: 80  
RESULT 446  
ID AAD33916 standard; cDNA; 2032 BP.  
DE Drosophila melanogaster scavenger receptor class CI (dsr-CI) cDNA.  
PN US6350859-B1.  
PD 26-FEB-2002.  
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
Percent Similarity: 36.1%      Conservative: 37  
Best Local Similarity: 23.5%      Mismatches: 108  
Query Match: 6.7%      Indels: 80  
RESULT 447  
ID ACA10147 standard; cDNA; 2570 BP.  
DE Human NOVX polynucleotide #37.  
PN WO200290504-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 33.8%      Conservative: 32  
Best Local Similarity: 25.6%      Mismatches: 172  
Query Match: 6.7%      Indels: 88  
RESULT 448  
ID ABL16368 standard; DNA; 7417 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 577.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 37.5%      Conservative: 50  
Best Local Similarity: 24.1%      Mismatches: 171  
Query Match: 6.7%      Indels: 65  
RESULT 449  
ID ABX72626 standard; cDNA; 31497 BP.  
DE Human cDNA encoding CA125 amino terminal extension.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Percent Similarity: 39.4%      Conservative: 47  
Best Local Similarity: 23.6%      Mismatches: 120  
Query Match: 6.7%      Indels: 61  
RESULT 450  
ID ABL13398 standard; cDNA; 39746 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 34676.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.9%      Conservative: 58  
Best Local Similarity: 23.1%      Mismatches: 137  
Query Match: 6.7%      Indels: 130  
RESULT 451  
ID ADP84154 standard; cDNA; 66765 BP.  
DE Human CA125 cDNA SeqID 4.  
PN WO2004045553-A2.  
PD 03-JUN-2004.  
PA (UYAR-) UNIV ARKANSAS.  
Percent Similarity: 39.4%      Conservative: 47  
Best Local Similarity: 23.6%      Mismatches: 120  
Query Match: 6.7%      Indels: 61  
RESULT 452  
ID ADR72872 standard; DNA; 66765 BP.  
DE Human ovarian cancer-related tumour marker CA125 DNA.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Percent Similarity: 39.4%      Conservative: 47  
Best Local Similarity: 23.6%      Mismatches: 120  
Query Match: 6.7%      Indels: 61  
RESULT 453  
ID AAD44410 standard; DNA; 1236 BP.  
DE Human huntington (htQ103) protein encoding DNA.  
PN WO200265136-A2.  
PD 22-AUG-2002.  
PA (UYCH-) UNIV CHICAGO.  
Percent Similarity: 41.4%      Conservative: 22

Best Local Similarity: 30.5%      Mismatches: 82  
Query Match: 6.7%      Indels: 38  
RESULT 454  
ID AEI77176 standard; DNA; 2529 BP.  
DE Caenorhabditis elegans heavy metal response gene DNA sequence SeqId 199.  
PN JP2006174802-A.  
PD 06-JUL-2006.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN KOKURITSU KENKO.  
PA (INTE-) INTER-UNIV RES INST CORP RES ORG.  
PA (GENE-) GENENET KK.  
Percent Similarity: 40.2%      Conservative: 34  
Best Local Similarity: 25.6%      Mismatches: 107  
Query Match: 6.7%      Indels: 33  
RESULT 455  
ID ABL28971 standard; DNA; 3736 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38386.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 35.8%      Conservative: 46  
Best Local Similarity: 22.8%      Mismatches: 156  
Query Match: 6.7%      Indels: 73  
RESULT 456  
ID ABL07579 standard; cDNA; 2709 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 17219.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.5%      Conservative: 42  
Best Local Similarity: 24.5%      Mismatches: 136  
Query Match: 6.6%      Indels: 87  
RESULT 457  
ID AAZ07198 standard; cDNA; 2113 BP.  
DE Human lung tumour protein SAL-104 5' cDNA sequence.  
PN WO9938973-A2.  
PD 05-AUG-1999.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 40.7%      Conservative: 25  
Best Local Similarity: 29.2%      Mismatches: 66  
Query Match: 6.6%      Indels: 62  
RESULT 458  
ID AAC79152 standard; cDNA; 2114 BP.  
DE Human lung tumour-specific cDNA #105.  
PN WO200060077-A2.  
PD 12-OCT-2000.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 40.7%      Conservative: 25  
Best Local Similarity: 29.2%      Mismatches: 66  
Query Match: 6.6%      Indels: 62  
RESULT 459  
ID AAD23227 standard; cDNA; 2114 BP.  
DE Human lung tumour-specific protein SAL-104 cDNA.  
PN WO200172295-A2.  
PD 04-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 40.7%      Conservative: 25  
Best Local Similarity: 29.2%      Mismatches: 66  
Query Match: 6.6%      Indels: 62  
RESULT 460  
ID ADD66466 standard; cDNA; 2114 BP.  
DE Human lung tumour-specific related cDNA, SEQ ID NO 158.  
PN WO200292001-A2.  
PD 21-NOV-2002.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 40.7%      Conservative: 25  
Best Local Similarity: 29.2%      Mismatches: 66  
Query Match: 6.6%      Indels: 62  
RESULT 461  
ID ADE87720 standard; cDNA; 2114 BP.  
DE Human lung tumour antigen cDNA #105.  
PN US2003118599-A1.  
PD 26-JUN-2003.  
PA (CORI-) CORIXA CORP.

Percent Similarity: 40.7% Conservative: 25  
Best Local Similarity: 29.2% Mismatches: 66  
Query Match: 6.6% Indels: 62  
RESULT 462  
ID ADO08326 standard; cDNA; 2511 BP.  
DE Human NOVX polynucleotide #37.  
PN US2004018594-A1.  
PD 29-JAN-2004.  
PA (ALSO/) ALSOBROOK J P.  
PA (ANDE/) ANDERSON D W.  
PA (BOLD/) BOLDOG F L.  
PA (BURG/) BURGESS C E.  
PA (CASM/) CASMAN S J.  
PA (CHAP/) CHAPOVAL A.  
PA (EDIN/) EDINGER S R.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUNT/) GUNTHER E.  
PA (GUOX/) GUO X S.  
PA (KEKU/) KEKUDA R.  
PA (LEPL/) LEFLEY D M..  
PA (LILL/) LI L.  
PA (LIUX/) LIU X.  
PA (MALY/) MALYANKAR U M.  
PA (MILL/) MILLER C E.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENNA C E A.  
PA (RIEG/) RIEGER D K.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (SPYT/) SPYTEK K A.  
PA (TAUP/) TAUPIER R J.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
Percent Similarity: 33.7% Conservative: 35  
Best Local Similarity: 24.7% Mismatches: 155  
Query Match: 6.6% Indels: 104  
RESULT 463  
ID ABQ18250 standard; DNA; 7593 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 4841.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 39.0% Conservative: 49  
Best Local Similarity: 23.8% Mismatches: 118  
Query Match: 6.6% Indels: 79  
RESULT 464  
ID ABQ18251 standard; DNA; 7593 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 4842.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 39.0% Conservative: 49  
Best Local Similarity: 23.8% Mismatches: 118  
Query Match: 6.6% Indels: 79  
RESULT 465  
ID AAN91235 standard; DNA; 1368 BP.  
DE DNA sequence of preprospasmolysin.  
PN DE3808456-A.  
PD 28-SEP-1989.  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
Percent Similarity: 35.5% Conservative: 44  
Best Local Similarity: 23.5% Mismatches: 155  
Query Match: 6.6% Indels: 81  
RESULT 466  
ID ABL28829 standard; DNA; 2291 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37960.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.

Percent Similarity: 36.5% Conservative: 35  
Best Local Similarity: 25.2% Mismatches: 118  
Query Match: 6.6% Indels: 79  
RESULT 467  
ID AAA70157 standard; DNA; 9408 BP.  
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:290.  
PN WO200025728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Percent Similarity: 35.7% Conservative: 56  
Best Local Similarity: 22.2% Mismatches: 158  
Query Match: 6.6% Indels: 108  
RESULT 468  
ID AAQ67190 standard; DNA; 9636 BP.  
DE P. falciparum transmission blocking target antigen Pfs230 DNA.  
PN WO9417187-A1.  
PD 04-AUG-1994.  
PA (USSH ) US SEC DEPT HEALTH.  
Percent Similarity: 35.7% Conservative: 56  
Best Local Similarity: 22.2% Mismatches: 158  
Query Match: 6.6% Indels: 108  
RESULT 469  
ID ABL20354 standard; DNA; 13631 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12535.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 33.2% Conservative: 48  
Best Local Similarity: 19.8% Mismatches: 163  
Query Match: 6.6% Indels: 76  
RESULT 470  
ID ABQ76371 standard; cDNA; 2156 BP.  
DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 167.  
PN WO200264766-A2.  
PD 22-AUG-2002.  
PA (JANC ) JANSSEN PHARM NV.  
Percent Similarity: 35.7% Conservative: 71  
Best Local Similarity: 21.1% Mismatches: 169  
Query Match: 6.5% Indels: 146  
RESULT 471  
ID ADI21446 standard; cDNA; 4115 BP.  
DE Novel human expressed sequence tag, EST #145.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.3% Conservative: 62  
Best Local Similarity: 22.3% Mismatches: 148  
Query Match: 6.5% Indels: 111  
RESULT 472  
ID ADY34541 standard; cDNA; 4327 BP.  
DE DPCR1 (1393 amino acid form) coding sequence.  
PN WO2005019257-A1.  
PD 03-MAR-2005.  
PA (CLLT ) CELLTECH R & D LTD.  
Percent Similarity: 37.3% Conservative: 62  
Best Local Similarity: 22.3% Mismatches: 148  
Query Match: 6.5% Indels: 111  
RESULT 473  
ID ADN39109 standard; cDNA; 4383 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:427.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (BOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 37.3% Conservative: 62  
Best Local Similarity: 22.3% Mismatches: 148  
Query Match: 6.5% Indels: 111  
RESULT 474  
ID ADI21918 standard; cDNA; 5238 BP.  
DE Novel human protein cDNA #177.  
PN WO2003025148-A2.



PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC. 37.3% Conservative: 62  
Best Local Similarity: 22.3% Mismatches: 148  
Query Match: 6.5% Indels: 111  
RESULT 475  
ID ACL26914 standard; cDNA; 1884 BP.  
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:870.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG. 41.2% Conservative: 24  
Best Local Similarity: 27.1% Mismatches: 68  
Query Match: 6.5% Indels: 32  
RESULT 476  
ID AEH37649 standard; DNA; 4941 BP.  
DE Cryptosporidium hominis gene SEQ ID NO:740.  
PN WO2006044045-A2.  
PD 27-APR-2006.  
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH. 33.3% Conservative: 28  
Best Local Similarity: 22.2% Mismatches: 136  
Query Match: 6.5% Indels: 32  
RESULT 477  
ID ABL27463 standard; DNA; 2517 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33862.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 30.8% Conservative: 32  
Best Local Similarity: 22.9% Mismatches: 168  
Query Match: 6.5% Indels: 110  
RESULT 478  
ID ABL16369 standard; DNA; 2607 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 580.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 36.9% Conservative: 56  
Best Local Similarity: 22.6% Mismatches: 127  
Query Match: 6.5% Indels: 121  
RESULT 479  
ID ABL27462 standard; DNA; 5146 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33859.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 30.8% Conservative: 32  
Best Local Similarity: 22.9% Mismatches: 168  
Query Match: 6.5% Indels: 110  
RESULT 480  
ID ABL25979 standard; DNA; 5388 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29410.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 38.4% Conservative: 48  
Best Local Similarity: 24.9% Mismatches: 150  
Query Match: 6.5% Indels: 69  
RESULT 481  
ID ABL25978 standard; DNA; 7782 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 29407.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 38.4% Conservative: 48  
Best Local Similarity: 24.9% Mismatches: 150  
Query Match: 6.5% Indels: 69  
RESULT 482  
ID AAL49163 standard; cDNA; 1881 BP.  
DE Murine gp100 coding sequence.  
PN EP1222928-A2.  
PD 17-JUL-2002.

PA (UYZU-) UNIV ZUERICH INST MEDIZINISCHE VIROLOGIE. 36.2% Conservative: 52  
Best Local Similarity: 23.3% Mismatches: 141  
Query Match: 6.5% Indels: 116  
RESULT 483  
ID ADW87785 standard; cDNA; 2086 BP.  
DE Mutant bovine Silver R93A cDNA sequence.  
PN FR2857979-A1.  
PD 28-JAN-2005.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE. 38.8% Conservative: 50  
Best Local Similarity: 24.6% Mismatches: 134  
Query Match: 6.5% Indels: 82  
RESULT 484  
ID ABL25662 standard; DNA; 2336 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28459.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. 43.3% Conservative: 32  
Best Local Similarity: 29.8% Mismatches: 108  
Query Match: 6.5% Indels: 30  
RESULT 485  
ID ADX83143 standard; DNA; 3789 BP.  
DE Human TEG26 polynucleotide SEQ ID NO 25.  
PN WO2005014818-A1.  
PD 17-FEB-2005.  
PA (PERS-) PERSEUS PROTEOMICS INC. 40.1% Conservative: 43  
Best Local Similarity: 25.5% Mismatches: 142  
Query Match: 6.5% Indels: 35  
RESULT 486  
PA (CHUS ) CHUGAI SEIYAKU KK. 36.3% Conservative: 37  
Best Local Similarity: 24.6% Mismatches: 112  
Query Match: 6.5% Indels: 91  
RESULT 487  
PA (ABUR/) ABURATANI H. 36.3% Conservative: 37  
Best Local Similarity: 24.6% Mismatches: 112  
Query Match: 6.5% Indels: 91  
RESULT 488  
ID AEH38295 standard; DNA; 5433 BP.  
DE Cryptosporidium hominis gene SEQ ID NO:1386.  
PN WO2006044045-A2.  
PD 27-APR-2006.  
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH. 35.4% Conservative: 64  
Best Local Similarity: 20.4% Mismatches: 165  
Query Match: 6.4% Indels: 112  
RESULT 489  
ID ADQ80323 standard; cDNA; 2917 BP.  
DE Human FLJ22751 fis cDNA clone.  
PN WO2004063709-A2.  
PD 29-JUL-2004.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO. 39.8% Conservative: 42  
Best Local Similarity: 25.5% Mismatches: 143  
Query Match: 6.4% Indels: 35  
RESULT 490  
ID AAK53131 standard; cDNA; 2981 BP.  
DE Human polynucleotide SEQ ID NO 2660.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC. 34.7% Conservative: 67  
Best Local Similarity: 21.6% Mismatches: 179  
Query Match: 6.4% Indels: 155  
RESULT 491  
ID AAA50043 standard; DNA; 12685 BP.  
DE Caenorhabditis elegans LOV-1 gene (non-coding strand).  
PN WO200040711-A2.

PD 13-JUL-2000.  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
Percent Similarity: 49.4% Conservative: 39  
Best Local Similarity: 25.0% Mismatches: 69  
Query Match: 6.4% Indels: 13  
RESULT 492  
ID ADN07622 standard; cDNA; 12685 BP.  
DE Caenorhabditis elegans location of vulva (LOV) -1 cDNA.  
PN US6723557-B1.  
PD 20-APR-2004.  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
Percent Similarity: 49.4% Conservative: 39  
Best Local Similarity: 25.0% Mismatches: 69  
Query Match: 6.4% Indels: 13  
RESULT 493  
ID ADW79939 standard; DNA; 12685 BP.  
DE Nematode location of vulva (lov-1) gene.  
PN US6849717-B1.  
PD 01-FEB-2005.  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
Percent Similarity: 49.4% Conservative: 39  
Best Local Similarity: 25.0% Mismatches: 69  
Query Match: 6.4% Indels: 13  
RESULT 494  
ID ADY34543 standard; cDNA; 2293 BP.  
DE DPCR1 (715 amino acid form) coding sequence.  
PN WO2005019257-A1.  
PD 03-MAR-2005.  
PA (CLLT ) CELLTech R & D LTD.  
Percent Similarity: 39.1% Conservative: 58  
Best Local Similarity: 22.6% Mismatches: 124  
Query Match: 6.4% Indels: 89  
RESULT 495  
ID ABL10403 standard; cDNA; 3263 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25691.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 38.0% Conservative: 44  
Best Local Similarity: 26.2% Mismatches: 147  
Query Match: 6.4% Indels: 87  
RESULT 496  
ID AEG97317 standard; DNA; 1905 BP.  
DE C. albicans hyphal growth regulator HWP1 DNA SEQ ID NO 86.  
PN WO2006036817-A2.  
PD 06-APR-2006.  
PA (MICR-) MICROBIA INC.  
Percent Similarity: 40.8% Conservative: 45  
Best Local Similarity: 24.3% Mismatches: 104  
Query Match: 6.4% Indels: 58  
RESULT 497  
ID AEL60498 standard; DNA; 2681 BP.  
DE Candida albicans hyphal wall protein 1 (HWP1) DNA.  
PN WO2006109283-A1.  
PD 19-OCT-2006.  
PA (UYNA-) UNIV NAT IRELAND GALWAY.  
Percent Similarity: 40.8% Conservative: 45  
Best Local Similarity: 24.3% Mismatches: 104  
Query Match: 6.4% Indels: 58  
RESULT 498  
ID AEL60483 standard; DNA; 2682 BP.  
DE Candida albicans hyphal wall protein 1 (HWP1) DNA SEQ ID NO 1.  
PN WO2006109283-A1.  
PD 19-OCT-2006.  
PA (UYNA-) UNIV NAT IRELAND GALWAY.  
Percent Similarity: 40.8% Conservative: 45  
Best Local Similarity: 24.3% Mismatches: 104  
Query Match: 6.4% Indels: 58  
RESULT 499  
ID ABA66656 standard; DNA; 3953 BP.  
DE Human foetal liver single exon nucleic acid probe #14961.  
PN WO200157277-A2.  
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 36.9% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 145  
Query Match: 6.4% Indels: 108  
RESULT 500  
ID ABA48746 standard; DNA; 3953 BP.  
DE Human breast cell single exon nucleic acid probe #7441.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 36.9% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 145  
Query Match: 6.4% Indels: 108  
RESULT 501  
ID ABA33721 standard; DNA; 3953 BP.  
DE Probe #12187 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 36.9% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 145  
Query Match: 6.4% Indels: 108  
RESULT 502  
ID AAK40813 standard; DNA; 3953 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 15370.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 36.9% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 145  
Query Match: 6.4% Indels: 108  
RESULT 503  
ID AAK15085 standard; DNA; 3953 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 15076.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 36.9% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 145  
Query Match: 6.4% Indels: 108  
RESULT 504  
ID ABS40392 standard; DNA; 3953 BP.  
DE Human liver single exon probe, SEQ ID No 15382.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 36.9% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 145  
Query Match: 6.4% Indels: 108  
RESULT 505  
ID AAI07277 standard; DNA; 3953 BP.  
DE Probe #7268 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 36.9% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 145  
Query Match: 6.4% Indels: 108  
RESULT 506  
ID ABS14767 standard; DNA; 3953 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14758.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 36.9% Conservative: 59  
Best Local Similarity: 22.2% Mismatches: 145  
Query Match: 6.4% Indels: 108  
RESULT 507  
ID ACH87407 standard; DNA; 3953 BP.  
DE Human genome derived single exon probe #20602.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.

PA (RANK/) RANK D R.  
PA (HANK/) HANZEL D K.  
Percent Similarity: 36.9%  
Best Local Similarity: 22.2%  
Query Match: 6.4%  
Conservative: 59  
Mismatches: 145  
Indels: 108  
RESULT 508  
ID ABL05381 standard; cDNA; 2032 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10625.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 37.0%  
Best Local Similarity: 23.7%  
Query Match: 6.4%  
Conservative: 28  
Mismatches: 78  
Indels: 55  
RESULT 509  
ID ABL05380 standard; cDNA; 4282 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10622.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 39.4%  
Best Local Similarity: 25.0%  
Query Match: 6.4%  
Conservative: 31  
Mismatches: 86  
Indels: 46  
RESULT 510  
ID ABX07541 standard; DNA; 13152 BP.  
DE S. pneumoniae type 4 strain coding region #1829.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 38.2%  
Best Local Similarity: 23.1%  
Query Match: 6.4%  
Conservative: 66  
Mismatches: 193  
Indels: 80  
RESULT 511  
ID ABX07543 standard; DNA; 14328 BP.  
DE S. pneumoniae type 4 strain coding region #1831.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 38.2%  
Best Local Similarity: 23.1%  
Query Match: 6.4%  
Conservative: 66  
Mismatches: 193  
Indels: 80  
RESULT 512  
ID ADM91975 standard; DNA; 14328 BP.  
DE S pneumoniae antigenic protein-encoding gene sequence SeqID172.  
PN WO2004020609-A2.  
PD 11-MAR-2004.  
PA (TUFT ) UNIV TUFTS.  
Percent Similarity: 38.2%  
Best Local Similarity: 23.1%  
Query Match: 6.4%  
Conservative: 66  
Mismatches: 193  
Indels: 80  
RESULT 513  
ID ADT49995 standard; DNA; 14328 BP.  
DE S pneumoniae hyperimmune serum reactive antigen DNA Seq 73.  
PN WO2004092209-A2.  
PD 28-OCT-2004.  
PA (INTE-) INTERCELL AG.  
Percent Similarity: 38.2%  
Best Local Similarity: 23.1%  
Query Match: 6.4%  
Conservative: 66  
Mismatches: 193  
Indels: 80  
RESULT 514  
ID ACA49624 standard; DNA; 14331 BP.  
DE Prokaryotic essential gene #31281.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 38.2%  
Best Local Similarity: 23.1%  
Query Match: 6.4%  
Conservative: 66  
Mismatches: 193  
Indels: 80  
RESULT 515  
ID AEK43399 standard; DNA; 107069 BP.  
DE Chlorothricin biological synthesis gene cluster.

PN CN1730657-A.  
PD 08-FEB-2006.  
PA (SHAN-) SHANGHAI ORGANIC CHEM INST.  
Percent Similarity: 33.5%  
Best Local Similarity: 23.5%  
Query Match: 6.4%  
Conservative: 35  
Mismatches: 122  
Indels: 110  
RESULT 516  
Percent Similarity: 38.2%  
Best Local Similarity: 23.1%  
Query Match: 6.4%  
Conservative: 66  
Mismatches: 193  
Indels: 80  
RESULT 517  
ID ABL07173 standard; cDNA; 6353 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 16001.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 41.7%  
Best Local Similarity: 29.5%  
Query Match: 6.3%  
Conservative: 32  
Mismatches: 95  
Indels: 61  
RESULT 518  
ID ABL07172 standard; cDNA; 8429 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15998.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 41.7%  
Best Local Similarity: 29.5%  
Query Match: 6.3%  
Conservative: 32  
Mismatches: 95  
Indels: 61  
RESULT 519  
ID AAT96035 standard; cDNA; 1795 BP.  
DE Human kidney injury related molecule (KIM) cDNA clone H13-10-85.  
PN WO9744460-A1.  
PD 27-NOV-1997.  
PA (BIOJ ) BIOGEN INC.  
Percent Similarity: 36.3%  
Best Local Similarity: 24.0%  
Query Match: 6.3%  
Conservative: 47  
Mismatches: 163  
Indels: 82  
RESULT 520  
ID ABL10368 standard; cDNA; 3463 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25586.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.8%  
Best Local Similarity: 21.3%  
Query Match: 6.3%  
Conservative: 57  
Mismatches: 157  
Indels: 76  
RESULT 521  
ID AAV20701 standard; DNA; 5318 BP.  
DE Cryptosporidium parvum GP900 antigen open reading frame and 3' region.  
PN WO9806430-A1.  
PD 19-FEB-1998.  
PA (REGC ) UNIV CALIFORNIA.  
Percent Similarity: 36.2%  
Best Local Similarity: 22.8%  
Query Match: 6.3%  
Conservative: 58  
Mismatches: 203  
Indels: 75  
RESULT 522  
ID ADZ51725 standard; DNA; 138203 BP.  
DE FR-008 polyketide gene cluster, SEQ ID 1.  
PN US2005089884-A1.  
PD 28-APR-2005.  
PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
PA (UYSH-) UNIV SHANGHAI JIAOTONG.  
Percent Similarity: 36.3%  
Best Local Similarity: 23.7%  
Query Match: 6.3%  
Conservative: 41  
Mismatches: 120  
Indels: 87  
RESULT 523  
ID AEH46706 standard; DNA; 138203 BP.  
DE Streptomyces FR-008 polyketone synthesis gene cluster - SEQ ID 1.  
PN CN1667123-A.  
PD 14-SEP-2005.  
PA (UYSH-) UNIV SHANGHAI JIAOTONG.  
Percent Similarity: 36.3%  
Best Local Similarity: 23.7%  
Conservative: 41  
Mismatches: 120



Query Match: 6.3% Indels: 87  
RESULT 524  
ID ACN44758 standard; DNA; 172569 BP.  
DE Human genomic sequence hCG20145.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 42.5%  
Best Local Similarity: 30.7%  
Query Match: 6.3%  
Indels: 17  
Conservative: 18  
Mismatches: 71  
Indels: 17  
RESULT 525  
ID AAX91461 standard; DNA; 867 BP.  
DE T. gondii ntG867 reverse complement sequence.  
PN WO9932633-A1.  
PD 01-JUL-1999.  
PA (HESK-) HESKA CORP.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 526  
ID AAX91460 standard; DNA; 867 BP.  
DE T. gondii immunogenic protein encoding DNA.  
PN WO9932633-A1.  
PD 01-JUL-1999.  
PA (HESK-) HESKA CORP.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 527  
ID AAS42783 standard; cDNA; 867 BP.  
DE T. gondii cDNA encoding immunogenic protein PTg288.  
PN US2001014447-A1.  
PD 16-AUG-2001.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 528  
ID AAS42784 standard; cDNA; 867 BP.  
DE Reverse complement of T. gondii cDNA ntG288.  
PN US2001014447-A1.  
PD 16-AUG-2001.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 529  
ID ADG17392 standard; DNA; 867 BP.  
DE T. gondii protein DNA #86.  
PN US2003194393-A1.  
PD 16-OCT-2003.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 530  
ID ADG17390 standard; cDNA; 867 BP.  
DE T. gondii protein cDNA #6.  
PN US2003194393-A1.  
PD 16-OCT-2003.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 531  
ID AEH92888 standard; DNA; 867 BP.  
DE T. gondii polynucleotide ntG(867) SEQ ID NO: 342.  
PN US2006115496-A1.  
PD 01-JUN-2006.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35

RESULT 532  
ID AEH92886 standard; cDNA; 867 BP.  
DE T. gondii polynucleotide ntG(867) SEQ ID NO: 340.  
PN US2006115496-A1.  
PD 01-JUN-2006.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 533  
ID ABL27929 standard; DNA; 1014 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35260.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.8%  
Best Local Similarity: 29.7%  
Query Match: 6.3%  
Indels: 56  
Conservative: 15  
Mismatches: 77  
Indels: 56  
RESULT 534  
ID AAX91462 standard; DNA; 1397 BP.  
DE T. gondii immunogenic protein encoding DNA.  
PN WO9932633-A1.  
PD 01-JUL-1999.  
PA (HESK-) HESKA CORP.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 535  
ID AAX91463 standard; DNA; 1397 BP.  
DE T. gondii ntG1397 reverse complement sequence.  
PN WO9932633-A1.  
PD 01-JUL-1999.  
PA (HESK-) HESKA CORP.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 536  
ID AAS42786 standard; cDNA; 1397 BP.  
DE Reverse complement of T. gondii cDNA ntG1397.  
PN US2001014447-A1.  
PD 16-AUG-2001.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 537  
ID AAS42785 standard; cDNA; 1397 BP.  
DE T. gondii cDNA encoding immunogenic protein PTg1397.  
PN US2001014447-A1.  
PD 16-AUG-2001.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 538  
ID ADG17395 standard; DNA; 1397 BP.  
DE T. gondii protein DNA #87.  
PN US2003194393-A1.  
PD 16-OCT-2003.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 539  
ID ADG17393 standard; cDNA; 1397 BP.  
DE T. gondii protein cDNA #7.  
PN US2003194393-A1.  
PD 16-OCT-2003.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 540  
ID ADG17394 standard; cDNA; 1397 BP.  
DE T. gondii protein cDNA #7.  
PN US2003194393-A1.  
PD 16-OCT-2003.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Indels: 35  
Conservative: 33  
Mismatches: 111  
Indels: 35

ID AEH92889 standard; cDNA; 1397 BP.  
DE T. gondii polynucleotide NTG(1397) SEQ ID NO: 343.  
PN US2006115496-A1.  
PD 01-JUN-2006.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 541  
ID AEH92891 standard; DNA; 1397 BP.  
DE T. gondii polynucleotide NTG(1397) SEQ ID NO: 345.  
PN US2006115496-A1.  
PD 01-JUN-2006.  
PA (MILH/) MILHAUSEN M J.  
Percent Similarity: 38.6%  
Best Local Similarity: 24.6%  
Query Match: 6.3%  
Conservative: 33  
Mismatches: 111  
Indels: 35  
RESULT 542  
ID ADS56141 standard; cDNA; 1976 BP.  
DE Bacterial polynucleotide #8128.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 35.5%  
Best Local Similarity: 24.2%  
Query Match: 6.3%  
Conservative: 36  
Mismatches: 97  
Indels: 108  
RESULT 543  
ID AAI67809 standard; cDNA; 3159 BP.  
DE Soybean alpha-glucosidase II alpha-subunit cDNA (clone srr3c.pk003.g3).  
PN US6316698-B1.  
PD 13-NOV-2001.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Percent Similarity: 38.5%  
Best Local Similarity: 24.3%  
Query Match: 6.3%  
Conservative: 46  
Mismatches: 131  
Indels: 69  
RESULT 544  
ID AAX26611 standard; DNA; 3183 BP.  
DE Trypanosoma cruzi alpha(2-3) trans-sialidase nucleotide sequence.  
PN WO9908511-A1.  
PD 25-FEB-1999.  
PA (NEOS-) NEOFSE TECHNOLOGIES INC.  
Percent Similarity: 37.9%  
Best Local Similarity: 27.8%  
Query Match: 6.3%  
Conservative: 34  
Mismatches: 137  
Indels: 73  
RESULT 545  
ID ABL24389 standard; DNA; 4116 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24640.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 42.4%  
Best Local Similarity: 28.1%  
Query Match: 6.3%  
Conservative: 29  
Mismatches: 54  
Indels: 63  
RESULT 546  
ID AAV20700 standard; DNA; 5163 BP.  
DE Cryptosporidium parvum GP900 antigen open reading frame.  
PN WO9806430-A1.  
PD 19-FEB-1998.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 35.6%  
Best Local Similarity: 22.3%  
Query Match: 6.3%  
Conservative: 58  
Mismatches: 204  
Indels: 77  
RESULT 547  
ID AAA61849 standard; DNA; 5163 BP.  
DE ORF encoding a portion of Cryptosporidium parvum NINC isolate GP900.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 35.6%  
Conservative: 58

Best Local Similarity: 22.3%  
Query Match: 6.3%  
Mismatches: 204  
Indels: 77  
RESULT 548  
ID ABT04778 standard; DNA; 5163 BP.  
DE C parvum GP900 gene fragment SEQ ID NO: 4.  
PN WO200194631-A1.  
PD 13-DEC-2001.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 35.6%  
Best Local Similarity: 22.3%  
Query Match: 6.3%  
Conservative: 58  
Mismatches: 204  
Indels: 77  
RESULT 549  
ID AAA61848 standard; DNA; 5318 BP.  
DE DNA encoding a portion of Cryptosporidium parvum NINC isolate GP900.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 35.6%  
Best Local Similarity: 22.3%  
Query Match: 6.3%  
Conservative: 58  
Mismatches: 204  
Indels: 77  
RESULT 550  
ID ABT04777 standard; DNA; 5318 BP.  
DE C parvum GP900 gene fragment SEQ ID NO: 3.  
PN WO200194631-A1.  
PD 13-DEC-2001.  
PA (REGC) UNIV CALIFORNIA.  
Percent Similarity: 35.6%  
Best Local Similarity: 22.3%  
Query Match: 6.3%  
Conservative: 58  
Mismatches: 204  
Indels: 77  
RESULT 551  
ID ABK94926 standard; cDNA; 5735 BP.  
DE Human novel polynucleotide #37.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 40.2%  
Best Local Similarity: 22.3%  
Query Match: 6.3%  
Conservative: 59  
Mismatches: 116  
Indels: 81  
RESULT 552  
ID ABK94980 standard; cDNA; 5735 BP.  
DE Human novel polynucleotide #91.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 40.2%  
Best Local Similarity: 22.3%  
Query Match: 6.3%  
Conservative: 59  
Mismatches: 116  
Indels: 81  
RESULT 553  
ID ABL24388 standard; DNA; 6116 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 24637.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 42.4%  
Best Local Similarity: 28.1%  
Query Match: 6.3%  
Conservative: 29  
Mismatches: 54  
Indels: 63  
RESULT 554  
ID ADR18911 standard; DNA; 5985 BP.  
DE Human mucin-like protein, SCS0004, coding sequence, SEQ ID 1.  
PN WO2004069136-A2.  
PD 19-AUG-2004.  
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.  
Percent Similarity: 40.0%  
Best Local Similarity: 26.6%  
Query Match: 6.2%  
Conservative: 39  
Mismatches: 118  
Indels: 59  
RESULT 555  
ID AEB35716 standard; DNA; 162147 BP.  
DE L. pneumophila DNA SEQ ID NO 48.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP) INST PASTEUR.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.

PA (CNRS ) CNRS CENT NAT RECH SCI.	Conservative: 47	
Percent Similarity: 37.0%	Mismatches: 101	
Best Local Similarity: 21.9%	Indels: 95	
Query Match: 6.2%		
RESULT 556		
ID ADT05874 standard; DNA; 171096 BP.		
DE Cercopithecine herpesvirus 15 complete genome.		
PN US2004214161-A1.		
PD 28-OCT-2004.		
PA (SMIT/) SMITH M.		
Percent Similarity: 34.6%	Conservative: 40	
Best Local Similarity: 23.3%	Mismatches: 118	
Query Match: 6.2%	Indels: 115	
RESULT 557		
ID ABL09095 standard; cDNA; 3150 BP.		
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21767.		
PN WO200171042-A2.		
PD 27-SEP-2001.		
PA (PEKE ) PE CORP NY.		
Percent Similarity: 33.0%	Conservative: 24	
Best Local Similarity: 26.0%	Mismatches: 160	
Query Match: 6.2%	Indels: 67	
RESULT 558		
ID ABQ78676 standard; DNA; 4518 BP.		
DE Nucleotide sequence of a human heart of glass polypeptide.		
PN WO200262205-A2.		
PD 15-AUG-2002.		
PA (GEHO ) GEN HOSPITAL CORP.		
Percent Similarity: 30.7%	Conservative: 21	
Best Local Similarity: 24.2%	Mismatches: 126	
Query Match: 6.2%	Indels: 97	
RESULT 559		
ID ABQ78675 standard; DNA; 4519 BP.		
DE Nucleotide sequence of a zebrafish heart of glass polypeptide.		
PN WO200262205-A2.		
PD 15-AUG-2002.		
PA (GEHO ) GEN HOSPITAL CORP.		
Percent Similarity: 30.7%	Conservative: 21	
Best Local Similarity: 24.2%	Mismatches: 126	
Query Match: 6.2%	Indels: 97	
RESULT 560		
ID ACH92120 standard; DNA; 1303 BP.		
DE Human genome derived single exon probe #25315.		
PN US2003194704-A1.		
PD 16-OCT-2003.		
PA (PENN/) PENN S G.		
PA (RANK/) RANK D R.		
PA (HANK/) HANZEL D K.		
Percent Similarity: 34.1%	Conservative: 50	
Best Local Similarity: 22.4%	Mismatches: 171	
Query Match: 6.2%	Indels: 112	
RESULT 561		
ID AAS32485 standard; DNA; 5664 BP.		
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 439.		
PN WO200155319-A2.		
PD 02-AUG-2001.		
PA (HUMA-) HUMAN GENOME SCI INC.		
Percent Similarity: 37.1%	Conservative: 41	
Best Local Similarity: 24.3%	Mismatches: 113	
Query Match: 6.2%	Indels: 90	
RESULT 562		
ID ABL09094 standard; cDNA; 5943 BP.		
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21764.		
PN WO200171042-A2.		
PD 27-SEP-2001.		
PA (PEKE ) PE CORP NY.		
Percent Similarity: 35.8%	Conservative: 39	
Best Local Similarity: 24.3%	Mismatches: 141	
Query Match: 6.2%	Indels: 77	
RESULT 563		
ID ABL09094 standard; cDNA; 5943 BP.		
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21764.		
PN WO200171042-A2.		
PD 27-SEP-2001.		
PA (PEKE ) PE CORP NY.		
Percent Similarity: 35.8%	Conservative: 39	
Best Local Similarity: 24.3%	Mismatches: 141	
Query Match: 6.2%	Indels: 77	
RESULT 564		
ID ADS47200 standard; cDNA; 1512 BP.		
DE Bacterial polynucleotide #1943.		
PN US2003233675-A1.		
PD 18-DEC-2003.		
PA (CAOY/) CAO Y.		
PA (HINK/) HINKLE G J.		
PA (SLAT/) SLATER S C.		
PA (CHEN/) CHEN X.		
PA (GOLD/) GOLDMAN B S.		
Percent Similarity: 45.5%	Conservative: 34	
Best Local Similarity: 28.3%	Mismatches: 102	
Query Match: 6.2%	Indels: 6	
RESULT 565		
ID AEG51911 standard; DNA; 1512 BP.		
DE Stress-related protein, SRP, DNA SEQ ID NO 169.		
PN WO2006032708-A2.		
PD 30-MAR-2006.		
PA (BADI ) BASF PLANT SCI GMBH.		
Percent Similarity: 45.5%	Conservative: 34	
Best Local Similarity: 28.3%	Mismatches: 102	
Query Match: 6.2%	Indels: 6	
RESULT 566		
ID ADF82805 standard; cDNA; 1923 BP.		
DE Aspergillus niger phospholipase PLP34 coding sequence.		
PN WO2003097825-A2.		
PD 27-NOV-2003.		
PA (STAM ) DSM IP ASSETS BV.		
Percent Similarity: 36.1%	Conservative: 59	
Best Local Similarity: 23.8%	Mismatches: 172	
Query Match: 6.2%	Indels: 135	
RESULT 567		
ID AAK52147 standard; cDNA; 3135 BP.		
DE Human polynucleotide SEQ ID NO 692.		
PN WO200157190-A2.		



Percent Similarity: 36.6% Conservative: 33  
Best Local Similarity: 25.4% Mismatches: 127  
Query Match: 6.2% Indels: 60  
RESULT 572  
ID ADI57706 standard; cDNA; 1808 BP.  
DE Human breast specific nucleic acid (BSNA) #77.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 30.6% Conservative: 41  
Best Local Similarity: 21.7% Mismatches: 146  
Query Match: 6.2% Indels: 174  
RESULT 573  
ID AEG97426 standard; DNA; 1905 BP.  
DE C. albicans cell wall protein HWP1 DNA SEQ ID NO 195.  
PN WO2006036817-A2.  
PD 06-APR-2006.  
PA (MICR-) MICROBIA INC.  
Percent Similarity: 40.4% Conservative: 45  
Best Local Similarity: 23.9% Mismatches: 105  
Query Match: 6.2% Indels: 58  
RESULT 574  
ID AAZ32027 standard; DNA; 3015 BP.  
DE Human METH1 related EST Z46970.  
PN WO9937660-A1.  
PD 29-JUL-1999.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
Percent Similarity: 34.7% Conservative: 48  
Best Local Similarity: 23.5% Mismatches: 173  
Query Match: 6.2% Indels: 111  
RESULT 575  
ID AAC90084 standard; DNA; 3015 BP.  
DE Z46970 cDNA clone.  
PN WO200071577-A1.  
PD 30-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
PA (JONA/) JONAK Z L.  
PA (TRUL/) TRULLI S H.  
PA (FORN/) FORNWALD J A.  
PA (TERR/) TERRETT J A.  
Percent Similarity: 34.7% Conservative: 48  
Best Local Similarity: 23.5% Mismatches: 173  
Query Match: 6.2% Indels: 111  
RESULT 576  
ID ABT14863 standard; DNA; 6783 BP.  
DE Pathogen specific antigen related staphylococcal DNA SEQ ID No 8.  
PN WO200259148-A2.  
PD 01-AUG-2002.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
Percent Similarity: 41.5% Conservative: 79  
Best Local Similarity: 21.3% Mismatches: 192  
Query Match: 6.2% Indels: 36  
RESULT 577  
ID ADA02498 standard; DNA; 37487 BP.  
DE Human MYC carcinoma associated gene, SEQ ID NO:1016.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 34.7% Conservative: 55  
Best Local Similarity: 21.9% Mismatches: 159  
Query Match: 6.2% Indels: 123  
RESULT 578  
ID ADB72236 standard; DNA; 37487 BP.  
DE Human MYC gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.

PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 34.7% Conservative: 55  
Best Local Similarity: 21.9% Mismatches: 159  
Query Match: 6.2% Indels: 123  
RESULT 579  
ID ADE82938 standard; DNA; 37487 BP.  
DE Human MYC genomic DNA sequence.  
PN WO2003080808-A2.  
PD 02-OCT-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 34.7% Conservative: 55  
Best Local Similarity: 21.9% Mismatches: 159  
Query Match: 6.2% Indels: 123  
RESULT 580  
ID ADE95746 standard; DNA; 37487 BP.  
DE Human MYC gene genomic DNA sequence.  
PN WO2003039484-A2.  
PD 15-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 34.7% Conservative: 55  
Best Local Similarity: 21.9% Mismatches: 159  
Query Match: 6.2% Indels: 123  
RESULT 581  
ID AEK60017 standard; DNA; 37487 BP.  
DE Human MYC genomic sequence, SEQ ID NO:4.  
PN US2006204982-A1.  
PD 14-SEP-2006.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Percent Similarity: 34.7% Conservative: 55  
Best Local Similarity: 21.9% Mismatches: 159  
Query Match: 6.2% Indels: 123  
RESULT 582  
ID ADO25291 standard; cDNA; 191010 BP.  
DE Human protein kinase C zeta I/zeta Ii genomic sequence.  
PN WO2004041212-A2.  
PD 21-MAY-2004.  
PA (SACK/) SACKTOR T C.  
PA (CRAR/) CRARY J F.  
PA (HERN/) HERNANDEZ A I.  
PA (MIRR/) MIRRA S.  
PA (SHAO/) SHAO C.  
Percent Similarity: 39.3% Conservative: 66  
Best Local Similarity: 22.7% Mismatches: 140  
Query Match: 6.2% Indels: 103  
RESULT 583  
ID AEI33649 standard; DNA; 889 BP.  
DE Soybean polymorphic locus, SEQ ID 6283.  
PN US2006135758-A1.  
PD 22-JUN-2006.  
PA (WUKK/) WU K.  
Percent Similarity: 42.2% Conservative: 31  
Best Local Similarity: 27.2% Mismatches: 86  
Query Match: 6.1% Indels: 34  
RESULT 584  
ID AEB65261 standard; DNA; 1718 BP.  
DE Rice genome derived DNA sequence, SEQ ID 406.  
PN JP2005185101-A.  
PD 14-JUL-2005.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.  
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.  
Percent Similarity: 37.9% Conservative: 56  
Best Local Similarity: 22.0% Mismatches: 124  
Query Match: 6.1% Indels: 96  
RESULT 585  
ID ADU01973 standard; cDNA; 2328 BP.  
DE Novel human polynucleotide seqid 440.  
PN WO2004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 45.3% Conservative: 27

Best Local Similarity: 25.9% Mismatches: 73  
Query Match: 6.1% Indels: 3  
RESULT 586  
ID ADQ67406 standard; cDNA; 3089 BP.  
DE Novel human cDNA sequence #2379.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 39.0% Conservative: 55  
Best Local Similarity: 24.1% Mismatches: 135  
Query Match: 6.1% Indels: 91  
RESULT 587  
ID ABK89101 standard; DNA; 3949 BP.  
DE Aspergillus oryzae galactose oxidase gene.  
PN JP2002165596-A.  
PD 11-JUN-2002.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN SHURUI SOGO KENKY.  
PA (GEKK-) GEKKEIKAN KK.  
Percent Similarity: 33.7% Conservative: 57  
Best Local Similarity: 21.5% Mismatches: 181  
Query Match: 6.1% Indels: 129  
RESULT 588  
ID ABL20362 standard; DNA; 5396 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12559.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 38.0% Conservative: 50  
Best Local Similarity: 23.8% Mismatches: 117  
Query Match: 6.1% Indels: 104  
RESULT 589  
ID ACA19870 standard; DNA; 6816 BP.  
DE Prokaryotic essential gene #1527.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 40.7% Conservative: 76  
Best Local Similarity: 21.1% Mismatches: 195  
Query Match: 6.1% Indels: 35  
RESULT 590  
ID ABO81845 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1101.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Percent Similarity: 35.0% Conservative: 38  
Best Local Similarity: 24.6% Mismatches: 135  
Query Match: 6.1% Indels: 104  
RESULT 591  
ID ADT18751 standard; cDNA; 1131 BP.  
DE Plant cDNA, Seq ID 4077.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Percent Similarity: 44.0% Conservative: 31  
Best Local Similarity: 28.5% Mismatches: 75  
Query Match: 6.1% Indels: 38  
RESULT 592  
ID AAV41733 standard; DNA; 1140 BP.  
DE Codon-optimised Ramy3D signal fused to prosubtilisin BPN' DNA.  
PN WO9836085-A1.  
PD 20-AUG-1998.  
PA (PHYT-) APPLIED PHYTOLOGICS INC.  
Percent Similarity: 41.3% Conservative: 44  
Best Local Similarity: 25.1% Mismatches: 94  
Query Match: 6.1% Indels: 66  
RESULT 593  
ID AEB65063 standard; DNA; 1475 BP.  
DE Rice genome derived DNA sequence, SEQ ID 208.  
PN JP2005185101-A.  
PD 14-JUL-2005.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.

PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.  
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.  
Percent Similarity: 35.5% Conservative: 52  
Best Local Similarity: 22.2% Mismatches: 108  
Query Match: 6.1% Indels: 146  
RESULT 594  
ID ADQ84536 standard; cDNA; 2398 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1350.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.7% Conservative: 71  
Best Local Similarity: 22.7% Mismatches: 190  
Query Match: 6.1% Indels: 108  
RESULT 595  
ID ADQ86498 standard; cDNA; 2398 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3371.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.7% Conservative: 71  
Best Local Similarity: 22.7% Mismatches: 190  
Query Match: 6.1% Indels: 108  
RESULT 596  
ID ACH87318 standard; DNA; 2412 BP.  
DE Human genome derived single exon probe #20513.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 36.0% Conservative: 50  
Best Local Similarity: 23.1% Mismatches: 153  
Query Match: 6.1% Indels: 96  
RESULT 597  
ID ADY34547 standard; cDNA; 2425 BP.  
DE DPCR1 (759 amino acid form) coding sequence.  
PN WO2005019257-A1.  
PD 03-MAR-2005.  
PA (CLLT ) CELLTECH R & D LTD.  
Percent Similarity: 36.6% Conservative: 60  
Best Local Similarity: 22.0% Mismatches: 136  
Query Match: 6.1% Indels: 126  
RESULT 598  
ID ADC30653 standard; cDNA; 6614 BP.  
DE Human novel cDNA sequence, SEQ ID NO:735.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.2% Conservative: 37  
Best Local Similarity: 25.7% Mismatches: 135  
Query Match: 6.1% Indels: 69  
RESULT 599  
ID ABL03416 standard; cDNA; 9402 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4730.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 36.4% Conservative: 66  
Best Local Similarity: 20.7% Mismatches: 140  
Query Match: 6.1% Indels: 127  
RESULT 600  
ID ADF89954 standard; cDNA; 1446 BP.  
DE N. crassa del12-desaturase (NCD12D) encoding cDNA.  
PN WO2003099216-A2.  
PD 04-DEC-2003.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Percent Similarity: 33.0% Conservative: 50  
Best Local Similarity: 21.7% Mismatches: 156

Query Match: 6.1% Indels: 142  
RESULT 601  
ID AEA10864 standard; DNA; 1446 BP.  
DE Neurospora crassa sub family 2 Delta-15 desaturase Nc2 DNA.  
PN WO2005047480-A2.  
PD 26-MAY-2005.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Percent Similarity: 33.0% Conservative: 50  
Best Local Similarity: 21.7% Mismatches: 156  
Query Match: 6.1% Indels: 142  
RESULT 602  
ID AEA12341 standard; cDNA; 1446 BP.  
DE DNA encoding delta12 desaturase polypeptide #8.  
PN WO2005047485-A2.  
PD 26-MAY-2005.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Percent Similarity: 33.0% Conservative: 50  
Best Local Similarity: 21.7% Mismatches: 156  
Query Match: 6.1% Indels: 142  
RESULT 603  
ID AEA14796 standard; DNA; 1446 BP.  
DE Sub-family 2 desaturase DNA SEQ ID NO 15.  
PN WO2005047479-A2.  
PD 26-MAY-2005.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Percent Similarity: 33.0% Conservative: 50  
Best Local Similarity: 21.7% Mismatches: 156  
Query Match: 6.1% Indels: 142  
RESULT 604  
ID AEH65581 standard; DNA; 1446 BP.  
DE N. crassa delta 12 desaturase DNA SEQ ID NO: 35.  
PN US2006094092-A1.  
PD 04-MAY-2006.  
PA (DAMU/) DAMUDE H G.  
PA (GILL/) GILLIES P J.  
PA (MACO/) MACOOL D J.  
PA (PICA/) PICATAGGIO S K.  
PA (POLL/) POLLAK D M W.  
PA (RAGG/) RAGGHianti J J.  
PA (XUEZ/) XUE Z.  
PA (YADA/) YADAV N S.  
PA (ZHAN/) ZHANG H.  
PA (ZHUQ/) ZHU Q Q.  
Percent Similarity: 33.0% Conservative: 50  
Best Local Similarity: 21.7% Mismatches: 156  
Query Match: 6.1% Indels: 142  
RESULT 605  
ID AEI06008 standard; DNA; 1446 BP.  
DE Neurospora crassa delta 12 desaturase coding sequence, SEQ ID 35.  
PN US2006115881-A1.  
PD 01-JUN-2006.  
PA (DAMU/) DAMUDE H G.  
PA (GILL/) GILLIES P J.  
PA (MACO/) MACOOL D J.  
PA (PICA/) PICATAGGIO S K.  
PA (POLL/) POLLAK D M W.  
PA (RAGG/) RAGGHianti J J.  
PA (XUEZ/) XUE Z.  
PA (YADA/) YADAV N S.  
PA (ZHAN/) ZHANG H.  
PA (ZHUQ/) ZHU Q Q.  
Percent Similarity: 33.0% Conservative: 50  
Best Local Similarity: 21.7% Mismatches: 156  
Query Match: 6.1% Indels: 142  
RESULT 606  
ID AEH96263 standard; DNA; 1446 BP.  
DE Delta-12 desaturase coding sequence - SEQ ID 40.  
PN US2006110806-A1.  
PD 25-MAY-2006.  
PA (DAMU/) DAMUDE H G.  
PA (GILL/) GILLIES P J.  
PA (MACO/) MACOOL D J.  
PA (PICA/) PICATAGGIO S K.

PA (RAGG/) RAGGHianti J J.  
PA (SEIP/) SEIP J E.  
PA (XUEZ/) XUE Z.  
PA (YADA/) YADAV N S.  
PA (ZHAN/) ZHANG H.  
PA (ZHUQ/) ZHU Q Q.  
Percent Similarity: 33.0% Conservative: 50  
Best Local Similarity: 21.7% Mismatches: 156  
Query Match: 6.1% Indels: 142  
RESULT 607  
ID AAD04178 standard; DNA; 1923 BP.  
DE Aspergillus niger lysophospholipase 1 (LLPL-1) DNA.  
PN WO200127251-A1.  
PD 19-APR-2001.  
PA (NOVO ) NOVOZYMES AS.  
Percent Similarity: 36.1% Conservative: 59  
Best Local Similarity: 23.8% Mismatches: 172  
Query Match: 6.1% Indels: 135  
RESULT 608  
ID ABL32439 standard; DNA; 5337 BP.  
DE Human immune system associated gene SEQ ID NO: 412.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 38.8% Conservative: 51  
Best Local Similarity: 24.6% Mismatches: 131  
Query Match: 6.1% Indels: 89  
RESULT 609  
ID AEJ07211 standard; DNA; 9931 BP.  
DE pTrex3g NSP24 vector containing Trichoderma reesei NSP24 gene.  
PN WO2006073839-A2.  
PD 13-JUL-2006.  
PA (GEMV ) GENENCOR INT INC.  
Percent Similarity: 36.1% Conservative: 53  
Best Local Similarity: 23.2% Mismatches: 128  
Query Match: 6.1% Indels: 136  
RESULT 610  
ID AEK59957 standard; DNA; 9931 BP.  
DE NSP24 protease coding sequence contained within a plasmid - SEQ ID 4.  
PN WO2006073843-A2.  
PD 13-JUL-2006.  
PA (GEMV ) GENENCOR INT INC.  
Percent Similarity: 36.1% Conservative: 53  
Best Local Similarity: 23.2% Mismatches: 128  
Query Match: 6.1% Indels: 136  
RESULT 611  
ID ADU47667 standard; DNA; 88400 BP.  
DE S. cyaneogriseus LL-F28249 compound full-length biosynthetic gene.  
PN EP1477563-A2.  
PD 17-NOV-2004.  
PA (AMHP ) WYETH.  
PA (FORT-) FORT DODGE ANIMAL HEALTH.  
Percent Similarity: 35.6% Conservative: 30  
Best Local Similarity: 24.9% Mismatches: 113  
Query Match: 6.1% Indels: 68  
RESULT 612  
Percent Similarity: 39.7% Conservative: 38  
Best Local Similarity: 26.7% Mismatches: 129  
Query Match: 6.1% Indels: 47  
RESULT 613  
ID AAH68531 standard; DNA; 349980 BP.  
DE C glutamicum coding sequence fragment SEQ ID NO: 7066.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 31.2% Conservative: 44  
Best Local Similarity: 22.8% Mismatches: 145  
Query Match: 6.1% Indels: 214  
RESULT 614  
ID AAH68532 standard; DNA; 349980 BP.  
DE C glutamicum coding sequence fragment SEQ ID NO: 7067.  
PN EP1108790-A2.  
PD 20-JUN-2001.



PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 31.2% Conservative: 44  
Best Local Similarity: 22.8% Mismatches: 145  
Query Match: 6.1% Indels: 214  
RESULT 615  
ID AAS84303 standard; cDNA; 569 BP.  
DE DNA encoding novel human diagnostic protein #20107.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC..  
Percent Similarity: 50.4% Conservative: 23  
Best Local Similarity: 32.6% Mismatches: 60  
Query Match: 6.1% Indels: 5  
RESULT 616  
ID AAD33861 standard; cDNA; 837 BP.  
DE Human secreted protein-encoding gene 17 cDNA clone HLDQZ72, SEQ ID NO:60.  
PN WO200224719-A1.  
PD 28-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 39.3% Conservative: 31  
Best Local Similarity: 25.4% Mismatches: 58  
Query Match: 6.1% Indels: 79  
RESULT 617  
ID AAS80389 standard; cDNA; 1209 BP.  
DE DNA encoding novel human diagnostic protein #16193.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 50.4% Conservative: 23  
Best Local Similarity: 32.6% Mismatches: 60  
Query Match: 6.1% Indels: 5  
RESULT 618  
ID AAS81401 standard; cDNA; 1209 BP.  
DE DNA encoding novel human diagnostic protein #17205.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 50.4% Conservative: 23  
Best Local Similarity: 32.6% Mismatches: 60  
Query Match: 6.1% Indels: 5  
RESULT 619  
ID ADS48415 standard; cDNA; 1274 BP.  
DE Bacterial polynucleotide #3158.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 34.4% Conservative: 32  
Best Local Similarity: 23.3% Mismatches: 95  
Query Match: 6.1% Indels: 94  
RESULT 620  
ID AEJ87551 standard; DNA; 1407 BP.  
DE B. subtilis yaad-Xa-basf1-his fusion DNA.  
PN WO2006082251-A2.  
PD 10-AUG-2006.  
PA (BADI ) BASF AG.  
Percent Similarity: 37.8% Conservative: 35  
Best Local Similarity: 23.7% Mismatches: 82  
Query Match: 6.1% Indels: 73  
RESULT 621  
ID AEK60806 standard; DNA; 1407 BP.  
DE Hydrophobin fusion construct yaad-Xa-basf-1-his DNA.  
PN WO2006082253-A2..  
PD 10-AUG-2006.  
PA (BADI ) BASF AG.  
Percent Similarity: 37.8% Conservative: 35  
Best Local Similarity: 23.7% Mismatches: 82  
Query Match: 6.1% Indels: 73  
RESULT 622  
ID AEL10480 standard; DNA; 1407 BP.

DE Bacillus subtilis yaad-Xa-hydrophobin basf1-his fusion DNA.  
PN DE102005015043-A1.  
PD 05-OCT-2006.  
PA (BADI ) BASF AG.  
Percent Similarity: 37.8% Conservative: 35  
Best Local Similarity: 23.7% Mismatches: 82  
Query Match: 6.1% Indels: 73  
RESULT 623  
ID AEL10520 standard; DNA; 1407 BP.  
DE Bacillus subtilis yaad-Xa-hydrophobin basf1-his fusion DNA.  
PN WO2006103230-A1.  
PD 05-OCT-2006.  
PA (BADI ) BASF AG.  
Percent Similarity: 37.8% Conservative: 35  
Best Local Similarity: 23.7% Mismatches: 82  
Query Match: 6.1% Indels: 73  
RESULT 624  
ID AEL10590 standard; DNA; 1407 BP.  
DE Bacillus subtilis yaad-Xa-hydrophobin basf1-his fusion DNA.  
PN WO2006103225-A1.  
PD 05-OCT-2006.  
PA (BADI ) BASF AG.  
Percent Similarity: 37.8% Conservative: 35  
Best Local Similarity: 23.7% Mismatches: 82  
Query Match: 6.1% Indels: 73  
RESULT 625  
ID AEL10555 standard; DNA; 1407 BP.  
DE Bacillus subtilis yaad-Xa-hydrophobin basf1-his fusion DNA.  
PN WO2006103251-A1.  
PD 05-OCT-2006.  
PA (BADI ) BASF AG.  
Percent Similarity: 37.8% Conservative: 35  
Best Local Similarity: 23.7% Mismatches: 82  
Query Match: 6.1% Indels: 73  
RESULT 626  
ID ABL61038 standard; DNA; 3783 BP.  
DE N. clavipes spidroin synthetic homologue S01S01.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Percent Similarity: 35.2% Conservative: 41  
Best Local Similarity: 23.5% Mismatches: 111  
Query Match: 6.1% Indels: 116  
RESULT 627  
ID ABL27121 standard; DNA; 4287 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32836.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 39.5% Conservative: 52  
Best Local Similarity: 24.0% Mismatches: 126  
Query Match: 6.1% Indels: 77  
RESULT 628  
ID ABL61040 standard; DNA; 5658 BP.  
DE N. clavipes spidroin synthetic homologue S01SM12.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Percent Similarity: 35.2% Conservative: 41  
Best Local Similarity: 23.5% Mismatches: 111  
Query Match: 6.1% Indels: 116  
RESULT 629  
ID AAV52204 standard; DNA; 32768 BP.  
DE Streptococcus pneumoniae genome fragment SEQ ID NO:71.  
PN WO9818931-A2.  
PD 07-MAY-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 39.2% Conservative: 73  
Best Local Similarity: 22.6% Mismatches: 187  
Query Match: 6.1% Indels: 83  
RESULT 630  
ID ADQ54163 standard; DNA; 654 BP.  
DE Novel canine microarray-related DNA sequence SeqID5465.

PN WO2004063324-A2.  
PD 29-JUL-2004.  
PA (GENE-) GENE LOGIC INC.  
PA (PFIZ ) PFIZER PROD INC.  
Percent Similarity: 34.3%  
Best Local Similarity: 24.9%  
Query Match: 6.0%  
RESULT 631  
ID ABZ68334 standard; DNA; 1098 BP.  
DE Nucleotide sequence of human TIM-1 allele 3.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Percent Similarity: 37.5%  
Best Local Similarity: 24.3%  
Query Match: 6.0%  
RESULT 632  
ID ADY98076 standard; cDNA; 1098 BP.  
DE Human TIM-1 allele 3.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Percent Similarity: 37.5%  
Best Local Similarity: 24.3%  
Query Match: 6.0%  
RESULT 633  
ID AED60520 standard; DNA; 1098 BP.  
DE Human TIM-1, allele 3, DNA SEQ ID NO:28.  
PN WO2005097211-A2.  
PD 20-OCT-2005.  
PA (TELO-) TELOS PHARM INC.  
Percent Similarity: 37.5%  
Best Local Similarity: 24.3%  
Query Match: 6.0%  
RESULT 634  
ID AAT90038 standard; cDNA to mRNA; 1542 BP.  
DE Hepatocyte growth factor activator inhibitor cDNA.  
PN EP759467-A2.  
PD 26-FEB-1997.  
PA (MITU ) MITSUBISHI CHEM CORP.  
Percent Similarity: 37.7%  
Best Local Similarity: 22.7%  
Query Match: 6.0%  
RESULT 635  
ID AAX02200 standard; DNA; 1542 BP.  
DE Human HAI-1 cDNA.  
PN JP11035480-A.  
PD 09-FEB-1999.  
PA (MITU ) MITSUBISHI CHEM CORP.  
Percent Similarity: 37.7%  
Best Local Similarity: 22.7%  
Query Match: 6.0%  
RESULT 636  
ID ADS47275 standard; cDNA; 1671 BP.  
DE Bacterial polynucleotide #2018.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 41.5%  
Best Local Similarity: 22.6%  
Query Match: 6.0%  
RESULT 637  
ID ABT42440 standard; DNA; 2636 BP.  
DE Toxicity modelling related rat gene SEQ ID No 2142.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 42.4%  
Conservative: 23

Best Local Similarity: 29.9%  
Query Match: 6.0%  
RESULT 638  
ID ADT47317 standard; cDNA; 3228 BP.  
DE Bacterial polynucleotide #22068.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 37.4%  
Best Local Similarity: 22.8%  
Query Match: 6.0%  
RESULT 639  
ID ABL28633 standard; DNA; 4777 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37372.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 31.8%  
Best Local Similarity: 20.2%  
Query Match: 6.0%  
RESULT 640  
Percent Similarity: 37.4%  
Best Local Similarity: 26.6%  
Query Match: 6.0%  
RESULT 641  
ID AAH77281 standard; cDNA; 1651 BP.  
DE Human hepatocyte growth factor activator inhibitor (HGF-AIh) #2 cDNA.  
PN WO200168707-A1.  
PD 20-SEP-2001.  
PA (ELIL ) LILLY & CO ELI.  
Percent Similarity: 34.2%  
Best Local Similarity: 21.9%  
Query Match: 6.0%  
RESULT 642  
ID AAD28495 standard; cDNA; 2601 BP.  
DE Human extracellular messenger (XMES) -5 cDNA.  
PN WO200194587-A2.  
PD 13-DEC-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 34.2%  
Best Local Similarity: 21.9%  
Query Match: 6.0%  
RESULT 643  
ID AAH17836 standard; cDNA; 3260 BP.  
DE Human cDNA sequence SEQ ID NO:17520.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 34.2%  
Best Local Similarity: 21.9%  
Query Match: 6.0%  
RESULT 644  
ID ABX71379 standard; cDNA; 4082 BP.  
DE Human testes-derived cDNA from clone DKFZphtes3\_2a11.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Percent Similarity: 34.9%  
Best Local Similarity: 23.6%  
Query Match: 6.0%  
RESULT 645  
ID ADC30325 standard; cDNA; 4082 BP.  
DE Human novel cDNA sequence, SEQ ID NO:407.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 34.7%  
Best Local Similarity: 22.9%  
Query Match: 6.0%  
Conservative: 56  
Mismatches: 174  
Indels: 141

RESULT 646  
ID ADZ70350 standard; cDNA; 4082 BP.  
DE Human cDNA from lung cancer marker gene FLJ12761.  
PN WO2005032495-A2.  
PD 14-APR-2005.  
PA (FARB ) BAYER PHARM CORP.  
Percent Similarity: 34.9%  
Best Local Similarity: 23.6%  
Query Match: 6.0%  
Conservative: 43  
Mismatches: 123  
Indels: 128  
RESULT 647  
ID ADZ80791 standard; cDNA; 4154 BP.  
DE Nucleotide sequence of human homologue of Drosophila gene CG11006.  
PN WO2005039635-A2.  
PD 06-MAY-2005.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS PHARMA GMBH.  
Percent Similarity: 34.9%  
Best Local Similarity: 23.6%  
Query Match: 6.0%  
Conservative: 43  
Mismatches: 123  
Indels: 128  
RESULT 648  
ID ABL05017 standard; cDNA; 4667 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 9533.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 33.6%  
Best Local Similarity: 20.7%  
Query Match: 6.0%  
Conservative: 55  
Mismatches: 152  
Indels: 133  
RESULT 649  
ID ACF74294 standard; DNA; 6813 BP.  
DE Staphylococcus aureus DNA #1974.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 41.1%  
Best Local Similarity: 21.6%  
Query Match: 6.0%  
Conservative: 76  
Mismatches: 192  
Indels: 37  
RESULT 650  
ID ABZ22900 standard; DNA; 6852 BP.  
DE Staphylococcus epidermidis DsqA encoding DNA SEQ ID NO:3.  
PN WO2002102829-A2.  
PD 27-DEC-2002.  
PA (INHI-) INHIBITEX INC.  
PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.  
PA (UYPA-) UNIV PAVIA.  
Percent Similarity: 41.1%  
Best Local Similarity: 21.6%  
Query Match: 6.0%  
Conservative: 76  
Mismatches: 192  
Indels: 37  
RESULT 651  
ID AAL07156 standard; DNA; 24387 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 9844.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 35.6%  
Best Local Similarity: 22.4%  
Query Match: 6.0%  
Conservative: 56  
Mismatches: 140  
Indels: 135  
RESULT 652  
ID ACH87193 standard; DNA; 461 BP.  
DE Human genome derived single exon probe #20388.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 45.8%  
Best Local Similarity: 26.0%  
Query Match: 6.0%  
Conservative: 26  
Mismatches: 69  
Indels: 2  
RESULT 653  
ID ABA35209 standard; DNA; 576 BP.  
DE Probe #13675 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.4%  
Best Local Similarity: 34.2%  
Query Match: 6.0%  
Conservative: 10  
Mismatches: 66  
Indels: 30  
RESULT 654  
ID AAK42331 standard; DNA; 576 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 16888.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.4%  
Best Local Similarity: 34.2%  
Query Match: 6.0%  
Conservative: 10  
Mismatches: 66  
Indels: 30  
RESULT 655  
ID AAK16577 standard; DNA; 576 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 16568.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.4%  
Best Local Similarity: 34.2%  
Query Match: 6.0%  
Conservative: 10  
Mismatches: 66  
Indels: 30  
RESULT 656  
ID AAI08759 standard; DNA; 576 BP.  
DE Probe #8750 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 40.4%  
Best Local Similarity: 34.2%  
Query Match: 6.0%  
Conservative: 10  
Mismatches: 66  
Indels: 30  
RESULT 657  
ID ACH91803 standard; DNA; 627 BP.  
DE Human genome derived single exon probe #24998.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 40.4%  
Best Local Similarity: 34.2%  
Query Match: 6.0%  
Conservative: 10  
Mismatches: 66  
Indels: 30  
RESULT 658  
ID AEB65941 standard; DNA; 1413 BP.  
DE Rice genome derived DNA sequence, SEQ ID 1086.  
PN JP2005185101-A.  
PD 14-JUL-2005.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
PA (SEIB-) SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.  
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.  
Percent Similarity: 38.8%  
Best Local Similarity: 26.2%  
Query Match: 6.0%  
Conservative: 41  
Mismatches: 114  
Indels: 86  
RESULT 659  
ID ABL61043 standard; DNA; 1908 BP.  
DE N. clavipes spideroin synthetic homologue SOL.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Percent Similarity: 36.7%  
Best Local Similarity: 26.0%  
Query Match: 6.0%  
Conservative: 36  
Mismatches: 154  
Indels: 62  
RESULT 660  
ID ABQ61126 standard; cDNA; 2114 BP.  
DE Human EXMAD-20 protein encoding sequence.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 32.9%  
Best Local Similarity: 20.9%  
Query Match: 6.0%  
Conservative: 50  
Mismatches: 124  
Indels: 156  
RESULT 661



ID AAZ45836 standard; cDNA; 2455 BP.  
DE cDNA of intestinal insect mucin isoform IIM14.  
PN WO9967373-A2.  
PD 29-DEC-1999.  
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.  
Percent Similarity: 40.6% Conservative: 15  
Best Local Similarity: 31.0% Mismatches: 78  
Query Match: 6.0% Indels: 14  
RESULT 662  
ID ADP04874 standard; cDNA; 2529 BP.  
DE Sea squirt cDNA with tissue specific expression in development Seq 469.  
PN JP2004057129-A.  
PD 26-FEB-2004.  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
Percent Similarity: 32.8% Conservative: 59  
Best Local Similarity: 20.3% Mismatches: 151  
Query Match: 6.0% Indels: 169  
RESULT 663  
ID AAZ45837 standard; cDNA; 2821 BP.  
DE cDNA of intestinal insect mucin isoform IIM22.  
PN WO9967373-A2.  
PD 29-DEC-1999.  
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.  
Percent Similarity: 40.6% Conservative: 15  
Best Local Similarity: 31.0% Mismatches: 78  
Query Match: 6.0% Indels: 14  
RESULT 664  
ID ABL61039 standard; DNA; 2985 BP.  
DE N. clavipes spidroin synthetic homologue SO1SM12.  
PN DE10113781-A1.  
PD 13-DEC-2001.  
PA (IPKP-) IPK INST PFLANZENGENETIK & KULTURPFLANZE.  
Percent Similarity: 36.7% Conservative: 36  
Best Local Similarity: 26.0% Mismatches: 154  
Query Match: 6.0% Indels: 62  
RESULT 665  
ID ABT10922 standard; cDNA; 4669 BP.  
DE Human breast cancer associated coding sequence SEQ ID NO: 1056.  
PN WO200259271-A2.  
PD 01-AUG-2002.  
PA (GENE-) GENE LOGIC INC.  
Percent Similarity: 35.1% Conservative: 56  
Best Local Similarity: 22.8% Mismatches: 130  
Query Match: 6.0% Indels: 167  
RESULT 666  
ID AAA61847 standard; DNA; 5511 BP.  
DE Cryptosporidium parvum Iowa isolate GP900 ORF.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Percent Similarity: 37.1% Conservative: 45  
Best Local Similarity: 23.3% Mismatches: 146  
Query Match: 6.0% Indels: 59  
RESULT 667  
ID ABT04776 standard; DNA; 5511 BP.  
DE C parvum GP900 gene fragment SEQ ID NO: 2.  
PN WO200194631-A1.  
PD 13-DEC-2001.  
PA (REGC ) UNIV CALIFORNIA.  
Percent Similarity: 37.1% Conservative: 45  
Best Local Similarity: 23.3% Mismatches: 146  
Query Match: 6.0% Indels: 59  
RESULT 668  
ID ADA83845 standard; DNA; 5610 BP.  
DE Human COL17A1 gene.  
PN WO2002103028-A2.  
PD 27-DEC-2002.  
PA (BIOM-) BIOMEDICAL CENT.  
Percent Similarity: 35.1% Conservative: 56  
Best Local Similarity: 22.8% Mismatches: 130  
Query Match: 6.0% Indels: 167  
RESULT 669  
ID ACN39117 standard; cDNA; 5610 BP.

DE Tumour-associated antigenic target (TAT) cDNA DNA325377, SEQ ID NO:3058.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.1% Conservative: 56  
Best Local Similarity: 22.8% Mismatches: 130  
Query Match: 6.0% Indels: 167  
RESULT 670  
ID ABQ60955 standard; cDNA; 5714 BP.  
DE Bullous pemphigoid BP180 encoding sequence.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 35.1% Conservative: 57  
Best Local Similarity: 22.6% Mismatches: 130  
Query Match: 6.0% Indels: 167  
RESULT 671  
ID AED73234 standard; cDNA; 5796 BP.  
DE Human placental protein encoding cDNA SEQ ID NO:62.  
PN US2005255114-A1.  
PD 17-NOV-2005.  
PA (NUVE-) NUVELO INC.  
Percent Similarity: 35.1% Conservative: 56  
Best Local Similarity: 22.8% Mismatches: 130  
Query Match: 6.0% Indels: 167  
RESULT 672  
ID AAA61846 standard; DNA; 7334 BP.  
DE Cryptosporidium parvum Iowa isolate GP900 DNA.  
PN US6071518-A.  
PD 06-JUN-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Percent Similarity: 37.1% Conservative: 45  
Best Local Similarity: 23.3% Mismatches: 146  
Query Match: 6.0% Indels: 59  
RESULT 673  
ID ABT04775 standard; DNA; 7334 BP.  
DE C parvum GP900 gene fragment SEQ ID NO: 1.  
PN WO200194631-A1.  
PD 13-DEC-2001.  
PA (REGC ) UNIV CALIFORNIA.  
Percent Similarity: 37.1% Conservative: 45  
Best Local Similarity: 23.3% Mismatches: 146  
Query Match: 6.0% Indels: 59  
RESULT 674  
ID ADN12161 standard; DNA; 172281 BP.  
DE Epstein-Barr virus genome B95-8.  
PN WO2004027036-A2.  
PD 01-APR-2004.  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Percent Similarity: 34.2% Conservative: 46  
Best Local Similarity: 21.6% Mismatches: 163  
Query Match: 6.0% Indels: 78  
RESULT 675  
ID ABQ93367 standard; cDNA; 12279 BP.  
DE Human cDNA SEQ ID NO 80.  
PN WO200218424-A2.  
PD 07-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 47.0% Conservative: 35  
Best Local Similarity: 28.1% Mismatches: 65  
Query Match: 5.9% Indels: 33  
RESULT 676  
ID AEE75855 standard; DNA; 73921 BP.  
DE Streptomyces tautomycetin polyketide synthase enzyme gene cluster.  
PN WO2005118797-A2.  
PD 15-DEC-2005.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Percent Similarity: 41.8% Conservative: 36  
Best Local Similarity: 26.8% Mismatches: 105  
Query Match: 5.9% Indels: 34  
RESULT 677  
ID AAA44382 standard; cDNA; 716 BP.  
DE Human secreted expressed sequence tag SEQ ID NO:957.

PN WO200021991-A1.  
PD 20-APR-2000.  
PA (GEMY ) GENETICS INST INC.  
Percent Similarity: 38.2%  
Best Local Similarity: 26.7%  
Query Match: 5.9%  
Conservative: 29  
Mismatches: 94  
Indels: 61  
RESULT 678  
ID ADJ48292 standard; DNA; 1428 BP.  
DE Maize oil-associated gene #110.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Percent Similarity: 38.1%  
Best Local Similarity: 27.1%  
Query Match: 5.9%  
Conservative: 37  
Mismatches: 111  
Indels: 101  
RESULT 679  
ID ADT17022 standard; cDNA; 1428 BP.  
DE Plant cDNA, Seq ID 2348.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Percent Similarity: 38.1%  
Best Local Similarity: 27.1%  
Query Match: 5.9%  
Conservative: 37  
Mismatches: 111  
Indels: 101  
RESULT 680  
ID ADS47261 standard; cDNA; 2178 BP.  
DE Bacterial polynucleotide #2004.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 33.6%  
Best Local Similarity: 19.5%  
Query Match: 5.9%  
Conservative: 64  
Mismatches: 185  
Indels: 118  
RESULT 681  
ID ADW72956 standard; DNA; 2391 BP.  
DE Bread wheat strain identification-related 1Bx14 subunit DNA.  
PN CN1428351-A.  
PD 09-JUL-2003.  
PA (GENE-) INST GENETICS CHINESE ACAD SCI.  
Percent Similarity: 38.4%  
Best Local Similarity: 23.5%  
Query Match: 5.9%  
Conservative: 57  
Mismatches: 166  
Indels: 72  
RESULT 682  
ID ABS51504 standard; cDNA; 4468 BP.  
DE Human cDNA encoding prey protein for Shigella ospC1 #29.  
PN WO200257303-A2.  
PD 25-JUL-2002.  
PA (HYBR-) HYBRIGENICS.  
Percent Similarity: 36.3%  
Best Local Similarity: 23.9%  
Query Match: 5.9%  
Conservative: 45  
Mismatches: 146  
Indels: 87  
RESULT 683  
ID ADR32198 standard; DNA; 4893 BP.  
DE Yeast FLO11 open reading frame, SEQ ID NO:3.  
PN WO2004067565-A1.  
PD 12-AUG-2004.  
PA (OSBO-) OSBORNE DISTRIBUIDORA SA.  
PA (UYDO/) UNIV DE OLAVIDE PABLO.  
Percent Similarity: 40.4%  
Best Local Similarity: 26.5%  
Query Match: 5.9%  
Conservative: 38  
Mismatches: 104  
Indels: 61  
RESULT 684  
ID ADS10393 standard; DNA; 7500 BP.  
DE Human therapeutic DNA - SEQ ID 630.  
PN WO2004080148-A2.

PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Percent Similarity: 36.3%  
Best Local Similarity: 23.9%  
Query Match: 5.9%  
Conservative: 45  
Mismatches: 146  
Indels: 87  
RESULT 685  
ID AEF92979 standard; DNA; 13125 BP.  
DE Human HectH9 ORF DNA sequence.  
PN WO2006018654-A1.  
PD 23-FEB-2006.  
PA (CANC-) CANCER RES TECHNOLOGY LTD.  
Percent Similarity: 36.3%  
Best Local Similarity: 23.9%  
Query Match: 5.9%  
Conservative: 45  
Mismatches: 146  
Indels: 87  
RESULT 686  
ID ADE79055 standard; DNA; 13855 BP.  
DE Human protein modification and maintenance molecule (PMM)-35 gene.  
PN WO2003063688-A2.  
PD 07-AUG-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 36.3%  
Best Local Similarity: 23.9%  
Query Match: 5.9%  
Conservative: 45  
Mismatches: 146  
Indels: 87  
RESULT 687  
ID ADQ97928 standard; DNA; 138808 BP.  
DE Human cancer associated sequence HD11-024, SEQ ID 905.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 41.1%  
Best Local Similarity: 26.5%  
Query Match: 5.9%  
Conservative: 22  
Mismatches: 75  
Indels: 14  
RESULT 688  
ID ACN44631 standard; cDNA; 1706 BP.  
DE Human mRNA sequence hCT1686293.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 39.0%  
Best Local Similarity: 25.5%  
Query Match: 5.9%  
Conservative: 51  
Mismatches: 118  
Indels: 112  
RESULT 689  
ID ADM41104 standard; cDNA; 1924 BP.  
DE Human CD43 (sialophorin, leukosialin)-encoding cDNA, SEQ ID NO:5.  
PN WO2004026120-A2.  
PD 01-APR-2004.  
PA (GEOH) GEN HOSPITAL CORP.  
Percent Similarity: 39.0%  
Best Local Similarity: 25.5%  
Query Match: 5.9%  
Conservative: 51  
Mismatches: 118  
Indels: 112  
RESULT 690  
ID ABZ35214 standard; cDNA; 2166 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 326.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
Percent Similarity: 36.8%  
Best Local Similarity: 22.6%  
Query Match: 5.9%  
Conservative: 57  
Mismatches: 139  
Indels: 113  
RESULT 691  
ID ADX52983 standard; cDNA; 2220 BP.  
DE Plant full length insert polynucleotide seqid 27723.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Percent Similarity: 39.1%  
Best Local Similarity: 23.6%  
Query Match: 5.9%  
Conservative: 46  
Mismatches: 136  
Indels: 45

RESULT 692  
ID AEK91705 standard; cDNA; 2235 BP.  
DE Breast cancer antigen Muc-1 RT-PCR amplified nucleic acid.  
PN WO2006105255-A2.  
PD 05-OCT-2006.  
PA (UNII ) UNIV ILLINOIS FOUND.  
Percent Similarity: 36.8%  
Best Local Similarity: 22.6%  
Query Match: 5.9%  
Conservative: 57  
Mismatches: 139  
Indels: 113  
RESULT 693  
ID ABL28816 standard; DNA; 2648 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37921.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 39.2%  
Best Local Similarity: 25.1%  
Query Match: 5.9%  
Conservative: 32  
Mismatches: 104  
Indels: 35  
RESULT 694  
ID ADZ13126 standard; cDNA; 2696 BP.  
DE Human cancer-associated cDNA #200.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 39.0%  
Best Local Similarity: 25.5%  
Query Match: 5.9%  
Conservative: 51  
Mismatches: 118  
Indels: 112  
RESULT 695  
ID AAT33007 standard; DNA; 10266 BP.  
DE Mouse SRY-related gene.  
PN JP08154685-A.  
PD 18-JUN-1996.  
PA (KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU.  
Percent Similarity: 43.0%  
Best Local Similarity: 24.6%  
Query Match: 5.9%  
Conservative: 56  
Mismatches: 136  
Indels: 39  
RESULT 696  
ID ADJ81505 standard; DNA; 14016 BP.  
DE Plant retroelement associated sequence #66.  
PN WO2003050259-A2.  
PD 19-JUN-2003.  
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.  
Percent Similarity: 36.4%  
Best Local Similarity: 25.9%  
Query Match: 5.9%  
Conservative: 40  
Mismatches: 159  
Indels: 83  
RESULT 697  
ID AEK18770 standard; DNA; 1971884 BP.  
DE T. parva strain Muguga chromosome 2 chr2\_complete SEQ ID NO:70.  
PN US2006210537-A1.  
PD 21-SEP-2006.  
PA (AUDO/) AUDONNET J F.  
PA (LOOS/) LOOSMORE S M.  
Percent Similarity: 32.3%  
Best Local Similarity: 21.4%  
Query Match: 5.9%  
Conservative: 41  
Mismatches: 131  
Indels: 126  
RESULT 698  
ID ADJ39821 standard; cDNA; 947 BP.  
DE Plant cDNA #821.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHE D.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 36.0%  
Best Local Similarity: 25.9%  
Conservative: 29  
Mismatches: 99

Query Match: 5.9% Indels: 84  
RESULT 699  
ID ADT18753 standard; cDNA; 1407 BP.  
DE Plant cDNA, Seq ID 4079.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Percent Similarity: 39.1%  
Best Local Similarity: 24.9%  
Query Match: 5.9%  
Conservative: 37  
Mismatches: 112  
Indels: 48  
RESULT 700  
ID ABT23249 standard; DNA; 1687 BP.  
DE Seed development embryo/endosperm size alteration DNA SEQ ID 40.  
PN WO200299063-A2.  
PD 12-DEC-2002.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
Percent Similarity: 40.0%  
Best Local Similarity: 25.8%  
Query Match: 5.9%  
Conservative: 32  
Mismatches: 105  
Indels: 31  
RESULT 701  
ID AEI36095 standard; DNA; 2042 BP.  
DE Soybean polymorphic locus, SEQ ID 8729.  
PN US2006135758-A1.  
PD 22-JUN-2006.  
PA (WUKK/) WU K.  
Percent Similarity: 37.7%  
Best Local Similarity: 24.9%  
Query Match: 5.9%  
Conservative: 42  
Mismatches: 113  
Indels: 93  
RESULT 702  
ID ADM02801 standard; cDNA; 2428 BP.  
DE Human cDNA of the invention SEQ ID NO:1486.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 36.8%  
Best Local Similarity: 23.2%  
Query Match: 5.9%  
Conservative: 50  
Mismatches: 128  
Indels: 107  
RESULT 703  
ID AEC85731 standard; cDNA; 2428 BP.  
DE Human cDNA clone PROST20100460, SEQ ID 1486.  
PN EP1580263-A1.  
PD 28-SEP-2005.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 36.8%  
Best Local Similarity: 23.2%  
Query Match: 5.9%  
Conservative: 50  
Mismatches: 128  
Indels: 107  
RESULT 704  
ID AAZ58824 standard; DNA; 2872 BP.  
DE Human MUC11 polypeptide encoding DNA.  
PN WO200004142-A1.  
PD 27-JAN-2000.  
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.  
Percent Similarity: 34.9%  
Best Local Similarity: 23.4%  
Query Match: 5.9%  
Conservative: 41  
Mismatches: 109  
Indels: 123  
RESULT 705  
ID AAI29501 standard; cDNA; 2872 BP.  
DE C900P determined cDNA sequence.  
PN WO200149716-A2.  
PD 12-JUL-2001.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 34.9%  
Best Local Similarity: 23.4%  
Query Match: 5.9%  
Conservative: 41  
Mismatches: 109  
Indels: 123  
RESULT 706  
ID ABZ33687 standard; cDNA; 2872 BP.  
DE Human colon tumour cDNA for clone C900P SEQ ID NO:1055.  
PN WO200283070-A2.  
PD 24-OCT-2002.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 34.9%  
Best Local Similarity: 23.4%  
Query Match: 5.9%  
Conservative: 41  
Mismatches: 109



Query Match: 5.9% Indels: 123  
RESULT 707  
ID ABL15838 standard; cDNA; 3983 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41996.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 35.3%  
Best Local Similarity: 21.9%  
Query Match: 5.9%  
Conservative: 44  
Mismatches: 133  
Indels: 80  
RESULT 708  
ID ADQ29629 standard; DNA; 4707 BP.  
DE Human colorectal cancer-associated protein coding sequence #51.  
PN EPI439393-A2.  
PD 21-JUL-2004.  
PA (FARB ) BAYER HEALTHCARE LLC.  
Percent Similarity: 39.1%  
Best Local Similarity: 23.5%  
Query Match: 5.9%  
Conservative: 44  
Mismatches: 122  
Indels: 50  
RESULT 709  
ID AED17896 standard; DNA; 4707 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 147.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC.  
Percent Similarity: 39.1%  
Best Local Similarity: 23.5%  
Query Match: 5.9%  
Conservative: 44  
Mismatches: 122  
Indels: 50  
RESULT 710  
ID AEF69941 standard; DNA; 4707 BP.  
DE Colorectal cancer-associated marker DNA SEQ ID NO:119.  
PN WO2006015047-A2.  
PD 09-FEB-2006.  
PA (FARB ) BAYER HEALTHCARE LLC.  
Percent Similarity: 39.1%  
Best Local Similarity: 23.5%  
Query Match: 5.9%  
Conservative: 44  
Mismatches: 122  
Indels: 50  
RESULT 711  
ID AAH98223 standard; cDNA; 4718 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 80.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 39.1%  
Best Local Similarity: 23.5%  
Query Match: 5.9%  
Conservative: 44  
Mismatches: 122  
Indels: 50  
RESULT 712  
ID ADI21512 standard; cDNA; 4718 BP.  
DE Novel human expressed sequence tag, EST #211.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 39.1%  
Best Local Similarity: 23.5%  
Query Match: 5.9%  
Conservative: 44  
Mismatches: 122  
Indels: 50  
RESULT 713  
ID AEG97264 standard; DNA; 5355 BP.  
DE Cryptococcus neoformans CRV1 DNA homolog SEQ ID NO 33.  
PN WO2006036817-A2.  
PD 06-APR-2006.  
PA (MICR-) MICROBIA INC.  
Percent Similarity: 36.1%  
Best Local Similarity: 24.2%  
Query Match: 5.9%  
Conservative: 32  
Mismatches: 112  
Indels: 61  
RESULT 714  
ID ACF74291 standard; DNA; 798 BP.  
DE Staphylococcus aureus DNA #1971.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 42.8%  
Conservative: 51

Best Local Similarity: 23.8%  
Query Match: 5.9%  
Mismatches: 131  
Indels: 23  
RESULT 715  
ID AAV75136 standard; DNA; 1099 BP.  
DE Staphylococcus aureus contig SEQ ID #825.  
PN EP786519-A2.  
PD 30-JUL-1997.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 42.8%  
Best Local Similarity: 23.8%  
Query Match: 5.9%  
Conservative: 51  
Mismatches: 131  
Indels: 23  
RESULT 716  
ID ADM99275 standard; DNA; 1719 BP.  
DE C heterostrophus strain C4 serine carboxypeptidase DNA SeqID 158.  
PN WO2004033668-A2.  
PD 22-APR-2004.  
PA (DIVE-) DIVERSA CORP.  
Percent Similarity: 33.6%  
Best Local Similarity: 24.5%  
Query Match: 5.9%  
Conservative: 33  
Mismatches: 148  
Indels: 93  
RESULT 717  
ID ABL28927 standard; DNA; 1767 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38254.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 39.1%  
Best Local Similarity: 23.5%  
Query Match: 5.9%  
Conservative: 48  
Mismatches: 119  
Indels: 69  
RESULT 718  
ID AAS72679 standard; cDNA; 2922 BP.  
DE DNA encoding novel human diagnostic protein #8483.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.1%  
Best Local Similarity: 27.1%  
Query Match: 5.9%  
Conservative: 22  
Mismatches: 87  
Indels: 52  
RESULT 719  
ID ABL28926 standard; DNA; 3767 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38251.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 39.1%  
Best Local Similarity: 23.5%  
Query Match: 5.9%  
Conservative: 48  
Mismatches: 119  
Indels: 69  
RESULT 720  
ID ABL10402 standard; cDNA; 16962 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25688.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 37.2%  
Best Local Similarity: 26.3%  
Query Match: 5.9%  
Conservative: 39  
Mismatches: 150  
Indels: 75  
RESULT 721  
ID ADU06921 standard; DNA; 20425 BP.  
DE Wheat plant genome region containing high molecular weight glutenin gene.  
PN AU2003259589-A1.  
PD 20-MAY-2004.  
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.  
PA (AWBA-) AWB LTD.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
PA (GRAI-) GRAINS RES & DEV CORP.  
Percent Similarity: 40.2%  
Best Local Similarity: 24.7%  
Query Match: 5.9%  
Conservative: 40  
Mismatches: 111  
Indels: 45  
RESULT 722  
ID ABZ68336 standard; DNA; 1095 BP.  
DE Nucleotide sequence of human TIM-1 allele 5.  
PN WO2003002722-A2.  
PD 09-JAN-2003.

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Percent Similarity: 37.5% Conservative: 42  
Best Local Similarity: 24.6% Mismatches: 144  
Query Match: 5.8% Indels: 60  
RESULT 723  
ID ADY98080 standard; cDNA; 1095 BP.  
DE Human TIM-1 allele 5.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBEN CANCER INST INC.  
Percent Similarity: 37.5% Conservative: 42  
Best Local Similarity: 24.6% Mismatches: 144  
Query Match: 5.8% Indels: 60  
RESULT 724  
ID AED60524 standard; DNA; 1095 BP.  
DE Human TIM-1, allele 5, DNA SEQ ID NO:32.  
PN WO2005097211-A2.  
PD 20-OCT-2005.  
PA (TELO-) TELOS PHARM INC.  
Percent Similarity: 37.5% Conservative: 42  
Best Local Similarity: 24.6% Mismatches: 144  
Query Match: 5.8% Indels: 60  
RESULT 725  
ID ADL93906 standard; DNA; 1374 BP.  
DE Human FOXp2 ORF isoform VI nucleotide sequence.  
PN WO2004022104-A2.  
PD 18-MAR-2004.  
PA (ISIS-) ISIS INNOVATION LTD.  
Percent Similarity: 36.0% Conservative: 22  
Best Local Similarity: 26.7% Mismatches: 109  
Query Match: 5.8% Indels: 44  
RESULT 726  
ID AEI88287 standard; cDNA; 1752 BP.  
DE cDNA encoding glucoamylase, SEQ ID NO:41.  
PN WO2006069289-A2.  
PD 29-JUN-2006.  
PA (NOVO ) NOVOZYMES NORTH AMERICA INC.  
PA (NOVO ) NOVOZYMES AS.  
Percent Similarity: 37.5% Conservative: 39  
Best Local Similarity: 25.0% Mismatches: 142  
Query Match: 5.8% Indels: 54  
RESULT 727  
ID AAD09400 standard; cDNA; 1815 BP.  
DE Zea mays neoxanthin cleavage enzyme, VP14 cDNA.  
PN EP1116794-A2.  
PD 18-JUL-2001.  
PA (RIKE ) RIKEN KK.  
Percent Similarity: 34.3% Conservative: 36  
Best Local Similarity: 22.7% Mismatches: 116  
Query Match: 5.8% Indels: 88  
RESULT 728  
ID AAC43180 standard; DNA; 1893 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38322.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (RIKE ) RIKEN KK.  
Percent Similarity: 36.4% Conservative: 41  
Best Local Similarity: 24.6% Mismatches: 140  
Query Match: 5.8% Indels: 81  
RESULT 729  
ID ADL93902 standard; DNA; 2223 BP.  
DE Human FOXp2 ORF isoform II nucleotide sequence.  
PN WO2004022104-A2.  
PD 18-MAR-2004.  
PA (ISIS-) ISIS INNOVATION LTD.  
Percent Similarity: 36.0% Conservative: 22  
Best Local Similarity: 26.7% Mismatches: 109  
Query Match: 5.8% Indels: 44  
RESULT 730  
ID AAF30256 standard; cDNA; 2249 BP.  
DE Human cDNA encoding protein associated with Iga nephropathy.  
PN WO200105803-A1.  
PD 25-JAN-2001.

PA (GENE-) GENE LOGIC INC..  
Percent Similarity: 37.7% Conservative: 55  
Best Local Similarity: 23.6% Mismatches: 162  
Query Match: 5.8% Indels: 82  
RESULT 731  
ID AEK56460 standard; cDNA; 2498 BP.  
DE Maize cDNA SEQ ID NO:17.  
PN WO2006098626-A2.  
PD 21-SEP-2006.  
PA (PLAN-) PLANT RES INT BV.  
PA (ROTH-) ROTHAMSTED RES LTD.  
Percent Similarity: 34.3% Conservative: 36  
Best Local Similarity: 22.7% Mismatches: 116  
Query Match: 5.8% Indels: 88  
RESULT 732  
ID ADS49143 standard; cDNA; 2714 BP.  
DE Bacterial polynucleotide #3886.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 38.5% Conservative: 44  
Best Local Similarity: 24.3% Mismatches: 133  
Query Match: 5.8% Indels: 58  
RESULT 733  
ID AEI34526 standard; DNA; 3020 BP.  
DE Soybean polymorphic locus, SEQ ID 7160.  
PN US2006135758-A1.  
PD 22-JUN-2006.  
PA (WUKK/) WU K.  
Percent Similarity: 35.3% Conservative: 37  
Best Local Similarity: 23.9% Mismatches: 110  
Query Match: 5.8% Indels: 101  
RESULT 734  
ID AEH37864 standard; DNA; 3600 BP.  
DE Cryptosporidium hominis gene SEQ ID NO:955.  
PN WO2006044045-A2.  
PD 27-APR-2006.  
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.  
Percent Similarity: 40.4% Conservative: 25  
Best Local Similarity: 24.4% Mismatches: 87  
Query Match: 5.8% Indels: 6  
RESULT 735  
ID AEA19839 standard; cDNA; 3809 BP.  
DE Novel human polynucleotide SEQ ID NO 533.  
PN WO2005049806-A2.  
PD 02-JUN-2005.  
PA (NUVE-) NUVELO INC.  
Percent Similarity: 34.6% Conservative: 40  
Best Local Similarity: 23.4% Mismatches: 110  
Query Match: 5.8% Indels: 123  
RESULT 736  
ID ADC30711 standard; cDNA; 3879 BP.  
DE Human novel cDNA sequence, SEQ ID NO:793.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 34.6% Conservative: 40  
Best Local Similarity: 23.4% Mismatches: 110  
Query Match: 5.8% Indels: 123  
RESULT 737  
ID AEA19838 standard; cDNA; 3893 BP.  
DE Novel human polynucleotide SEQ ID NO 532.  
PN WO2005049806-A2.  
PD 02-JUN-2005.  
PA (NUVE-) NUVELO INC.  
Percent Similarity: 34.6% Conservative: 40  
Best Local Similarity: 23.4% Mismatches: 110  
Query Match: 5.8% Indels: 123  
RESULT 738

ID AAS76405 standard; cDNA; 4074 BP.  
DE DNA encoding novel human diagnostic protein #12209.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. Conservative: 40  
Percent Similarity: 46.3% Mismatches: 91  
Best Local Similarity: 28.8% Indels: 33  
Query Match: 33  
RESULT 739  
ID ACC50985 standard; cDNA; 4209 BP.  
DE Human bladder cancer associated cDNA sequence SEQ ID NO:63.  
PN WO2003003906-A2.  
PD 16-JAN-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC. Conservative: 39  
Percent Similarity: 35.6% Mismatches: 128  
Best Local Similarity: 24.0% Indels: 87  
Query Match: 87  
RESULT 740  
ID ADM98727 standard; DNA; 4725 BP.  
DE HMG-CoA reductase DNA #62.  
PN US2004072323-A1.  
PD 15-APR-2004.  
PA (MATS/) MATSUDA S P T. Conservative: 26  
Percent Similarity: 43.2% Mismatches: 70  
Best Local Similarity: 28.4% Indels: 30  
Query Match: 30  
RESULT 741  
ID ABL29442 standard; DNA; 11847 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 39799.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. Conservative: 55  
Percent Similarity: 39.8% Mismatches: 138  
Best Local Similarity: 24.1% Indels: 73  
Query Match: 73  
RESULT 742  
ID AAS57196 standard; DNA; 11847 BP.  
DE DNA encoding Drosophila G-protein coupled receptor, GCPR #63.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. Conservative: 55  
Percent Similarity: 39.8% Mismatches: 138  
Best Local Similarity: 24.1% Indels: 73  
Query Match: 73  
RESULT 743  
ID ADC35935 standard; DNA; 11847 BP.  
DE Drosophila G protein coupled receptor genomic DNA seq id 63.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP. Conservative: 55  
Percent Similarity: 39.8% Mismatches: 138  
Best Local Similarity: 24.1% Indels: 73  
Query Match: 73  
RESULT 744  
ID ABO41714 standard; DNA; 1127 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28305.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG. Conservative: 24  
Percent Similarity: 40.6% Mismatches: 94  
Best Local Similarity: 31.1% Indels: 59  
Query Match: 59  
RESULT 745  
ID ABO41715 standard; DNA; 1127 BP.  
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28306.  
PN WO200218632-A2.  
PD 07-MAR-2002.  
PA (EPIG-) EPIGENOMICS AG. Conservative: 24  
Percent Similarity: 40.6% Mismatches: 94  
Best Local Similarity: 31.1% Indels: 59  
Query Match: 59  
RESULT 746

ID AAT63302 standard; cDNA to mRNA; 1538 BP.  
DE A. chrysogenum O-acetylhomoserine sulphydrylase coding sequence.  
PN JP08336391-A.  
PD 24-DEC-1996.  
PA (ASAH ) ASahi KASEI KOGYO KK. Conservative: 38  
Percent Similarity: 38.6% Mismatches: 89  
Best Local Similarity: 26.4% Indels: 103  
Query Match: 103  
RESULT 747  
ID AEJ43446 standard; DNA; 2391 BP.  
DE Wheat somatic cell like 13 glutelin subunit related DNA.  
PN CN1710075-A.  
PD 21-DEC-2005.  
PA (UYSH-) UNIV SHANDONG. Conservative: 65  
Percent Similarity: 39.7% Mismatches: 163  
Best Local Similarity: 24.0% Indels: 89  
Query Match: 89  
RESULT 748  
ID ACA30008 standard; DNA; 2880 BP.  
DE Prokaryotic essential gene #11665.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC. Conservative: 52  
Percent Similarity: 36.1% Mismatches: 119  
Best Local Similarity: 21.4% Indels: 108  
Query Match: 108  
RESULT 749  
ID ADU01669 standard; cDNA; 3540 BP.  
DE Novel human polynucleotide seqid 136.  
PN WO2004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC. Conservative: 50  
Percent Similarity: 39.4% Mismatches: 115  
Best Local Similarity: 24.7% Indels: 92  
Query Match: 92  
RESULT 750  
ID AAH81794 standard; DNA; 4373 BP.  
DE Human differential transcription-associated cDNA SEQ ID 303.  
PN WO200157058-A2.  
PD 09-AUG-2001.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH. Conservative: 51  
Percent Similarity: 35.0% Mismatches: 129  
Best Local Similarity: 22.3% Indels: 135  
Query Match: 135  
RESULT 751  
ID ABL20278 standard; DNA; 5162 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12307.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. Conservative: 41  
Percent Similarity: 34.3% Mismatches: 137  
Best Local Similarity: 23.6% Indels: 114  
Query Match: 114  
RESULT 752  
ID AED18170 standard; DNA; 5894 BP.  
DE Fibrotic disorder associated polynucleotide SEQ ID NO 421.  
PN WO2005098041-A2.  
PD 20-OCT-2005.  
PA (UYFL ) UNIV FLORIDA RES FOUND INC. Conservative: 51  
Percent Similarity: 35.0% Mismatches: 129  
Best Local Similarity: 22.3% Indels: 135  
Query Match: 135  
RESULT 753  
ID AAH81795 standard; DNA; 9027 BP.  
DE Human differential transcription-associated cDNA SEQ ID 304.  
PN WO200157058-A2.  
PD 09-AUG-2001.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH. Conservative: 51  
Percent Similarity: 35.0% Mismatches: 129  
Best Local Similarity: 22.3% Indels: 135  
Query Match: 135  
RESULT 754  
ID ADN60277 standard; cDNA; 9027 BP.



DE Human serine/arginine repetitive matrix 2 encoding cDNA.  
PN WO2004039955-A2.  
PD 13-MAY-2004.  
PA (RIGE-) RIGEL PHARM INC.  
Percent Similarity: 35.0%      Conservative: 51  
Best Local Similarity: 22.3%      Mismatches: 129  
Query Match: 5.8%      Indels: 135  
RESULT 755  
ID ADP24101 standard; cDNA; 9027 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:1279.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 35.0%      Conservative: 51  
Best Local Similarity: 22.3%      Mismatches: 129  
Query Match: 5.8%      Indels: 135  
RESULT 756  
ID ADY91654 standard; DNA; 9027 BP.  
DE Human prostatic cancer marker, splicing coactivator SRM300 DNA.  
PN JP2005080524-A.  
PD 31-MAR-2005.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.  
Percent Similarity: 35.0%      Conservative: 51  
Best Local Similarity: 22.3%      Mismatches: 129  
Query Match: 5.8%      Indels: 135  
RESULT 757  
ID ADZ49494 standard; DNA; 9027 BP.  
DE Insulin signaling pathway related gene, SEQ ID 823.  
PN US2005085436-A1.  
PD 21-APR-2005.  
PA (LIHH/) LI H.  
PA (MAJJ/) MA J.  
Percent Similarity: 35.0%      Conservative: 51  
Best Local Similarity: 22.3%      Mismatches: 129  
Query Match: 5.8%      Indels: 135  
RESULT 758  
ID AEE49547 standard; cDNA; 9027 BP.  
DE Human ser/arg repetitive matrix 2 cDNA.  
PN WO2005116205-A1.  
PD 08-DEC-2005.  
PA (NICA-) JAPAN FOUND CANCER RES.  
PA (NIBI-) JAPAN BIOLOGICAL INFORMATICS CONSORTIUM.  
PA (YOSH/) YOSHIMOTO M.  
Percent Similarity: 35.0%      Conservative: 51  
Best Local Similarity: 22.3%      Mismatches: 129  
Query Match: 5.8%      Indels: 135  
RESULT 759  
ID AAK85753 standard; DNA; 9893 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40565.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 37.0%      Conservative: 55  
Best Local Similarity: 23.0%      Mismatches: 136  
Query Match: 5.8%      Indels: 114  
RESULT 760  
ID ACN44303 standard; cDNA; 11895 BP.  
DE Human mRNA sequence hCT32001.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 36.7%      Conservative: 40  
Best Local Similarity: 24.5%      Mismatches: 141  
Query Match: 5.8%      Indels: 66  
RESULT 761  
ID ACF42746 standard; cDNA; 12598 BP.  
DE Human ALMS1 cDNA sequence.  
PN WO2003034072-A2.  
PD 24-APR-2003.  
PA (UYSO-) UNIV SOUTHAMPTON.  
Percent Similarity: 36.7%      Conservative: 40  
Best Local Similarity: 24.5%      Mismatches: 141  
Query Match: 5.8%      Indels: 66

RESULT 762  
ID AED20700 standard; cDNA; 12598 BP.  
DE Human ALMS1 encoding cDNA, SEQ ID 2.  
PN US2005214757-A1.  
PD 29-SEP-2005.  
PA (WILS/) WILSON D I.  
PA (HEAR/) HEARN T.  
PA (WALK/) WALKER M.  
Percent Similarity: 36.7%      Conservative: 40  
Best Local Similarity: 24.5%      Mismatches: 141  
Query Match: 5.8%      Indels: 66  
RESULT 763  
ID AEH14311 standard; DNA; 12922 BP.  
DE Human alstrom syndrome 1 cDNA SEQ ID NO:1.  
PN FR2876705-A1.  
PD 21-APR-2006.  
PA (INMR ) BIOMERIEUX SA.  
Percent Similarity: 36.7%      Conservative: 40  
Best Local Similarity: 24.5%      Mismatches: 141  
Query Match: 5.8%      Indels: 66  
RESULT 764  
ID AAQ20685 standard; DNA; 14704 BP.  
DE PKS 741 insert contg. Sry.  
PN WO200375-A.  
PD 09-JAN-1992.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
Percent Similarity: 39.0%      Conservative: 58  
Best Local Similarity: 21.2%      Mismatches: 130  
Query Match: 5.8%      Indels: 69  
RESULT 765  
ID AAK74017 standard; DNA; 15270 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28829.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 35.7%      Conservative: 53  
Best Local Similarity: 21.9%      Mismatches: 140  
Query Match: 5.8%      Indels: 108  
RESULT 766  
ID AAK85754 standard; DNA; 15270 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40566.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 35.7%      Conservative: 53  
Best Local Similarity: 21.9%      Mismatches: 140  
Query Match: 5.8%      Indels: 108  
RESULT 767  
ID AAA81457 standard; DNA; 49646 BP.  
DE N. meningitidis partial DNA sequence gnm\_5 SEQ ID NO:5.  
PN WO200022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 37.2%      Conservative: 62  
Best Local Similarity: 23.0%      Mismatches: 145  
Query Match: 5.8%      Indels: 131  
RESULT 768  
Percent Similarity: 37.2%      Conservative: 62  
Best Local Similarity: 23.0%      Mismatches: 145  
Query Match: 5.8%      Indels: 131  
RESULT 769  
Percent Similarity: 36.7%      Conservative: 40  
Best Local Similarity: 24.5%      Mismatches: 141  
Query Match: 5.8%      Indels: 66  
RESULT 770  
ID ADH69807 standard; DNA; 684973 BP.  
DE Human Vbeta gene.  
PN US2002150891-A1.  
PD 17-OCT-2002.  
PA (HOOD/) HOOD L E.  
PA (ROWE/) ROWEN L.  
Percent Similarity: 43.4%      Conservative: 37  
Best Local Similarity: 25.9%      Mismatches: 84

Query Match: 5.8% Indels: 36  
RESULT 771  
Percent Similarity: 36.7% Conservative: 40  
Best Local Similarity: 24.5% Mismatches: 141  
Query Match: 5.8% Indels: 66  
RESULT 772  
ID ACN44302 standard; DNA; 198073 BP.  
DE Human genomic sequence hCG40741.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 36.7% Conservative: 40  
Best Local Similarity: 24.5% Mismatches: 141  
Query Match: 5.8% Indels: 66  
RESULT 773  
ID ABL68560 standard; DNA; 267156 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:6897.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 43.4% Conservative: 37  
Best Local Similarity: 25.9% Mismatches: 84  
Query Match: 5.8% Indels: 36  
RESULT 774  
ID AAF21607 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:108.  
PN WO200066791-A1.  
PD 09-NOV-2000.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 37.2% Conservative: 62  
Best Local Similarity: 23.0% Mismatches: 145  
Query Match: 5.8% Indels: 131  
RESULT 775  
ID AAF21608 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.  
PN WO200066791-A1.  
PD 09-NOV-2000.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 37.2% Conservative: 62  
Best Local Similarity: 23.0% Mismatches: 145  
Query Match: 5.8% Indels: 131  
RESULT 776  
ID ADT47265 standard; cDNA; 1818 BP.  
DE Bacterial polynucleotide #22016.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 39.3% Conservative: 46  
Best Local Similarity: 23.2% Mismatches: 131  
Query Match: 5.8% Indels: 42  
RESULT 777  
ID ADI57677 standard; cDNA; 1882 BP.  
DE Human breast specific nucleic acid (BSNA) #48.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 33.7% Conservative: 37  
Best Local Similarity: 23.3% Mismatches: 124  
Query Match: 5.8% Indels: 112  
RESULT 778  
ID ABL08459 standard; cDNA; 2885 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19859.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 40.9% Conservative: 55  
Best Local Similarity: 22.0% Mismatches: 132

Query Match: 5.8% Indels: 41  
RESULT 779  
ID ADV97740 standard; cDNA; 3345 BP.  
DE CDNA sequence encoding a murine protein kinase Seq 60.  
PN WO2005000200-A2.  
PD 06-JAN-2005.  
PA (SUGE-) SUGEN INC.  
Percent Similarity: 35.6% Conservative: 45  
Best Local Similarity: 23.5% Mismatches: 164  
Query Match: 5.8% Indels: 80  
RESULT 780  
ID AEG97266 standard; DNA; 3507 BP.  
DE Eremothecium gossypii CRV1 DNA homolog SEQ ID NO 35.  
PN WO2006036817-A2.  
PD 06-APR-2006.  
PA (MICR-) MICROBIA INC.  
Percent Similarity: 39.7% Conservative: 46  
Best Local Similarity: 24.0% Mismatches: 136  
Query Match: 5.8% Indels: 41  
RESULT 781  
ID ABL08458 standard; cDNA; 5004 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19856.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 40.9% Conservative: 55  
Best Local Similarity: 22.0% Mismatches: 132  
Query Match: 5.8% Indels: 41  
RESULT 782  
ID ADM47088 standard; DNA; 5615 BP.  
DE Ogataea minuta LEU2 gene.  
PN WO2003091431-A1.  
PD 06-NOV-2003.  
PA (KIRI ) KIRIN BEER KK.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Percent Similarity: 42.5% Conservative: 45  
Best Local Similarity: 24.6% Mismatches: 108  
Query Match: 5.8% Indels: 38  
RESULT 783  
ID AEL31410 standard; DNA; 6138 BP.  
DE Mouse HCFC1 DNA SEQ ID NO 27.  
PN WO2006110264-A2.  
PD 19-OCT-2006.  
PA (KIMM-) KIMMEL CANCER CENT SIDNEY.  
Percent Similarity: 30.0% Conservative: 49  
Best Local Similarity: 20.3% Mismatches: 145  
Query Match: 5.8% Indels: 210  
RESULT 784  
ID ADX62221 standard; cDNA; 6159 BP.  
DE Plant full length insert polynucleotide seqid 33064.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Percent Similarity: 36.5% Conservative: 45  
Best Local Similarity: 22.7% Mismatches: 121  
Query Match: 5.8% Indels: 86  
RESULT 785  
Percent Similarity: 40.0% Conservative: 17  
Best Local Similarity: 29.7% Mismatches: 68  
Query Match: 5.8% Indels: 31  
RESULT 786  
Percent Similarity: 40.0% Conservative: 17  
Best Local Similarity: 29.7% Mismatches: 68  
Query Match: 5.8% Indels: 31  
RESULT 787  
ID ACH92224 standard; DNA; 572 BP.  
DE Human genome derived single exon probe #25419.  
PN US2003194704-A1.

PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 43.5%  
Best Local Similarity: 25.6%  
Query Match: 5.8%  
Indels: 34  
Conservative: 37  
Mismatches: 83  
Indels: 34

RESULT 788  
ID ADE36591 standard; cDNA; 1017 BP.  
DE Human NOV1a encoding cDNA SEQ ID NO:1.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 789  
ID ADE36617 standard; DNA; 1017 BP.  
DE Plasmid pCR2.1-CG57008-03-S843 15B nucleotide insert SEQ ID NO:27.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 790  
ID AEC32060 standard; DNA; 1017 BP.  
DE Human CG57008-03 DNA, SEQ ID NO: 5.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 791  
ID ACC72709 standard; cDNA; 1080 BP.  
DE Human cancer related protein encoding cDNA SEQ ID NO:48.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 792  
ID ABZ68333 standard; DNA; 1080 BP.  
DE Nucleotide sequence of human TIM-1 allele 2.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 793  
ID ABZ68332 standard; DNA; 1080 BP.  
DE Nucleotide sequence of human TIM-1 allele 1.  
PN WO2003002722-A2.  
PD 09-JAN-2003.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 794  
ID ADY98074 standard; cDNA; 1080 BP.  
DE Human TIM-1 allele 2.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 795  
ID ADY98072 standard; cDNA; 1080 BP.  
DE Human TIM-1 allele 1.  
PN WO2005027854-A2.  
PD 31-MAR-2005.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (DAND ) DANA FARBER CANCER INST INC.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 796  
ID AED60516 standard; DNA; 1080 BP.  
DE Human TIM-1, allele 1, DNA SEQ ID NO:24.  
PN WO2005097211-A2.  
PD 20-OCT-2005.  
PA (TELO-) TELOS PHARM INC.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 797  
ID AED60518 standard; DNA; 1080 BP.  
DE Human TIM-1, allele 2, DNA SEQ ID NO:26.  
PN WO2005097211-A2.  
PD 20-OCT-2005.  
PA (TELO-) TELOS PHARM INC.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 798  
ID AEC32068 standard; DNA; 1099 BP.  
DE Human CG57008-07 DNA, SEQ ID NO: 13.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 799  
ID AEC32070 standard; DNA; 1111 BP.  
DE Human CG57008-08 DNA, SEQ ID NO: 15.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 800  
ID ACL38953 standard; cDNA; 1380 BP.  
DE HAVCR1 coding sequence, SEQ ID 10.  
PN WO2005001092-A2.  
PD 06-JAN-2005.  
PA (AMHP ) WYETH.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 801  
ID ADE36593 standard; cDNA; 1440 BP.  
DE Human NOV1b encoding cDNA SEQ ID NO:3.  
PN WO2003080856-A2.  
PD 02-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 36.9%  
Best Local Similarity: 24.0%  
Query Match: 5.8%  
Indels: 65  
Conservative: 42  
Mismatches: 141  
Indels: 65

RESULT 802  
ID ADN38983 standard; cDNA; 1440 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:301.  
PN WO2003042661-A2.  
PD 22-MAY-2003.



PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Percent Similarity: 36.9% Conservative: 42  
Best Local Similarity: 24.0% Mismatches: 141  
Query Match: 5.8% Indels: 65  
RESULT 803  
ID AEC32056 standard; DNA; 1440 BP.  
DE Human CG57008-01 DNA, SEQ ID NO: 1.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9% Conservative: 42  
Best Local Similarity: 24.0% Mismatches: 141  
Query Match: 5.8% Indels: 65  
RESULT 804  
ID AEC32096 standard; DNA; 1440 BP.  
DE Human CG57008-01-SNP A96V DNA, SEQ ID NO: 41.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9% Conservative: 42  
Best Local Similarity: 24.0% Mismatches: 141  
Query Match: 5.8% Indels: 65  
RESULT 805  
ID AEC32090 standard; DNA; 1440 BP.  
DE Human CG57008-01-SNP P174L DNA, SEQ ID NO: 35.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9% Conservative: 42  
Best Local Similarity: 24.0% Mismatches: 141  
Query Match: 5.8% Indels: 65  
RESULT 806  
ID AEC32088 standard; DNA; 1440 BP.  
DE Human CG57008-01-SNP T202A DNA, SEQ ID NO: 33.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9% Conservative: 42  
Best Local Similarity: 24.0% Mismatches: 141  
Query Match: 5.8% Indels: 65  
RESULT 807  
ID AED01587 standard; cDNA; 1440 BP.  
DE Human cDNA encoding tim-1.  
PN WO2005090573-A2.  
PD 29-SEP-2005.  
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
Percent Similarity: 36.9% Conservative: 42  
Best Local Similarity: 24.0% Mismatches: 141  
Query Match: 5.8% Indels: 65  
RESULT 808  
ID AEH40439 standard; DNA; 1524 BP.  
DE Cryptosporidium hominis gene SEQ ID NO:3530.  
PN WO2006044045-A2.  
PD 27-APR-2006.  
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.  
Percent Similarity: 36.9% Conservative: 39  
Best Local Similarity: 23.4% Mismatches: 105  
Query Match: 5.8% Indels: 79  
RESULT 809  
ID ADI57708 standard; cDNA; 1630 BP.  
DE Human breast specific nucleic acid (BSNA) #79.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.

Percent Similarity: 32.1% Conservative: 40  
Best Local Similarity: 22.6% Mismatches: 134  
Query Match: 5.8% Indels: 152  
RESULT 810  
ID ABQ99274 standard; cDNA; 2030 BP.  
DE Human coding sequence SEQ ID 7.  
PN WO200259260-A2.  
PD 01-AUG-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 38.9% Conservative: 39  
Best Local Similarity: 26.1% Mismatches: 125  
Query Match: 5.8% Indels: 60  
RESULT 811  
ID ADR25292 standard; DNA; 2197 BP.  
DE Breast cancer prognosis marker #1153.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Percent Similarity: 35.7% Conservative: 45  
Best Local Similarity: 24.8% Mismatches: 164  
Query Match: 5.8% Indels: 102  
RESULT 812  
ID ADS51623 standard; DNA; 2197 BP.  
DE Human CAF-1 p60 protein encoding DNA.  
PN WO2004085644-A2.  
PD 07-OCT-2004.  
PA (BADI ) BASF PLANT SCI GMBH.  
Percent Similarity: 35.7% Conservative: 45  
Best Local Similarity: 24.8% Mismatches: 164  
Query Match: 5.8% Indels: 102  
RESULT 813  
ID AEG70588 standard; cDNA; 2197 BP.  
DE Human p53 mutational status predicting gene SEQ ID NO:62.  
PN US2006074565-A1.  
PD 06-APR-2006.  
PA (MILL/) MILLER L D.  
PA (GEOR/) GEORGE J.  
PA (VEGA/) VEGA V B.  
Percent Similarity: 35.7% Conservative: 45  
Best Local Similarity: 24.8% Mismatches: 164  
Query Match: 5.8% Indels: 102  
RESULT 814  
ID AAC66909 standard; cDNA; 2364 BP.  
DE Human EXMAD-20 coding sequence SEQ ID NO: 45.  
PN WO200068380-A2.  
PD 16-NOV-2000.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 38.1% Conservative: 39  
Best Local Similarity: 25.6% Mismatches: 120  
Query Match: 5.8% Indels: 74  
RESULT 815  
ID AEC55828 standard; DNA; 2838 BP.  
DE Candida albicans CanDT80 protein (CaNdt80p) DNA, SEQ ID NO: 3.  
PN US2005192240-A1.  
PD 01-SEP-2005.  
PA (YANG/) YANG Y.  
PA (CHEN/) CHEN C.  
PA (LOHH/) LO H.  
Percent Similarity: 35.6% Conservative: 44  
Best Local Similarity: 23.0% Mismatches: 119  
Query Match: 5.8% Indels: 107  
RESULT 816  
ID ABL28547 standard; DNA; 2973 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37114.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.8% Conservative: 61  
Best Local Similarity: 21.8% Mismatches: 147  
Query Match: 5.8% Indels: 158  
RESULT 817  
ID ADS46610 standard; cDNA; 3969 BP.

DE Bacterial polynucleotide #1353.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 37.3%  
 Best Local Similarity: 22.5%  
 Query Match: 5.8%  
 RESULT 818  
 ID AAQ21604 standard; DNA; 4394 BP.  
 DE Alpha galactosidase gene.  
 PN GB2247238-A.  
 PD 26-FEB-1992.  
 PA (GNSS ) GUINNESS & SON CO LTD ARTHUR.  
 Percent Similarity: 38.1%  
 Best Local Similarity: 25.0%  
 Query Match: 5.8%  
 RESULT 819  
 ID AAS84306 standard; cDNA; 10578 BP.  
 DE DNA encoding novel human diagnostic protein #20110.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 48.0%  
 Best Local Similarity: 27.6%  
 Query Match: 5.8%  
 RESULT 820  
 ID AAA92301 standard; DNA; 30690 BP.  
 DE S. avermitilis avermectin aglycon synthase DNA aveAI SEQ ID NO:1.  
 PN WO200050605-A1.  
 PD 31-AUG-2000.  
 PA (KITA ) KITASATO INST.  
 Percent Similarity: 37.3%  
 Best Local Similarity: 25.3%  
 Query Match: 5.8%  
 RESULT 821  
 ID AAH79277 standard; DNA; 30690 BP.  
 DE Streptomyces avermitilis coding sequences SEQ ID NO: 1.  
 PN WO200162939-A1.  
 PD 30-AUG-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA (KITA ) KITASATO INST.  
 Percent Similarity: 37.3%  
 Best Local Similarity: 25.3%  
 Query Match: 5.8%  
 RESULT 822  
 ID ADW43464 standard; DNA; 39912 BP.  
 DE S. avermitilis avermectin aglycon biosynthesis gene cluster aveA3-4 DNA.  
 PN WO2004111230-A1.  
 PD 23-DEC-2004.  
 PA (KITA ) KITASATO INST.  
 Percent Similarity: 37.3%  
 Best Local Similarity: 25.3%  
 Query Match: 5.8%  
 RESULT 823  
 ID ADT89084 standard; DNA; 80393 BP.  
 DE Arabidopsis thaliana T-DNA insertion mutant DNA, SALKO41951.  
 PN US2004210962-A1.  
 PD 21-OCT-2004.  
 PA (UYNE-) UNIV NEBRASKA.  
 Percent Similarity: 40.9%  
 Best Local Similarity: 27.9%  
 Query Match: 5.8%  
 RESULT 824  
 ID AEL87435 standard; DNA; 80393 BP.  
 DE Thale cress T-DNA insertion mutant DNA SEQ ID: 4.  
 PN US2006248613-A1.  
 PD 02-NOV-2006.  
 PA (MACK/) MACKENZIE S.  
 PA (ABDE/) ABDELNOOR R V.

Percent Similarity: 40.9%  
 Best Local Similarity: 27.9%  
 Query Match: 5.8%  
 RESULT 825  
 ID AEL86867 standard; DNA; 80393 BP.  
 DE Thale cress T-DNA insertion mutant DNA SEQ ID: 4.  
 PN US2006248614-A1.  
 PD 02-NOV-2006.  
 PA (MACK/) MACKENZIE S.  
 PA (ABDE/) ABDELNOOR R V.  
 Percent Similarity: 40.9%  
 Best Local Similarity: 27.9%  
 Query Match: 5.8%  
 RESULT 826  
 ID ABQ81842 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 genomic sequence SEQ ID NO:1.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST ) SOC PROD NESTLE SA.  
 Percent Similarity: 33.9%  
 Best Local Similarity: 21.1%  
 Query Match: 5.8%  
 RESULT 827  
 ID AAI23782 standard; DNA; 1667 BP.  
 DE Probe #13715 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 39.6%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 RESULT 828  
 ID ABA68895 standard; DNA; 1667 BP.  
 DE Human foetal liver single exon nucleic acid probe #17200.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 39.6%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 RESULT 829  
 ID AAI49092 standard; DNA; 1667 BP.  
 DE Probe #17778 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 39.6%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 RESULT 830  
 ID ABA50917 standard; DNA; 1667 BP.  
 DE Human breast cell single exon nucleic acid probe #9612.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 39.6%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 RESULT 831  
 ID ABA35846 standard; DNA; 1667 BP.  
 DE Probe #14312 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 39.6%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 RESULT 832  
 ID AAK43013 standard; DNA; 1667 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 17570.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.

Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 833  
ID AAK17227 standard; DNA; 1667 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 17218.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 834  
ID ABS42655 standard; DNA; 1667 BP.  
DE Human liver single exon probe, SEQ ID No 17645.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 835  
ID AAI09388 standard; DNA; 1667 BP.  
DE Probe #9379 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 836  
ID AAA30736 standard; DNA; 1854 BP.  
DE DNA encoding human mutant G protein-coupled receptor H9b (F236K).  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 837  
ID AB281156 standard; cDNA; 1854 BP.  
DE Human GPR50 allelic variant encoding cDNA SEQ ID NO:6.  
PN WO2003006504-A2.  
PD 23-JAN-2003.  
PA (ALKU) AKZO NOBEL NV.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 838  
ID AB281155 standard; cDNA; 1854 BP.  
DE Human GPR50 allelic variant encoding cDNA SEQ ID NO:5.  
PN WO2003006504-A2.  
PD 23-JAN-2003.  
PA (ALKU) AKZO NOBEL NV.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 839  
ID AB281157 standard; cDNA; 1854 BP.  
DE Human GPR50 allelic variant encoding cDNA SEQ ID NO:7.  
PN WO2003006504-A2.  
PD 23-JAN-2003.  
PA (ALKU) AKZO NOBEL NV.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 840  
ID AB281158 standard; cDNA; 1854 BP.  
DE Human GPR50 allelic variant encoding cDNA SEQ ID NO:8.  
PN WO2003006504-A2.  
PD 23-JAN-2003.  
PA (ALKU) AKZO NOBEL NV.  
Percent Similarity: 39.6%  
Conservative: 40  
Mismatch: 109  
Indels: 52

Best Local Similarity: 24.5%  
Query Match: 5.7%  
Mismatch: 109  
Indels: 52  
RESULT 841  
ID ADC22736 standard; cDNA; 1854 BP.  
DE Human G protein-coupled receptor cDNA #67.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 842  
ID ADH14209 standard; cDNA; 1854 BP.  
DE Mutated human H9b cDNA.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAW/) LIAW C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 843  
ID AAI14586 standard; DNA; 1958 BP.  
DE Probe #4519 for gene expression analysis in human cervical cell sample.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 844  
ID ABA56312 standard; DNA; 1958 BP.  
DE Human foetal liver single exon nucleic acid probe #4617.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 845  
ID AAI35956 standard; DNA; 1958 BP.  
DE Probe #4642 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 846  
ID ABA45798 standard; DNA; 1958 BP.  
DE Human breast cell single exon nucleic acid probe #4493.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 847  
ID ABA25952 standard; DNA; 1958 BP.  
DE Probe #4418 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
RESULT 848  
ID AAK29990 standard; DNA; 1958 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 4547.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6%  
Conservative: 40  
Mismatch: 109  
Indels: 52



Percent Similarity: 39.6% Conservative: 40  
Best Local Similarity: 24.5% Mismatches: 109  
Query Match: 5.7% Indels: 52  
RESULT 849  
ID AAK04492 standard; DNA; 1958 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 4483.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6% Conservative: 40  
Best Local Similarity: 24.5% Mismatches: 109  
Query Match: 5.7% Indels: 52  
RESULT 850  
ID ABS29649 standard; DNA; 1958 BP.  
DE Human liver single exon probe, SEQ ID No 4639.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6% Conservative: 40  
Best Local Similarity: 24.5% Mismatches: 109  
Query Match: 5.7% Indels: 52  
RESULT 851  
ID AAI04397 standard; DNA; 1958 BP.  
DE Probe #4388 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 39.6% Conservative: 40  
Best Local Similarity: 24.5% Mismatches: 109  
Query Match: 5.7% Indels: 52  
RESULT 852  
ID AEI34363 standard; DNA; 1967 BP.  
DE Soybean polymorphic locus, SEQ ID 6997.  
PN US2006135758-A1.  
PD 22-JUN-2006.  
PA (WUKK/) WU K.  
Percent Similarity: 33.5% Conservative: 50  
Best Local Similarity: 23.2% Mismatches: 178  
Query Match: 5.7% Indels: 148  
RESULT 853  
ID ACN43073 standard; cDNA; 2131 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1948.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 39.6% Conservative: 40  
Best Local Similarity: 24.5% Mismatches: 109  
Query Match: 5.7% Indels: 52  
RESULT 854  
ID ABL08537 standard; cDNA; 2175 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 20093.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.1% Conservative: 53  
Best Local Similarity: 20.1% Mismatches: 122  
Query Match: 5.7% Indels: 127  
RESULT 855  
ID ADP07664 standard; DNA; 2335 BP.  
DE Human secreted protein encoding DNA, seq id 147.  
PN WO2004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 35.7% Conservative: 43  
Best Local Similarity: 23.1% Mismatches: 132  
Query Match: 5.7% Indels: 89  
RESULT 856  
ID ADX26007 standard; DNA; 3378 BP.  
DE Novel cell pain response detection method-related mouse gene SeqID353.  
PN WO2005014849-A2.  
PD 17-FEB-2005.  
PA (EURO-) EUROCELTIQUE SA.  
Percent Similarity: 32.5% Conservative: 59

Best Local Similarity: 21.0% Mismatches: 137  
Query Match: 5.7% Indels: 208  
RESULT 857  
ID AEG97401 standard; DNA; 3783 BP.  
DE C. albicans cell wall protein ALS1b DNA SEQ ID NO 170.  
PN WO2006036817-A2.  
PD 06-APR-2006.  
PA (MICR-) MICROBIA INC.  
Percent Similarity: 36.4% Conservative: 64  
Best Local Similarity: 21.4% Mismatches: 181  
Query Match: 5.7% Indels: 90  
RESULT 858  
ID AAD62305 standard; DNA; 3786 BP.  
DE Candida albicans agglutinin-like sequence (ALS) 1 gene.  
PN US2003124134-A1.  
PD 03-JUL-2003.  
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.  
Percent Similarity: 36.4% Conservative: 64  
Best Local Similarity: 21.4% Mismatches: 181  
Query Match: 5.7% Indels: 90  
RESULT 859  
ID AEI26925 standard; DNA; 3786 BP.  
DE Candida albicans agglutinin-like sequence 1 gene, SEQ ID NO: 7.  
PN US7067138-B1.  
PD 27-JUN-2006.  
PA (ANGE-) LOS ANGELES BIOMEDICAL RES INST AT HARBO.  
Percent Similarity: 36.4% Conservative: 64  
Best Local Similarity: 21.4% Mismatches: 181  
Query Match: 5.7% Indels: 90  
RESULT 860  
ID AAS27718 standard; DNA; 3915 BP.  
DE DNA encoding novel signal transduction pathway protein, Seq ID 1378.  
PN WO200154733-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 34.1% Conservative: 28  
Best Local Similarity: 25.2% Mismatches: 89  
Query Match: 5.7% Indels: 118  
RESULT 861  
ID ADB94521 standard; DNA; 3915 BP.  
DE Novel human protein DNA #130.  
PN US2002168711-A1.  
PD 14-NOV-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Percent Similarity: 34.1% Conservative: 28  
Best Local Similarity: 25.2% Mismatches: 89  
Query Match: 5.7% Indels: 118  
RESULT 862  
ID ABA95683 standard; DNA; 7542 BP.  
DE Human protein kinase gene.  
PN WO200192492-A2.  
PD 06-DEC-2001.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 34.1% Conservative: 28  
Best Local Similarity: 25.2% Mismatches: 89  
Query Match: 5.7% Indels: 118  
RESULT 863  
ID ABL68626 standard; DNA; 10708 BP.  
DE Kidney cancer related gene sequence SEQ ID NO:6963.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 38.5% Conservative: 47  
Best Local Similarity: 24.2% Mismatches: 120  
Query Match: 5.7% Indels: 82  
RESULT 864  
ID ADS36503 standard; DNA; 24345 BP.  
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1717.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.

Percent Similarity: 34.1%      Conservative: 28  
Best Local Similarity: 25.2%      Mismatches: 89  
Query Match: 5.7%      Indels: 118  
RESULT 865  
ID ADS36474 standard; DNA; 40947 BP.  
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1688.  
PN WO2004083403-A2.  
PD 30-SEP-2004.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 34.1%      Conservative: 28  
Best Local Similarity: 25.2%      Mismatches: 89  
Query Match: 5.7%      Indels: 118  
RESULT 866  
ID AAH64966 standard; DNA; 349980 BP.  
DE C glutamicum coding sequence fragment SEQ ID NO: 1.  
PN EP1108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Percent Similarity: 37.2%      Conservative: 63  
Best Local Similarity: 22.3%      Mismatches: 157  
Query Match: 5.7%      Indels: 109  
RESULT 867  
ID AAT07199 standard; DNA; 913 BP.  
DE Cotton fibre-specific H6 protein gene.  
PN US5474925-A.  
PD 12-DEC-1995.  
PA (CETU ) AGRACETUS INC.  
Percent Similarity: 42.3%      Conservative: 31  
Best Local Similarity: 26.3%      Mismatches: 80  
Query Match: 5.7%      Indels: 33  
RESULT 868  
ID AAT13034 standard; cDNA; 913 BP.  
DE Cotton fibre-specific cDNA clone H6.  
PN US5495070-A.  
PD 27-FEB-1996.  
PA (CETU ) AGRACETUS INC.  
Percent Similarity: 42.3%      Conservative: 31  
Best Local Similarity: 26.3%      Mismatches: 80  
Query Match: 5.7%      Indels: 33  
RESULT 869  
ID AAT30253 standard; DNA; 913 BP.  
DE Cotton fibre cell-specific cDNA clone CKFB15A1-H6.  
PN US5521078-A.  
PD 28-MAY-1996.  
PA (CETU ) AGRACETUS INC.  
Percent Similarity: 42.3%      Conservative: 31  
Best Local Similarity: 26.3%      Mismatches: 80  
Query Match: 5.7%      Indels: 33  
RESULT 870  
ID AAT62610 standard; cDNA to mRNA; 913 BP.  
DE Cotton fibre specific cDNA clone CKFB15A1-H6.  
PN US5597718-A.  
PD 28-JAN-1997.  
PA (CETU ) AGRACETUS.  
Percent Similarity: 42.3%      Conservative: 31  
Best Local Similarity: 26.3%      Mismatches: 80  
Query Match: 5.7%      Indels: 33  
RESULT 871  
ID AAT70041 standard; cDNA; 913 BP.  
DE Cotton fibre specific cDNA clone H6.  
PN US5620882-A.  
PD 15-APR-1997.  
PA (CETU ) AGRACETUS INC.  
Percent Similarity: 42.3%      Conservative: 31  
Best Local Similarity: 26.3%      Mismatches: 80  
Query Match: 5.7%      Indels: 33  
RESULT 872  
ID AAZ35545 standard; DNA; 913 BP.  
DE cDNA sequence a cotton fibre gene from clone CDFB15A1H6.  
PN US5981834-A.  
PD 09-NOV-1999.  
PA (MONS ) MONSANTO CO.  
Percent Similarity: 42.3%      Conservative: 31

Best Local Similarity: 26.3%      Mismatches: 80  
Query Match: 5.7%      Indels: 33  
RESULT 873  
ID AEC32094 standard; DNA; 1440 BP.  
DE Human CG57008-01-SNP S51L DNA, SEQ ID NO: 39.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9%      Conservative: 42  
Best Local Similarity: 24.0%      Mismatches: 141  
Query Match: 5.7%      Indels: 65  
RESULT 874  
ID AEC32092 standard; DNA; 1440 BP.  
DE Human CG57008-01-SNP V138I DNA, SEQ ID NO: 37.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 36.9%      Conservative: 43  
Best Local Similarity: 23.7%      Mismatches: 141  
Query Match: 5.7%      Indels: 65  
RESULT 875  
ID AEL57388 standard; cDNA; 1661 BP.  
DE Mouse podocalypsin-like protein 1 precursor gene, SEQ ID NO: 1851.  
PN US2006216722-A1.  
PD 28-SEP-2006.  
PA (BETS/) BETSHOLTZ C.  
PA (TRYG/) TRYGGVASON K.  
PA (TAKE/) TAKEMOTO M.  
PA (HELL/) HE L.  
PA (PATR/) PATRAKKAS J.  
Percent Similarity: 34.1%      Conservative: 33  
Best Local Similarity: 23.1%      Mismatches: 123  
Query Match: 5.7%      Indels: 74  
RESULT 876  
ID ADY34545 standard; cDNA; 1804 BP.  
DE DPCR1 (552 amino acid form) coding sequence.  
PN WO2005019257-A1.  
PD 03-MAR-2005.  
PA (CLLT ) CELLTech R & D LTD.  
Percent Similarity: 37.2%      Conservative: 51  
Best Local Similarity: 21.9%      Mismatches: 134  
Query Match: 5.7%      Indels: 75  
RESULT 877  
ID AAH25852 standard; DNA; 2131 BP.  
DE Murine PCLP1 coding sequence.  
PN WO200134797-A1.  
PD 17-MAY-2001.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Percent Similarity: 34.1%      Conservative: 33  
Best Local Similarity: 23.1%      Mismatches: 123  
Query Match: 5.7%      Indels: 74  
RESULT 878  
ID ADC01839 standard; DNA; 2217 BP.  
DE C. albicans DNA encoding dimorphism-specific protein 2400.  
PN DE10142743-A1.  
PD 13-MAR-2003.  
PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.  
Percent Similarity: 33.9%      Conservative: 63  
Best Local Similarity: 19.7%      Mismatches: 161  
Query Match: 5.7%      Indels: 131  
RESULT 879  
ID ACL28658 standard; cDNA; 2403 BP.  
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:2614.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 34.9%      Conservative: 47  
Best Local Similarity: 21.9%      Mismatches: 132  
Query Match: 5.7%      Indels: 103

RESULT 880  
ID AED11382 standard; DNA; 2800 BP.  
DE Modified human CDH4 gene CpG island nucleotide sequence SEQ ID NO:3.  
PN EP1584629-A1.  
PD 12-OCT-2005.  
PA (UYFE-) UNIV FERRARA.  
Percent Similarity: 33.1%  
Best Local Similarity: 25.2%  
Query Match: 5.7%  
Conservative: 21  
Mismatches: 119  
Indels: 60  
RESULT 881  
ID AEH38832 standard; DNA; 3981 BP.  
DE Cryptosporidium hominis gene SEQ ID NO:1923.  
PN WO2006044045-A2.  
PD 27-APR-2006.  
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.  
Percent Similarity: 37.0%  
Best Local Similarity: 24.0%  
Query Match: 5.7%  
Conservative: 44  
Mismatches: 153  
Indels: 65  
RESULT 882  
ID AEL57386 standard; cDNA; 5302 BP.  
DE Mouse podocalypsin-like protein 1 precursor gene, SEQ ID NO: 1849.  
PN US2006216722-A1.  
PD 28-SEP-2006.  
PA (BETS/) BETSHOLTZ C.  
PA (TRYG/) TRYGVASON K.  
PA (TAKE/) TAKEMOTO M.  
PA (HELL/) HE L.  
PA (PATR/) PATRAKKAS J.  
Percent Similarity: 34.1%  
Best Local Similarity: 23.1%  
Query Match: 5.7%  
Conservative: 33  
Mismatches: 123  
Indels: 74  
RESULT 883  
ID AAS70562 standard; cDNA; 7715 BP.  
DE DNA encoding novel human diagnostic protein #6366.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 32.2%  
Best Local Similarity: 20.7%  
Query Match: 5.7%  
Conservative: 46  
Mismatches: 123  
Indels: 149  
RESULT 884  
ID ADO28931 standard; cDNA; 8194 BP.  
DE Human novel GPCR PGR17 polynucleotide, SEQ ID NO:30.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Percent Similarity: 32.2%  
Best Local Similarity: 20.7%  
Query Match: 5.7%  
Conservative: 46  
Mismatches: 123  
Indels: 149  
RESULT 885  
ID ADQ10013 standard; DNA; 8762 BP.  
DE Borrelia afzelii strain ACAI vls silent cassette locus DNA SeqID 57.  
PN WO2004058181-A2.  
PD 15-JUL-2004.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Percent Similarity: 36.0%  
Best Local Similarity: 23.2%  
Query Match: 5.7%  
Conservative: 58  
Mismatches: 172  
Indels: 119  
RESULT 886  
ID ABL08376 standard; cDNA; 11230 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19610.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 42.2%  
Best Local Similarity: 29.4%  
Query Match: 5.7%  
Conservative: 23  
Mismatches: 73  
Indels: 31  
RESULT 887  
ID AAZ58381 standard; DNA; 12381 BP.  
DE Streptomyces avermitilis avermectin polyketide synthase modules 1+2.  
PN WO200001827-A2.  
PD 13-JAN-2000.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.

PA (PFIZ) PFIZER INC.  
Percent Similarity: 35.3%  
Best Local Similarity: 25.5%  
Query Match: 5.7%  
Conservative: 36  
Mismatches: 155  
Indels: 81  
RESULT 888  
ID ADB54255 standard; DNA; 12781 BP.  
DE Pretreated genomic DNA region 179.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 34.6%  
Best Local Similarity: 22.6%  
Query Match: 5.7%  
Conservative: 45  
Mismatches: 156  
Indels: 90  
RESULT 889  
ID ADY95168 standard; DNA; 1009 BP.  
DE DNA of gene 118b from Loblolly pine which encodes a glycine rich protein.  
PN WO2005030988-A1.  
PD 07-APR-2005.  
PA (CELL-) CELLFOR INC.  
Percent Similarity: 44.0%  
Best Local Similarity: 29.3%  
Query Match: 5.7%  
Conservative: 22  
Mismatches: 69  
Indels: 15  
RESULT 890  
ID AAF08222 standard; cDNA; 1021 BP.  
DE Fusarium venenatum EST SEQ ID NO:745.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO) NOVO NORDISK BIOTECH INC.  
PA (NOVO) NOVO NORDISK AS.  
Percent Similarity: 42.9%  
Best Local Similarity: 30.6%  
Query Match: 5.7%  
Conservative: 24  
Mismatches: 70  
Indels: 43  
RESULT 891  
ID ADU52263 standard; cDNA; 1021 BP.  
DE Fusarium venenatum CCl-3 EST, SEQ ID NO:745.  
PN US2004229367-A1.  
PD 18-NOV-2004.  
PA (NOVO) NOVOZYMES BIOTECH INC.  
PA (NOVO) NOVOZYMES INC AS.  
Percent Similarity: 42.9%  
Best Local Similarity: 30.6%  
Query Match: 5.7%  
Conservative: 24  
Mismatches: 70  
Indels: 43  
RESULT 892  
ID ADZ90266 standard; cDNA; 1021 BP.  
DE Fusarium venenatum expressed sequence tag cDNA SEQ ID NO 745.  
PN US6902887-B1.  
PD 07-JUN-2005.  
PA (NOVO) NOVOZYMES BIOTECH INC.  
PA (NOVO) NOVOZYMES AS.  
Percent Similarity: 42.9%  
Best Local Similarity: 30.6%  
Query Match: 5.7%  
Conservative: 24  
Mismatches: 70  
Indels: 43  
RESULT 893  
ID ACL70863 standard; DNA; 1059 BP.  
DE M. xanthus gene sequence, seq id 7326.  
PN US6833447-B1.  
PD 21-DEC-2004.  
PA (MONS) MONSANTO TECHNOLOGY LLC.  
Percent Similarity: 37.8%  
Best Local Similarity: 26.7%  
Query Match: 5.7%  
Conservative: 24  
Mismatches: 78  
Indels: 57  
RESULT 894  
ID AAZ99653 standard; DNA; 1079 BP.  
DE DNA coding for the extracellular domain of syndecan-3.  
PN WO200014103-A1.  
PD 16-MAR-2000.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
Percent Similarity: 39.1%  
Best Local Similarity: 26.2%  
Query Match: 5.7%  
Conservative: 32  
Mismatches: 111  
Indels: 40  
RESULT 895  
ID AAI21687 standard; DNA; 1161 BP.  
DE Probe #11620 for gene expression analysis in human cervical cell sample.



PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 896  
ID ABA66765 standard; DNA; 1161 BP.  
DE Human foetal liver single exon nucleic acid probe #15070.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 897  
ID AAI46976 standard; DNA; 1161 BP.  
DE Probe #15662 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 898  
ID ABA48852 standard; DNA; 1161 BP.  
DE Human breast cell single exon nucleic acid probe #7547.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 899  
ID ABA33829 standard; DNA; 1161 BP.  
DE Probe #12295 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 900  
ID AAK40921 standard; DNA; 1161 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 15478.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 901  
ID AAK15196 standard; DNA; 1161 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 15187.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 902  
ID ABS40502 standard; DNA; 1161 BP.  
DE Human liver single exon probe, SEQ ID No 15492.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 903  
ID AAI07377 standard; DNA; 1161 BP.  
DE Probe #7368 used to measure gene expression in human breast sample.  
PN WO200157270-A2.

PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 35.9%  
Best Local Similarity: 22.1%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 147  
Indels: 106  
RESULT 904  
ID ADS49128 standard; CDNA; 1239 BP.  
DE Bacterial polynucleotide #3871.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 34.8%  
Best Local Similarity: 21.2%  
Query Match: 5.7%  
Conservative: 54  
Mismatches: 125  
Indels: 134  
RESULT 905  
ID AAF11900 standard; CDNA; 1446 BP.  
DE Aspergillus oryzae EST SEQ ID NO:4423.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
Percent Similarity: 33.1%  
Best Local Similarity: 22.8%  
Query Match: 5.7%  
Conservative: 39  
Mismatches: 137  
Indels: 117  
RESULT 906  
ID ADU55941 standard; CDNA; 1446 BP.  
DE Aspergillus oryzae strain strain A1560/strain AL-1 EST, SEQ ID NO:4423.  
PN US2004229367-A1.  
PD 18-NOV-2004.  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES INC AS.  
Percent Similarity: 33.1%  
Best Local Similarity: 22.8%  
Query Match: 5.7%  
Conservative: 39  
Mismatches: 137  
Indels: 117  
RESULT 907  
ID AD293944 standard; CDNA; 1446 BP.  
DE Aspergillus oryzae expressed sequence tag cDNA SEQ ID NO 4423.  
PN US6902887-B1.  
PD 07-JUN-2005.  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES AS.  
Percent Similarity: 33.1%  
Best Local Similarity: 22.8%  
Query Match: 5.7%  
Conservative: 39  
Mismatches: 137  
Indels: 117  
RESULT 908  
ID ADK41684 standard; CDNA; 1821 BP.  
DE Maize amino acid transporter gene.  
PN WO2003066879-A2.  
PD 14-AUG-2003.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Percent Similarity: 34.8%  
Best Local Similarity: 23.4%  
Query Match: 5.7%  
Conservative: 38  
Mismatches: 131  
Indels: 88  
RESULT 909  
ID AAC69572 standard; DNA; 2084 BP.  
DE Human secreted protein gene 61 clone HAJBG14.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 36.9%  
Best Local Similarity: 23.0%  
Query Match: 5.7%  
Conservative: 57  
Mismatches: 164  
Indels: 94  
RESULT 910  
ID ADA53108 standard; CDNA; 2256 BP.  
DE Human coding sequence, SEQ ID 676.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

Percent Similarity: 34.2%      Conservative: 43  
Best Local Similarity: 22.9%      Mismatches: 126  
Query Match: 5.7%      Indels: 127  
RESULT 911  
ID ABL08377 standard; cDNA; 2636 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19613.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 44.1%      Conservative: 19  
Best Local Similarity: 30.8%      Mismatches: 64  
Query Match: 5.7%      Indels: 16  
RESULT 912  
ID ACN38055 standard; cDNA; 2733 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA324424, SEQ ID NO:1338.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 37.6%      Conservative: 38  
Best Local Similarity: 25.4%      Mismatches: 134  
Query Match: 5.7%      Indels: 62  
RESULT 913  
ID ADS48534 standard; cDNA; 3078 BP.  
DE Bacterial polynucleotide #3277.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 35.7%      Conservative: 40  
Best Local Similarity: 25.3%      Mismatches: 147  
Query Match: 5.7%      Indels: 102  
RESULT 914  
ID ABL23385 standard; DNA; 3906 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21628.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 33.2%      Conservative: 46  
Best Local Similarity: 22.0%      Mismatches: 153  
Query Match: 5.7%      Indels: 122  
RESULT 915  
ID ACL64233 standard; DNA; 4039 BP.  
DE M. xanthus DNA fragment, seq id 696.  
PN US6833447-B1.  
PD 21-DEC-2004.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Percent Similarity: 37.8%      Conservative: 24  
Best Local Similarity: 26.7%      Mismatches: 78  
Query Match: 5.7%      Indels: 57  
RESULT 916  
ID ABL08392 standard; cDNA; 5296 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19658.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 35.4%      Conservative: 39  
Best Local Similarity: 21.3%      Mismatches: 114  
Query Match: 5.7%      Indels: 66  
RESULT 917  
ID ADZ72162 standard; DNA; 5301 BP.  
DE P. luminescens toxin A gene A0 with N- and C-terminal truncation.  
PN US2005102713-A1.  
PD 12-MAY-2005.  
PA (MERL/) MERLO D J.  
PA (LIUD/) LIU D.  
PA (BURT/) BURTON S L.  
PA (GLAN/) GLANCY T P.  
Percent Similarity: 36.8%      Conservative: 58  
Best Local Similarity: 24.6%      Mismatches: 165  
Query Match: 5.7%      Indels: 137

RESULT 918  
ID ADZ72160 standard; DNA; 5561 BP.  
DE P. luminescens toxin A full length gene A1 SEQ ID NO:7.  
PN US2005102713-A1.  
PD 12-MAY-2005.  
PA (MERL/) MERLO D J.  
PA (LIUD/) LIU D.  
PA (BURT/) BURTON S L.  
PA (GLAN/) GLANCY T P.  
Percent Similarity: 36.8%      Conservative: 58  
Best Local Similarity: 24.6%      Mismatches: 165  
Query Match: 5.7%      Indels: 137  
RESULT 919  
ID ADM10942 standard; cDNA; 5738 BP.  
DE Human O645genomicContig2 cDNA.  
PN US2003206918-A1.  
PD 06-NOV-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 35.2%      Conservative: 50  
Best Local Similarity: 22.8%      Mismatches: 153  
Query Match: 5.7%      Indels: 109  
RESULT 920  
ID ADJ11272 standard; DNA; 5738 BP.  
DE Human ovarian tumour antigen DNA SeqID 273.  
PN US2003232056-A1.  
PD 18-DEC-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 35.2%      Conservative: 50  
Best Local Similarity: 22.8%      Mismatches: 153  
Query Match: 5.7%      Indels: 109  
RESULT 921  
ID ADM43533 standard; DNA; 5738 BP.  
DE Human ovarian cancer cDNA homologous DNA #18.  
PN US2003129192-A1.  
PD 10-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 35.2%      Conservative: 50  
Best Local Similarity: 22.8%      Mismatches: 153  
Query Match: 5.7%      Indels: 109  
RESULT 922  
ID AEG35782 standard; DNA; 5738 BP.  
DE Human ovarian tumor antigen O648S contig DNA sequence SEQ ID NO: 273.  
PN US2006057141-A1.  
PD 16-MAR-2006.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 35.2%      Conservative: 50  
Best Local Similarity: 22.8%      Mismatches: 153  
Query Match: 5.7%      Indels: 109  
RESULT 923  
ID ADZ72161 standard; DNA; 5816 BP.  
DE P. luminescens toxin A gene A1 with C-terminal truncation SEQ ID NO:8.  
PN US2005102713-A1.  
PD 12-MAY-2005.  
PA (MERL/) MERLO D J.  
PA (LIUD/) LIU D.  
PA (BURT/) BURTON S L.  
PA (GLAN/) GLANCY T P.  
Percent Similarity: 36.8%      Conservative: 58  
Best Local Similarity: 24.6%      Mismatches: 165  
Query Match: 5.7%      Indels: 137  
RESULT 924  
ID AEG64418 standard; DNA; 5901 BP.  
DE B. longum narrowly conserved hypothetical protein encoding DNA.  
PN US2006068461-A1.  
PD 30-MAR-2006.  
PA (AJIN ) AJINOMOTO CO INC.  
Percent Similarity: 41.6%      Conservative: 23  
Best Local Similarity: 29.5%      Mismatches: 72  
Query Match: 5.7%      Indels: 40  
RESULT 925  
ID AEL42510 standard; DNA; 5901 BP.  
DE Bifidobacterium longum NCC2705 genomic DNA.  
PN US2006223140-A1.

PD 05-OCT-2006.  
PA (AJIN ) AJINOMOTO CO INC.  
Percent Similarity: 41.6%  
Best Local Similarity: 29.5%  
Query Match: 5.7%  
RESULT 926  
ID ABL23384 standard; DNA; 5983 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21625.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 33.2%  
Best Local Similarity: 22.0%  
Query Match: 5.7%  
RESULT 927  
ID AAD55736 standard; DNA; 6052 BP.  
DE Plectreury's tristis fibroin 3 DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Percent Similarity: 38.4%  
Best Local Similarity: 22.0%  
Query Match: 5.7%  
RESULT 928  
ID AD72159 standard; DNA; 7302 BP.  
DE P. luminescens toxin A gene A0 with N-terminal truncation SEQ ID NO:6.  
PN US2005102713-A1.  
PD 12-MAY-2005.  
PA (MERL/) MERLO D J.  
PA (LIUD/) LIU D.  
PA (BURT/) BURTON S L.  
PA (GLAN/) GLANCY T P.  
Percent Similarity: 36.8%  
Best Local Similarity: 24.6%  
Query Match: 5.7%  
RESULT 929  
ID AD72158 standard; DNA; 7560 BP.  
DE P. luminescens toxin A full length gene A0 SEQ ID NO:5.  
PN US2005102713-A1.  
PD 12-MAY-2005.  
PA (MERL/) MERLO D J.  
PA (LIUD/) LIU D.  
PA (BURT/) BURTON S L.  
PA (GLAN/) GLANCY T P.  
Percent Similarity: 36.8%  
Best Local Similarity: 24.6%  
Query Match: 5.7%  
RESULT 930  
ID AAF58780 standard; DNA; 7577 BP.  
DE Modified Photorhabdus tcdA toxin coding sequence.  
PN WO200111029-A1.  
PD 15-FEB-2001.  
PA (DOWC ) DOW AGROSCIENCES LLC.  
Percent Similarity: 36.8%  
Best Local Similarity: 24.6%  
Query Match: 5.7%  
RESULT 931  
ID AAF58783 standard; DNA; 7621 BP.  
DE TcdA toxin-zein ER signal peptide fusion protein coding sequence.  
PN WO200111029-A1.  
PD 15-FEB-2001.  
PA (DOWC ) DOW AGROSCIENCES LLC.  
Percent Similarity: 36.8%  
Best Local Similarity: 24.6%  
Query Match: 5.7%  
RESULT 932  
ID ABD33215 standard; DNA; 43865 BP.  
DE Human cancer-associated (CA) gene HD07-034.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 33.2%  
Best Local Similarity: 24.2%  
Conservative: 33  
Mismatches: 159  
Indels: 88

Query Match: 5.7%  
Indels: 88  
RESULT 933  
ID AEJ13218 standard; DNA; 43865 BP.  
DE Cancer-associated gene sequence - SEQ ID 226.  
PN US2006154250-A1.  
PD 13-JUL-2006.  
PA (MORR/) MORRIS D W.  
PA (MALA/) MALANDRO M S.  
Percent Similarity: 33.2%  
Best Local Similarity: 24.2%  
Query Match: 5.7%  
RESULT 934  
ID ABQ81844 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1100.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Percent Similarity: 41.6%  
Best Local Similarity: 29.5%  
Query Match: 5.7%  
RESULT 935  
ID ADT95863 standard; cDNA; 1111 BP.  
DE Colon cancer associated human cDNA sequence #1382.  
PN US2003087818-A1.  
PD 08-MAY-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 43.0%  
Best Local Similarity: 27.6%  
Query Match: 5.7%  
RESULT 936  
ID ADX42345 standard; cDNA; 1111 BP.  
DE Human cDNA encoding colon cancer protein SEQ ID NO 1382.  
PN WO200274156-A2.  
PD 26-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 43.0%  
Best Local Similarity: 27.6%  
Query Match: 5.7%  
RESULT 937  
ID AAQ75858 standard; DNA; 1352 BP.  
DE Glucomyrase gene.  
PN JP06303984-A.  
PD 01-NOV-1994.  
PA (NISB ) JAPAN TOBACCO INC.  
Percent Similarity: 33.6%  
Best Local Similarity: 23.2%  
Query Match: 5.7%  
RESULT 938  
ID ABT23537 standard; DNA; 1395 BP.  
DE Cellobiohydrolase I activity polynucleotide SEQ ID No 49.  
PN WO2003000941-A2.  
PD 03-JAN-2003.  
PA (NOVO ) NOVOZYMES AS.  
Percent Similarity: 36.0%  
Best Local Similarity: 22.5%  
Query Match: 5.7%  
RESULT 939  
ID AEI60832 standard; cDNA; 1541 BP.  
DE Soybean coding sequence, SEQ ID NO: 5299.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Percent Similarity: 36.6%  
Best Local Similarity: 24.1%  
Query Match: 5.7%  
RESULT 940  
ID ADQ23348 standard; DNA; 1679 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6168.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Percent Similarity: 36.8%  
Best Local Similarity: 23.0%  
Conservative: 45  
Mismatches: 143



Query Match: 5.7% Indels: 64  
RESULT 941  
ID ADS61404 standard; cDNA; 1817 BP.  
DE Bacterial polynucleotide #13391.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 32.6% Conservative: 38  
Best Local Similarity: 23.6% Mismatches: 131  
Query Match: 5.7% Indels: 152  
RESULT 942  
ID ADR96639 standard; DNA; 1860 BP.  
DE M. tuberculosis antigen Rv0312 DNA SEQ ID NO:65.  
PN WO2004083448-A2.  
PD 30-SEP-2004.  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
PA (STAT-) STATENS SERUM INST.  
Percent Similarity: 47.8% Conservative: 11  
Best Local Similarity: 35.6% Mismatches: 36  
Query Match: 5.7% Indels: 11  
RESULT 943  
ID ABI99688 standard; cDNA; 2215 BP.  
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:726.  
PN WO200188188-A2.  
PD 22-NOV-2001.  
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
Percent Similarity: 39.5% Conservative: 56  
Best Local Similarity: 22.2% Mismatches: 131  
Query Match: 5.7% Indels: 66  
RESULT 944  
ID ACC46555 standard; cDNA; 2382 BP.  
DE Human dithp secreted/extracellular matrix protein-encoding cDNA.  
PN WO200297031-A2.  
PD 05-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 38.4% Conservative: 51  
Best Local Similarity: 25.7% Mismatches: 153  
Query Match: 5.7% Indels: 98  
RESULT 945  
ID ABL28391 standard; DNA; 2532 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 36646.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 37.5% Conservative: 45  
Best Local Similarity: 23.9% Mismatches: 129  
Query Match: 5.7% Indels: 80  
RESULT 946  
ID ADH71761 standard; DNA; 2623 BP.  
DE Human gene of the invention NOV28k SEQ ID NO:657.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.7% Indels: 117  
RESULT 947  
ID ADN00733 standard; DNA; 2671 BP.  
DE Human LDLR coding sequence, SEQ ID 6.  
PN WO2004024881-A2.  
PD 25-MAR-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.7% Indels: 117  
RESULT 948  
ID ABQ76406 standard; cDNA; 2717 BP.  
DE S. cerevisiae BAX-associated cDNA fragment SEQ ID 237.  
PN WO200264766-A2.

PD 22-AUG-2002.  
PA (JANC ) JANSSEN PHARM NV.  
Percent Similarity: 42.4% Conservative: 51  
Best Local Similarity: 24.8% Mismatches: 111  
Query Match: 5.7% Indels: 57  
RESULT 949  
ID AAD07130 standard; cDNA; 2805 BP.  
DE Canine retinitis pigmentosa GTPase regulator (RPGR) cDNA.  
PN WO200138578-A1.  
PD 31-MAY-2001.  
PA (CORR ) CORNELL RES FOUND INC.  
Percent Similarity: 36.4% Conservative: 72  
Best Local Similarity: 19.4% Mismatches: 139  
Query Match: 5.7% Indels: 131  
RESULT 950  
ID ADR84702 standard; DNA; 2832 BP.  
DE Aspergillus fumigatus essential gene genomic sequence #513.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Percent Similarity: 35.8% Conservative: 54  
Best Local Similarity: 21.3% Mismatches: 135  
Query Match: 5.7% Indels: 104  
RESULT 951  
ID AAA81463 standard; DNA; 78845 BP.  
DE N. meningitidis partial DNA sequence gnm\_11 SEQ ID NO:11.  
PN WO200022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 36.1% Conservative: 61  
Best Local Similarity: 22.9% Mismatches: 157  
Query Match: 5.7% Indels: 140  
RESULT 952  
ID ADU47667 standard; DNA; 88400 BP.  
DE S. cyaneogriseus LL-F28249 compound full-length biosynthetic gene.  
PN EP1477563-A2.  
PD 17-NOV-2004.  
PA (AMHP ) WYETH.  
PA (FORT-) FORT DODGE ANIMAL HEALTH.  
Percent Similarity: 36.4% Conservative: 65  
Best Local Similarity: 22.3% Mismatches: 162  
Query Match: 5.7% Indels: 134  
RESULT 953  
Percent Similarity: 36.1% Conservative: 61  
Best Local Similarity: 22.9% Mismatches: 157  
Query Match: 5.7% Indels: 140  
RESULT 954  
Percent Similarity: 32.3% Conservative: 38  
Best Local Similarity: 23.0% Mismatches: 142  
Query Match: 5.7% Indels: 135  
RESULT 955  
Percent Similarity: 38.4% Conservative: 26  
Best Local Similarity: 26.4% Mismatches: 104  
Query Match: 5.7% Indels: 29  
RESULT 956  
ID AED46970 standard; DNA; 1242 BP.  
DE Membrane construction and membrane transport protein DNA SEQ ID 247.  
PN US2005244935-A1.  
PD 03-NOV-2005.  
PA (BADI ) BASF AG.  
Percent Similarity: 36.7% Conservative: 62  
Best Local Similarity: 22.0% Mismatches: 159  
Query Match: 5.7% Indels: 109  
RESULT 957  
ID ABK71704 standard; cDNA; 1430 BP.  
DE Human dithp polynucleotide #170.  
PN WO200220754-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 36.9% Conservative: 48  
Best Local Similarity: 23.8% Mismatches: 125  
Query Match: 5.7% Indels: 110

RESULT 958  
 ID ADM86778 standard; cDNA; 1430 BP.  
 DE Human cDNA #39 differentially expressed in lung cancer.  
 PN US2003175704-A1.  
 PD 18-SEP-2003.  
 PA (LASE/) LASEK A K W.  
 PA (SHYJ/) SHYJAN A W.  
 PA (TURN/) TURNER C M.  
 Percent Similarity: 36.9%  
 Best Local Similarity: 23.8%  
 Query Match: 5.7%  
 Conservative: 48  
 Mismatches: 125  
 Indels: 110  
 RESULT 959  
 ID ADL13149 standard; cDNA; 1430 BP.  
 DE Human steroid-induced C3A liver cell cDNA #878.  
 PN US6673549-B1.  
 PD 06-JAN-2004.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 36.9%  
 Best Local Similarity: 23.8%  
 Query Match: 5.7%  
 Conservative: 48  
 Mismatches: 125  
 Indels: 110  
 RESULT 960  
 ID AAF07488 standard; cDNA; 1463 BP.  
 DE Fusarium venenatum EST SEQ ID NO:11.  
 PN WO200056762-A2.  
 PD 28-SEP-2000.  
 PA (NOVO ) NOVO NORDISK BIOTECH INC.  
 PA (NOVO ) NOVO NORDISK AS.  
 Percent Similarity: 39.3%  
 Best Local Similarity: 21.9%  
 Query Match: 5.7%  
 Conservative: 63  
 Mismatches: 130  
 Indels: 90  
 RESULT 961  
 ID ADU51529 standard; cDNA; 1463 BP.  
 DE Fusarium venenatum CC1-3 EST, SEQ ID NO:11.  
 PN US2004229367-A1.  
 PD 18-NOV-2004.  
 PA (NOVO ) NOVOZYMES BIOTECH INC.  
 PA (NOVO ) NOVOZYMES INC AS.  
 Percent Similarity: 39.3%  
 Best Local Similarity: 21.9%  
 Query Match: 5.7%  
 Conservative: 63  
 Mismatches: 130  
 Indels: 90  
 RESULT 962  
 ID ADZ89532 standard; cDNA; 1463 BP.  
 DE Fusarium venenatum expressed sequence tag cDNA SEQ ID NO 11.  
 PN US6902887-B1.  
 PD 07-JUN-2005.  
 PA (NOVO ) NOVOZYMES BIOTECH INC.  
 PA (NOVO ) NOVOZYMES AS.  
 Percent Similarity: 39.3%  
 Best Local Similarity: 21.9%  
 Query Match: 5.7%  
 Conservative: 63  
 Mismatches: 130  
 Indels: 90  
 RESULT 963  
 ID ABL16653 standard; DNA; 1529 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1432.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 40.4%  
 Best Local Similarity: 29.2%  
 Query Match: 5.7%  
 Conservative: 31  
 Mismatches: 119  
 Indels: 47  
 RESULT 964  
 ID AAI49456 standard; DNA; 1887 BP.  
 DE Probe #18142 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.0%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 Conservative: 62  
 Mismatches: 147  
 Indels: 78  
 RESULT 965  
 ID ABA51281 standard; DNA; 1887 BP.  
 DE Human breast cell single exon nucleic acid probe #9976.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.0%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 Conservative: 62  
 Mismatches: 147  
 Indels: 78  
 RESULT 966  
 ID ABS17477 standard; DNA; 1887 BP.  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 17468.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.0%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 Conservative: 62  
 Mismatches: 147  
 Indels: 78  
 RESULT 967  
 ID AAI36327 standard; DNA; 1972 BP.  
 DE Probe #5013 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.0%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 Conservative: 62  
 Mismatches: 147  
 Indels: 78  
 RESULT 968  
 ID ABA46169 standard; DNA; 1972 BP.  
 DE Human breast cell single exon nucleic acid probe #4864.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.0%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 Conservative: 62  
 Mismatches: 147  
 Indels: 78  
 RESULT 969  
 ID ABS04966 standard; DNA; 1972 BP.  
 DE Human genome-derived single exon probe from lung SEQ ID No 4957.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 41.0%  
 Best Local Similarity: 24.5%  
 Query Match: 5.7%  
 Conservative: 62  
 Mismatches: 147  
 Indels: 78  
 RESULT 970  
 ID ACC61564 standard; DNA; 2000 BP.  
 DE Gene sequence #SEQ ID 1910.  
 PN EP1258494-A1.  
 PD 20-NOV-2002.  
 PA (CELL-) CELLZOME AG.  
 Percent Similarity: 42.6%  
 Best Local Similarity: 27.7%  
 Query Match: 5.7%  
 Conservative: 42  
 Mismatches: 126  
 Indels: 37  
 RESULT 971  
 ID ADK64447 standard; DNA; 2000 BP.  
 DE Disease treating protein complex-derived gene #1152.  
 PN EP1338608-A2.  
 PD 27-AUG-2003.  
 PA (CELL-) CELLZOME AG.  
 Percent Similarity: 42.6%  
 Best Local Similarity: 27.7%  
 Query Match: 5.7%  
 Conservative: 42  
 Mismatches: 126  
 Indels: 37  
 RESULT 972  
 ID AAT17864 standard; DNA; 2093 BP.  
 DE Hepatitis A virus receptor DNA.  
 PN WO9604376-A1.  
 PD 15-FEB-1996.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 Percent Similarity: 41.0%  
 Best Local Similarity: 23.4%  
 Query Match: 5.7%  
 Conservative: 43  
 Mismatches: 110  
 Indels: 35  
 RESULT 973  
 ID AAI60599 standard; cDNA; 2177 BP.  
 DE Human polynucleotide SEQ ID NO 4588.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.

Percent Similarity: 39.1% Conservative: 46  
Best Local Similarity: 23.5% Mismatches: 117  
Query Match: 5.7% Indels: 63  
RESULT 974  
ID AAD30798 standard; DNA; 2337 BP.  
DE Saccharomyces diastaticus-derived glucoamylase gene, STAL.  
PN WO200212509-A1.  
PD 14-FEB-2002.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
Percent Similarity: 35.8% Conservative: 35  
Best Local Similarity: 22.8% Mismatches: 86  
Query Match: 5.7% Indels: 87  
RESULT 975  
ID AAV02953 standard; DNA; 2753 BP.  
DE S. diastaticus STAL genomic DNA.  
PN JP09299090-A.  
PD 25-NOV-1997.  
PA (SUNR ) SUNTORY LTD.  
Percent Similarity: 35.8% Conservative: 35  
Best Local Similarity: 22.8% Mismatches: 86  
Query Match: 5.7% Indels: 87  
RESULT 976  
ID AAN60834 standard; DNA; 2764 BP.  
DE Sequence of plasmid pSTAL.  
PN JP60262593-A.  
PD 25-DEC-1985.  
PA (MITK ) MITSUI TOATSU CHEM INC.  
Percent Similarity: 35.8% Conservative: 35  
Best Local Similarity: 22.8% Mismatches: 86  
Query Match: 5.7% Indels: 87  
RESULT 977  
ID ADW10463 standard; DNA; 2818 BP.  
DE Colon proliferative disorder associated human DNA fragment, SEQ ID 268.  
PN US2004265833-A1.  
PD 30-DEC-2004.  
PA (LOFT/) LOFTON-DAY C.  
PA (SLED/) SLEDZIEWSKI A.  
PA (THOM/) THOMAS J.  
PA (DAYR/) DAY R W.  
PA (TONN/) TONNES-PRIDDY L.  
PA (CARD/) CARDON K.  
Percent Similarity: 34.9% Conservative: 43  
Best Local Similarity: 21.7% Mismatches: 138  
Query Match: 5.7% Indels: 76  
RESULT 978  
ID ADW10457 standard; DNA; 2818 BP.  
DE Colon proliferative disorder associated human DNA fragment, SEQ ID 262.  
PN US2004265833-A1.  
PD 30-DEC-2004.  
PA (LOFT/) LOFTON-DAY C.  
PA (SLED/) SLEDZIEWSKI A.  
PA (THOM/) THOMAS J.  
PA (DAYR/) DAY R W.  
PA (TONN/) TONNES-PRIDDY L.  
PA (CARD/) CARDON K.  
Percent Similarity: 34.9% Conservative: 43  
Best Local Similarity: 21.7% Mismatches: 138  
Query Match: 5.7% Indels: 76  
RESULT 979  
ID ABN92052 standard; DNA; 2835 BP.  
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1515.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 40.5% Conservative: 76  
Best Local Similarity: 20.5% Mismatches: 160  
Query Match: 5.7% Indels: 66  
RESULT 980  
ID ABL25807 standard; DNA; 3381 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28894.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.

Percent Similarity: 33.9% Conservative: 51  
Best Local Similarity: 22.1% Mismatches: 158  
Query Match: 5.7% Indels: 130  
RESULT 981  
ID ABN92222 standard; DNA; 3561 BP.  
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1685.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 40.5% Conservative: 76  
Best Local Similarity: 20.5% Mismatches: 160  
Query Match: 5.7% Indels: 66  
RESULT 982  
ID ADS02014 standard; DNA; 3561 BP.  
DE Staphylococcus epidermis polynucleotide segid 1309.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
Percent Similarity: 40.5% Conservative: 76  
Best Local Similarity: 20.5% Mismatches: 160  
Query Match: 5.7% Indels: 66  
RESULT 983  
ID AEI08097 standard; DNA; 3561 BP.  
DE Staphylococcus epidermidis protein coding sequence - SEQ ID 1309.  
PN US7060458-B1.  
PD 13-JUN-2006.  
PA (AMHP ) WYETH.  
Percent Similarity: 40.5% Conservative: 76  
Best Local Similarity: 20.5% Mismatches: 160  
Query Match: 5.7% Indels: 66  
RESULT 984  
ID ABL16652 standard; DNA; 3591 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1429.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 40.4% Conservative: 31  
Best Local Similarity: 29.2% Mismatches: 119  
Query Match: 5.7% Indels: 47  
RESULT 985  
ID AAA59701 standard; DNA; 4998 BP.  
DE DNA encoding murine neural plakophilin related armidillo protein.  
PN WO200047615-A2.  
PD 17-AUG-2000.  
PA (UTOR ) UNIV TORONTO GOVERNING COUNCIL.  
Percent Similarity: 34.9% Conservative: 62  
Best Local Similarity: 22.0% Mismatches: 193  
Query Match: 5.7% Indels: 122  
RESULT 986  
ID ABL25806 standard; DNA; 5381 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28891.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 33.9% Conservative: 51  
Best Local Similarity: 22.1% Mismatches: 158  
Query Match: 5.7% Indels: 130  
RESULT 987  
ID ABN92163 standard; DNA; 6414 BP.  
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1626.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 40.5% Conservative: 76  
Best Local Similarity: 20.5% Mismatches: 160  
Query Match: 5.7% Indels: 66  
RESULT 988  
ID ADS01884 standard; DNA; 6414 BP.  
DE Staphylococcus epidermis polynucleotide segid 1179.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.



PA (BUSH/) BUSH D.  
Percent Similarity: 40.5%  
Best Local Similarity: 20.5%  
Query Match: 5.7%  
Conservative: 76  
Mismatches: 160  
Indels: 66  
RESULT 989  
ID AEI07967 standard; DNA; 6414 BP.  
DE Staphylococcus epidermidis protein coding sequence - SEQ ID 1179.  
PN US7060458-B1.  
PD 13-JUN-2006.  
PA (AMHP ) WYETH.  
Percent Similarity: 40.5%  
Best Local Similarity: 20.5%  
Query Match: 5.7%  
Conservative: 76  
Mismatches: 160  
Indels: 66  
RESULT 990  
ID AAS84050 standard; cDNA; 6458 BP.  
DE DNA encoding novel human diagnostic protein #19854.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.2%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
Conservative: 43  
Mismatches: 119  
Indels: 95  
RESULT 991  
ID ADZ13121 standard; cDNA; 8382 BP.  
DE Murine cancer-associated cDNA #70.  
PN WO2005031001-A2.  
PD 07-APR-2005.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 37.6%  
Best Local Similarity: 23.9%  
Query Match: 5.7%  
Conservative: 47  
Mismatches: 138  
Indels: 76  
RESULT 992  
ID AAS68117 standard; cDNA; 9012 BP.  
DE DNA encoding novel human diagnostic protein #3921.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 41.0%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
Conservative: 62  
Mismatches: 147  
Indels: 78  
RESULT 993  
ID AAS72748 standard; cDNA; 9012 BP.  
DE DNA encoding novel human diagnostic protein #8552.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 41.0%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
Conservative: 62  
Mismatches: 147  
Indels: 78  
RESULT 994  
ID ACN40983 standard; cDNA; 9633 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA327008, SEQ ID NO:6123.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 41.0%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
Conservative: 62  
Mismatches: 147  
Indels: 78  
RESULT 995  
ID AAS88071 standard; cDNA; 10184 BP.  
DE DNA encoding novel human diagnostic protein #23875.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 41.0%  
Best Local Similarity: 24.5%  
Query Match: 5.7%  
Conservative: 62  
Mismatches: 147  
Indels: 78  
RESULT 996  
ID ADA02558 standard; DNA; 21526 BP.  
DE Human LY6E carcinoma associated gene, SEQ ID NO:1076.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 31.4%  
Conservative: 26

Percent Similarity: 34.6%  
Best Local Similarity: 22.9%  
Query Match: 5.7%  
Conservative: 42  
Mismatches: 137  
Indels: 98  
RESULT 997  
ID ADB72296 standard; DNA; 21526 BP.  
DE Human LY6E gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 34.6%  
Best Local Similarity: 22.9%  
Query Match: 5.7%  
Conservative: 42  
Mismatches: 137  
Indels: 98  
RESULT 998  
ID ADE95806 standard; DNA; 21526 BP.  
DE Human LY6E gene genomic DNA sequence.  
PN WO2003039484-A2.  
PD 15-MAY-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Percent Similarity: 34.6%  
Best Local Similarity: 22.9%  
Query Match: 5.7%  
Conservative: 42  
Mismatches: 137  
Indels: 98  
RESULT 999  
ID AEK60077 standard; DNA; 21526 BP.  
DE Human LY6E genomic sequence, SEQ ID NO: 64.  
PN US2006204982-A1.  
PD 14-SEP-2006.  
PA (MORR/) MORRIS D W.  
PA (ENGE/) ENGELHARD E K.  
Percent Similarity: 34.6%  
Best Local Similarity: 22.9%  
Query Match: 5.7%  
Conservative: 42  
Mismatches: 137  
Indels: 98  
RESULT 1000  
ID ABD32538 standard; DNA; 46030 BP.  
DE Mouse cancer-associated genomic DNA MD7-023.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 39.4%  
Best Local Similarity: 27.3%  
Query Match: 5.7%  
Conservative: 35  
Mismatches: 116  
Indels: 59  
RESULT 1001  
Percent Similarity: 35.5%  
Best Local Similarity: 26.3%  
Query Match: 5.7%  
Conservative: 27  
Mismatches: 112  
Indels: 77  
RESULT 1002  
Percent Similarity: 35.5%  
Best Local Similarity: 26.3%  
Query Match: 5.7%  
Conservative: 27  
Mismatches: 112  
Indels: 77  
RESULT 1003  
ID ABN77933 standard; cDNA; 702 BP.  
DE Human ORF2880 cDNA, SEQ ID NO:5759.  
PN WO200190366-A2.  
PD 29-NOV-2001.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 43.9%  
Best Local Similarity: 28.5%  
Query Match: 5.6%  
Conservative: 34  
Mismatches: 98  
Indels: 27  
RESULT 1004  
ID ABI57142 standard; cDNA; 1209 BP.  
DE Thale cress coding sequence, SEQ ID NO: 1609.  
PN US2006143729-A1.  
PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Percent Similarity: 36.9%  
Best Local Similarity: 23.6%  
Query Match: 5.6%  
Conservative: 41  
Mismatches: 125  
Indels: 71  
RESULT 1005  
ID AAQ82821 standard; cDNA; 1425 BP.  
DE A. aculeatus protease II gene.  
PN WO9502044-A1.  
PD 19-JAN-1995.  
PA (NOVO ) NOVO-NORDISK AS.  
Percent Similarity: 31.4%  
Conservative: 26

Best Local Similarity: 24.9% Mismatches: 133  
Query Match: 5.6% Indels: 145  
RESULT 1006  
ID ABL19993 standard; DNA; 1439 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11452.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 35.0% Conservative: 32  
Best Local Similarity: 24.5% Mismatches: 103  
Query Match: 5.6% Indels: 96  
RESULT 1007  
ID ADQ96833 standard; DNA; 1944 BP.  
DE CrtWcrtY nucleotide sequence.  
PN CN1380415-A.  
PD 20-NOV-2002.  
PA (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.  
Percent Similarity: 35.4% Conservative: 41  
Best Local Similarity: 23.1% Mismatches: 120  
Query Match: 5.6% Indels: 96  
RESULT 1008  
ID ADQ96933 standard; DNA; 1966 BP.  
DE CrtWcrtY nucleotide sequence.  
PN CN1380415-A.  
PD 20-NOV-2002.  
PA (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.  
Percent Similarity: 35.4% Conservative: 41  
Best Local Similarity: 23.1% Mismatches: 120  
Query Match: 5.6% Indels: 96  
RESULT 1009  
ID AED70477 standard; DNA; 2175 BP.  
DE Corynebacterium glutamicum MCP gene SEQ ID NO:653.  
PN US6962989-B1.  
PD 08-NOV-2005.  
PA (BADI ) BASF AG.  
Percent Similarity: 31.7% Conservative: 34  
Best Local Similarity: 22.9% Mismatches: 110  
Query Match: 5.6% Indels: 153  
RESULT 1010  
ID AED70479 standard; DNA; 2175 BP.  
DE Corynebacterium glutamicum MCP gene SEQ ID NO:655.  
PN US6962989-B1.  
PD 08-NOV-2005.  
PA (BADI ) BASF AG.  
Percent Similarity: 31.7% Conservative: 34  
Best Local Similarity: 22.9% Mismatches: 110  
Query Match: 5.6% Indels: 153  
RESULT 1011  
ID AAQ80010 standard; DNA; 2414 BP.  
DE Genomic DNA encoding cystathionine gamma lyase.  
PN JP06292586-A.  
PD '21-OCT-1994.  
PA (ASAH ) ASahi KASEI KOGYO KK.  
Percent Similarity: 38.1% Conservative: 49  
Best Local Similarity: 24.4% Mismatches: 153  
Query Match: 5.6% Indels: 70  
RESULT 1012  
ID ADC30199 standard; cDNA; 3007 BP.  
DE Human novel cDNA sequence, SEQ ID NO:281.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 36.0% Conservative: 32  
Best Local Similarity: 25.3% Mismatches: 111  
Query Match: 5.6% Indels: 81  
RESULT 1013  
ID ADZ03671 standard; cDNA; 3117 BP.  
DE PRG4-Lub:3 cDNA construct.  
PN WO2005016130-A2.  
PD 24-FEB-2005.  
PA (AMHP ) WYETH.  
Percent Similarity: 38.2% Conservative: 59  
Best Local Similarity: 23.4% Mismatches: 162

Query Match: 5.6% Indels: 85  
RESULT 1014  
ID AEF99542 standard; cDNA; 3891 BP.  
DE C. botulinum active BONT/A modified open reading frame, SEQ ID No:29.  
PN WO2006017749-A2.  
PD 16-FEB-2006.  
PA (ALLR ) ALLERGAN INC.  
Percent Similarity: 36.6% Conservative: 38  
Best Local Similarity: 23.8% Mismatches: 137  
Query Match: 5.6% Indels: 52  
RESULT 1015  
ID ADT87027 standard; DNA; 3921 BP.  
DE Yeast Stress-related protein gene YR014W.  
PN WO2004092398-A2.  
PD 28-OCT-2004.  
PA (BADI ) BASF PLANT SCI GMBH.  
Percent Similarity: 39.4% Conservative: 51  
Best Local Similarity: 23.2% Mismatches: 146  
Query Match: 5.6% Indels: 45  
RESULT 1016  
ID AEJ50086 standard; DNA; 3921 BP.  
DE Saccharomyces cerevisiae stress-related protein coding seq - SEQ ID 5.  
PN US2006137043-A1.  
PD 22-JUN-2006.  
PA (BADI ) BASF PLANT SCI GMBH.  
Percent Similarity: 39.4% Conservative: 51  
Best Local Similarity: 23.2% Mismatches: 146  
Query Match: 5.6% Indels: 45  
RESULT 1017  
ID AED53819 standard; DNA; 8994 BP.  
DE Ulkenia sp. PUFA-PKS DNA fragment SEQ ID NO 3.  
PN WO2005097982-A2.  
PD 20-OCT-2005.  
PA (NUTR-) NUTRINOVA NUTRITION SPECIALTIES & FOOD.  
Percent Similarity: 40.5% Conservative: 56  
Best Local Similarity: 24.2% Mismatches: 142  
Query Match: 5.6% Indels: 64  
RESULT 1018  
ID AED53817 standard; DNA; 43372 BP.  
DE Cosmid containing PUFA-PKS open reading frames SEQ ID NO 1.  
PN WO2005097982-A2.  
PD 20-OCT-2005.  
PA (NUTR-) NUTRINOVA NUTRITION SPECIALTIES & FOOD.  
Percent Similarity: 40.5% Conservative: 56  
Best Local Similarity: 24.2% Mismatches: 142  
Query Match: 5.6% Indels: 64  
RESULT 1019  
Percent Similarity: 37.6% Conservative: 49  
Best Local Similarity: 21.9% Mismatches: 96  
Query Match: 5.6% Indels: 99  
RESULT 1020  
ID ABQ81849 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1105.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Percent Similarity: 33.2% Conservative: 41  
Best Local Similarity: 22.0% Mismatches: 137  
Query Match: 5.6% Indels: 109  
RESULT 1021  
ID ADX28535 standard; cDNA; 865 BP.  
DE Plant full length insert polynucleotide seqid 11355.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Percent Similarity: 41.1% Conservative: 27  
Best Local Similarity: 26.5% Mismatches: 72  
Query Match: 5.6% Indels: 37

RESULT 1022  
ID ACH87528 standard; DNA; 1083 BP.  
DE Human genome derived single exon probe #20723.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 38.3%  
Best Local Similarity: 25.8%  
Query Match: 5.6%  
Conservative: 16  
Mismatches: 79  
Indels: 0  
RESULT 1023  
ID AAS92828 standard; cDNA; 1200 BP.  
DE DNA encoding novel human diagnostic protein #28632.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 46.2%  
Best Local Similarity: 27.3%  
Query Match: 5.6%  
Conservative: 27  
Mismatches: 71  
Indels: 8  
RESULT 1024  
ID AEB67470 standard; DNA; 1351 BP.  
DE Rice genome derived DNA sequence, SEQ ID 2615.  
PN JP2005185101-A.  
PD 14-JUL-2005.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
PA (SEIB-) SEIBUTSUKI TOKUTEI SANGYO GIJUTSU.  
PA (DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.  
PA (KOKU-) ZH KOKUSAI KAGAKU SHINKO ZAIDAN.  
Percent Similarity: 38.6%  
Best Local Similarity: 26.0%  
Query Match: 5.6%  
Conservative: 40  
Mismatches: 105  
Indels: 91  
RESULT 1025  
ID ADS48557 standard; cDNA; 1451 BP.  
DE Bacterial polynucleotide #3300.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 37.2%  
Best Local Similarity: 23.7%  
Query Match: 5.6%  
Conservative: 49  
Mismatches: 147  
Indels: 82  
RESULT 1026  
ID ADT18746 standard; cDNA; 1463 BP.  
DE Plant cDNA, Seq ID 4072.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Percent Similarity: 42.9%  
Best Local Similarity: 27.0%  
Query Match: 5.6%  
Conservative: 30  
Mismatches: 70  
Indels: 38  
RESULT 1027  
ID AAH78220 standard; DNA; 1464 BP.  
DE Nucleotide sequence of a human secreted polypeptide.  
PN WO200166690-A2.  
PD 13-SEP-2001.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Percent Similarity: 36.0%  
Best Local Similarity: 23.8%  
Query Match: 5.6%  
Conservative: 49  
Mismatches: 160  
Indels: 97  
RESULT 1028  
ID ADO05413 standard; DNA; 1795 BP.  
DE Human GPR50 polymorphic genomic fragment, SEQ ID NO:43.  
PN WO2003104381-A2.  
PD 18-DEC-2003.  
PA (ASTR) ASTRAZENECA AB.  
PA (ASTR) ASTRAZENECA UK LTD.  
Percent Similarity: 38.9%  
Best Local Similarity: 24.2%  
Conservative: 39  
Mismatches: 111

Query Match: 5.6% Indels: 52  
RESULT 1029  
ID AEH37863 standard; DNA; 2199 BP.  
DE Cryptosporidium hominis gene SEQ ID NO:954.  
PN WO2006044045-A2.  
PD 27-APR-2006.  
PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.  
Percent Similarity: 36.3%  
Best Local Similarity: 24.4%  
Query Match: 5.6%  
Conservative: 16  
Mismatches: 86  
Indels: 0  
RESULT 1030  
ID ABL01969 standard; cDNA; 2268 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 389.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Percent Similarity: 31.8%  
Best Local Similarity: 23.0%  
Query Match: 5.6%  
Conservative: 41  
Mismatches: 157  
Indels: 162  
RESULT 1031  
ID AAH15971 standard; cDNA; 2566 BP.  
DE Human cDNA sequence SEQ ID NO:14580.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Percent Similarity: 39.3%  
Best Local Similarity: 26.5%  
Query Match: 5.6%  
Conservative: 35  
Mismatches: 82  
Indels: 84  
RESULT 1032  
ID ADK60438 standard; DNA; 2566 BP.  
DE Angiogenesis differentially expressed gene GS-N13.  
PN FR2836687-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Percent Similarity: 39.3%  
Best Local Similarity: 26.5%  
Query Match: 5.6%  
Conservative: 35  
Mismatches: 82  
Indels: 84  
RESULT 1033  
ID ADK60739 standard; DNA; 2566 BP.  
DE Angiogenesis differentially expressed gene GS-N13.  
PN FR2836686-A1.  
PD 05-SEP-2003.  
PA (GENE-) GENE SIGNAL.  
PA (ALMA/) AL MAHMOOD S.  
Percent Similarity: 39.3%  
Best Local Similarity: 26.5%  
Query Match: 5.6%  
Conservative: 35  
Mismatches: 82  
Indels: 84  
RESULT 1034  
ID ADP73061 standard; DNA; 2566 BP.  
DE Angiogenesis inhibitor human DNA sequence, GS-N13.  
PN FR2843753-A1.  
PD 27-FEB-2004.  
PA (GENE/) GENE S.  
PA (ALMS/) AL M S.  
Percent Similarity: 39.3%  
Best Local Similarity: 26.5%  
Query Match: 5.6%  
Conservative: 35  
Mismatches: 82  
Indels: 84  
RESULT 1035  
ID AAN60473 standard; DNA; 2790 BP.  
DE Sequence encoding the Falciparum Interspersed Repeat Antigen (FIRA).  
PN WO8601802-A.  
PD 27-MAR-1986.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
Percent Similarity: 39.3%  
Best Local Similarity: 25.4%  
Query Match: 5.6%  
Conservative: 34  
Mismatches: 104  
Indels: 44  
RESULT 1036  
ID ADB62373 standard; cDNA; 2821 BP.  
DE Human cDNA encoding clone FCBBF30125460.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.



PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 38.5%  
 Best Local Similarity: 22.8%  
 Query Match: 5.6%  
 RESULT 1037  
 ID ADM99269 standard; DNA; 3002 BP.  
 DE C heterostrophus strain C4 serine carboxypeptidase gene SeqID 152.  
 PN WO2004033668-A2.  
 PD 22-APR-2004.  
 PA (DIVE-) DIVERSA CORP.  
 Percent Similarity: 32.0%  
 Best Local Similarity: 22.5%  
 Query Match: 5.6%  
 RESULT 1038  
 ID ABZ11405 standard; cDNA; 3429 BP.  
 DE Human polynucleotide SEQ ID NO 287.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 39.3%  
 Best Local Similarity: 26.5%  
 Query Match: 5.6%  
 RESULT 1039  
 ID ADM43923 standard; cDNA; 3604 BP.  
 DE Novel human arginine-rich protein cDNA #287.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Percent Similarity: 39.3%  
 Best Local Similarity: 26.5%  
 Query Match: 5.6%  
 RESULT 1040  
 ID ADX64026 standard; cDNA; 4072 BP.  
 DE Plant full length insert polynucleotide seqid 34869.  
 PN US2004034888-A1.  
 PD 19-FEB-2004.  
 PA (LIUJ/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 Percent Similarity: 35.5%  
 Best Local Similarity: 20.4%  
 Query Match: 5.6%  
 RESULT 1041  
 ID ADS48728 standard; cDNA; 4566 BP.  
 DE Bacterial polynucleotide #3471.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 34.4%  
 Best Local Similarity: 22.4%  
 Query Match: 5.6%  
 RESULT 1042  
 ID ADY18478 standard; DNA; 5095 BP.  
 DE DNA encoding a PRO polypeptide, SEQ ID NO 4284.  
 PN WO2005016962-A2.  
 PD 24-FEB-2005.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 39.3%  
 Best Local Similarity: 26.5%  
 Query Match: 5.6%  
 RESULT 1043  
 ID ABX72552 standard; cDNA; 5465 BP.  
 DE Human CA125 cDNA encoding the amino terminal domain.  
 PN WO200283866-A2.

Conservative: 63  
 Mismatches: 160  
 Indels: 87

Conservative: 45  
 Mismatches: 189  
 Indels: 132

Conservative: 35  
 Mismatches: 82  
 Indels: 84

Conservative: 75  
 Mismatches: 144  
 Indels: 177

Conservative: 54  
 Mismatches: 181  
 Indels: 116

Conservative: 35  
 Mismatches: 82  
 Indels: 84

PD 24-OCT-2002.  
 PA (UYAR-) UNIV ARKANSAS.  
 Percent Similarity: 37.3%  
 Best Local Similarity: 23.5%  
 Query Match: 5.6%  
 RESULT 1044  
 ID ADO28933 standard; cDNA; 7710 BP.  
 DE Mouse novel GPCR PGR17 polynucleotide, SEQ ID NO:32.  
 PN WO2004040000-A2.  
 PD 13-MAY-2004.  
 PA (PRIM-) PRIMAL INC.  
 Percent Similarity: 37.3%  
 Best Local Similarity: 22.6%  
 Query Match: 5.6%  
 RESULT 1045  
 ID AAD53014 standard; DNA; 18404 BP.  
 DE Human mucin (MUC-16B) DNA.  
 PN WO200292836-A2.  
 PD 21-NOV-2002.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Percent Similarity: 37.3%  
 Best Local Similarity: 23.5%  
 Query Match: 5.6%  
 RESULT 1046  
 ID ACL68541 standard; DNA; 24459 BP.  
 DE M. xanthus gene sequence, seq id 5004.  
 PN US6833447-B1.  
 PD 21-DEC-2004.  
 PA (MONS) MONSANTO TECHNOLOGY LLC.  
 Percent Similarity: 35.7%  
 Best Local Similarity: 21.7%  
 Query Match: 5.6%  
 RESULT 1047  
 ID ACL64784 standard; DNA; 32241 BP.  
 DE M. xanthus DNA fragment, seq id 1247.  
 PN US6833447-B1.  
 PD 21-DEC-2004.  
 PA (MONS) MONSANTO TECHNOLOGY LLC.  
 Percent Similarity: 35.7%  
 Best Local Similarity: 21.7%  
 Query Match: 5.6%  
 RESULT 1048  
 ID AAI21781 standard; DNA; 1075 BP.  
 DE Probe #11714 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 44.2%  
 Best Local Similarity: 25.6%  
 Query Match: 5.6%  
 RESULT 1049  
 ID ABA66852 standard; DNA; 1075 BP.  
 DE Human foetal liver single exon nucleic acid probe #15157.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 44.2%  
 Best Local Similarity: 25.6%  
 Query Match: 5.6%  
 RESULT 1050  
 ID AAI47064 standard; DNA; 1075 BP.  
 DE Probe #15750 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 44.2%  
 Best Local Similarity: 25.6%  
 Query Match: 5.6%  
 RESULT 1051  
 ID ABA48937 standard; DNA; 1075 BP.  
 DE Human breast cell single exon nucleic acid probe #7632.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.

Conservative: 46  
 Mismatches: 103  
 Indels: 107

Conservative: 57  
 Mismatches: 158  
 Indels: 86

Conservative: 46  
 Mismatches: 103  
 Indels: 107

Conservative: 66  
 Mismatches: 162  
 Indels: 141

Conservative: 66  
 Mismatches: 162  
 Indels: 141

Conservative: 24  
 Mismatches: 69  
 Indels: 3

Conservative: 24  
 Mismatches: 69  
 Indels: 3

Conservative: 24  
 Mismatches: 69  
 Indels: 3

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1052  
ID ABA33921 standard; DNA; 1075 BP.  
DE Probe #12387 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1053  
ID AAK41011 standard; DNA; 1075 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 15568.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1054  
ID AAK15288 standard; DNA; 1075 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 15279.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1055  
ID ABS40603 standard; DNA; 1075 BP.  
DE Human liver single exon probe, SEQ ID No 15593.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1056  
ID AAI07466 standard; DNA; 1075 BP.  
DE Probe #7457 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1057  
ID ABS14983 standard; DNA; 1075 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID No 14974.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1058  
ID ADO00111 standard; cDNA; 1113 BP.  
DE Novel human cDNA sequence #926.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Percent Similarity: 41.5%  
Best Local Similarity: 22.1%  
Query Match: 58  
Indels: 47  
RESULT 1059  
ID ADN98542 standard; cDNA; 1113 BP.  
DE Novel human cDNA sequence #142.  
PN WO2004038003-A2.  
PD 06-MAY-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

Percent Similarity: 41.5%  
Best Local Similarity: 22.1%  
Query Match: 58  
Indels: 47  
RESULT 1060  
ID AAI12593 standard; DNA; 1403 BP.  
DE Probe #2526 for gene expression analysis in human cervical cell sample.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1061  
ID ABA54290 standard; DNA; 1403 BP.  
DE Human foetal liver single exon nucleic acid probe #2595.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1062  
ID AAI33941 standard; DNA; 1403 BP.  
DE Probe #2627 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1063  
ID ABA43834 standard; DNA; 1403 BP.  
DE Human breast cell single exon nucleic acid probe #2529.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1064  
ID ABA24047 standard; DNA; 1403 BP.  
DE Probe #2513 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1065  
ID AAK28010 standard; DNA; 1403 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 2567.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1066  
ID AAK02574 standard; DNA; 1403 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 2565.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3  
RESULT 1067  
ID ABS27605 standard; DNA; 1403 BP.  
DE Human liver single exon probe, SEQ ID No 2595.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2%  
Best Local Similarity: 24  
Query Match: 69  
Indels: 3

Best Local Similarity: 25.6% Mismatches: 69  
Query Match: 5.6% Indels: 3  
RESULT 1068  
ID AAI02498 standard; DNA; 1403 BP.  
DE Probe #2489 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2% Conservative: 24  
Best Local Similarity: 25.6% Mismatches: 69  
Query Match: 5.6% Indels: 3  
RESULT 1069  
ID ABS02482 standard; DNA; 1403 BP.  
DE Human genome-derived single exon probe from lung SEQ ID No 2473.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 44.2% Conservative: 24  
Best Local Similarity: 25.6% Mismatches: 69  
Query Match: 5.6% Indels: 3  
RESULT 1070  
ID ADA70624 standard; DNA; 1755 BP.  
DE Rice gene, SEQ ID 3947.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 44.1% Conservative: 28  
Best Local Similarity: 29.3% Mismatches: 81  
Query Match: 5.6% Indels: 24  
RESULT 1071  
ID ADJ39721 standard; cDNA; 1755 BP.  
DE Plant cDNA #721.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 44.1% Conservative: 28  
Best Local Similarity: 29.3% Mismatches: 81  
Query Match: 5.6% Indels: 24  
RESULT 1072  
ID ADC30239 standard; cDNA; 2139 BP.  
DE Human novel cDNA sequence, SEQ ID NO:321.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 36.1% Conservative: 53  
Best Local Similarity: 23.2% Mismatches: 127  
Query Match: 5.6% Indels: 140  
RESULT 1073  
ID AAH98444 standard; cDNA; 2283 BP.  
DE Yeast EST-derived coding sequence SEQ ID NO: 301.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.7% Conservative: 34  
Best Local Similarity: 26.0% Mismatches: 141  
Query Match: 5.6% Indels: 43  
RESULT 1074  
ID ABK55571 standard; cDNA; 2474 BP.  
DE Human cDNA encoding NOV5f.  
PN WO200216600-A2.  
PD 28-FEB-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 38.2% Conservative: 81

Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1075  
ID ADH71753 standard; DNA; 2474 BP.  
DE Human gene of the invention NOV28g SEQ ID NO:649.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1076  
ID ADD93417 standard; cDNA; 2856 BP.  
DE Human lipid-associated molecule LIPAM-5 polynucleotide.  
PN WO2003083081-A2.  
PD 09-OCT-2003.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1077  
ID ADI27140 standard; DNA; 2892 BP.  
DE Human LRP binding family protein DNA #16.  
PN WO2003106657-A2.  
PD 24-DEC-2003.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1078  
ID ABN68049 standard; DNA; 2910 BP.  
DE Streptococcus polynucleotide SEQ ID NO 4011.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 37.9% Conservative: 60  
Best Local Similarity: 22.6% Mismatches: 151  
Query Match: 5.6% Indels: 91  
RESULT 1079  
ID ABK55569 standard; cDNA; 3039 BP.  
DE Human cDNA encoding NOV5d.  
PN WO200216600-A2.  
PD 28-FEB-2002.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1080  
ID ADH71749 standard; DNA; 3039 BP.  
DE Human gene of the invention NOV28e SEQ ID NO:645.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1081  
ID ABL15152 standard; cDNA; 3090 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 39938.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 37.1% Conservative: 27  
Best Local Similarity: 27.3% Mismatches: 117  
Query Match: 5.6% Indels: 57  
RESULT 1082  
ID ADN00734 standard; DNA; 3322 BP.  
DE Human LDLR coding sequence, SEQ ID 7.  
PN WO2004024881-A2.  
PD 25-MAR-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 38.2% Conservative: 81





Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1099  
ID ABL28909 standard; DNA; 4443 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38200.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 38.0% Conservative: 49  
Best Local Similarity: 24.7% Mismatches: 129  
Query Match: 5.6% Indels: 100  
RESULT 1100  
ID ABL66481 standard; DNA; 4468 BP.  
DE Lung cancer related gene sequence SEQ ID NO:4818.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1101  
ID ADN00732 standard; DNA; 4468 BP.  
DE Human LDLR coding sequence, SEQ ID 5.  
PN WO2004024881-A2.  
PD 25-MAR-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1102  
ID AEC82956 standard; cDNA; 4468 BP.  
DE Breast cancer associated cDNA SEQ ID NO 524.  
PN WO2005083429-A2.  
PD 09-SEP-2005.  
PA (VERI-) VERIDEX LLC.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1103  
ID ADH71763 standard; DNA; 4607 BP.  
DE Human gene of the invention NOV281 SEQ ID NO:659.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1104  
ID ADN00728 standard; DNA; 4607 BP.  
DE Human LDLR coding sequence, SEQ ID 1.  
PN WO2004024881-A2.  
PD 25-MAR-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1105  
ID ADO19503 standard; cDNA; 4607 BP.  
DE Human PRO polynucleotide #217.  
PN WO2004043361-A2.  
PD 27-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1106  
ID ADY15957 standard; DNA; 4607 BP.  
DE DNA encoding a PRO polypeptide, SEQ ID NO 1763.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158

Query Match: 5.6% Indels: 117  
RESULT 1107  
ID AEG59841 standard; cDNA; 4607 BP.  
DE Human breast cancer marker gene, SEQ ID NO:146.  
PN WO2006015312-A2.  
PD 09-FEB-2006.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Percent Similarity: 38.2% Conservative: 81  
Best Local Similarity: 20.0% Mismatches: 158  
Query Match: 5.6% Indels: 117  
RESULT 1108  
ID ABL34357 standard; DNA; 5660 BP.  
DE Human immune system associated gene SEQ ID NO: 2330.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 39.7% Conservative: 43  
Best Local Similarity: 24.5% Mismatches: 102  
Query Match: 5.6% Indels: 68  
RESULT 1109  
ID ABL02900 standard; cDNA; 6007 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3182.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.2% Conservative: 47  
Best Local Similarity: 22.6% Mismatches: 149  
Query Match: 5.6% Indels: 121  
RESULT 1110  
ID ADM10522 standard; DNA; 17220 BP.  
DE Colon proliferative disorder associated human DNA fragment, SEQ ID 327.  
PN US2004265833-A1.  
PD 30-DEC-2004.  
PA (LOFT/) LOFTON-DAY C.  
PA (SLED/) SLEDZIEWSKI A.  
PA (THOM/) THOMAS J.  
PA (DAYR/) DAY R W.  
PA (TONN/) TONNES-PRIDDY L.  
PA (CARD/) CARDON K.  
Percent Similarity: 35.5% Conservative: 41  
Best Local Similarity: 23.8% Mismatches: 136  
Query Match: 5.6% Indels: 92  
RESULT 1111  
ID ABS79084 standard; DNA; 48012 BP.  
DE E. coli CFT073 genomic sequence #251.  
PN WO200259320-A2.  
PD 01-AUG-2002.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
Percent Similarity: 35.6% Conservative: 69  
Best Local Similarity: 22.0% Mismatches: 143  
Query Match: 5.6% Indels: 188  
RESULT 1112  
ID ADH80651 standard; DNA; 48012 BP.  
DE Escherichia coli CFT073 genome contig #251.  
PN US2003165870-A1.  
PD 04-SEP-2003.  
PA (BLAT/) BLATTNER F R.  
PA (WELC/) WELCH R A.  
PA (BURL/) BURLAND V D.  
Percent Similarity: 35.6% Conservative: 69  
Best Local Similarity: 22.0% Mismatches: 143  
Query Match: 5.6% Indels: 188  
RESULT 1113  
Percent Similarity: 37.9% Conservative: 60  
Best Local Similarity: 22.6% Mismatches: 151  
Query Match: 5.6% Indels: 91  
RESULT 1114  
ID ABD32653 standard; DNA; 117750 BP.  
DE Human cancer-associated genomic DNA HD13-060.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.

Percent Similarity: 35.2%      Conservative: 34  
Best Local Similarity: 25.1%      Mismatches: 136  
Query Match: 5.6%      Indels: 84  
RESULT 1115  
ID ABL22175 standard; DNA; 1110 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 17998.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.8%      Conservative: 40  
Best Local Similarity: 23.8%      Mismatches: 141  
Query Match: 5.6%      Indels: 98  
RESULT 1116  
ID ADS56260 standard; cDNA; 1398 BP.  
DE Bacterial polynucleotide #8247.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 36.8%      Conservative: 19  
Best Local Similarity: 27.8%      Mismatches: 85  
Query Match: 5.6%      Indels: 49  
RESULT 1117  
ID AAQ29276 standard; cDNA; 1452 BP.  
DE Encodes transmembrane form of H23-ETA antigen.  
PN WO9207000-A1.  
PD 30-APR-1992.  
PA (TRGE ) TRANSGENE SA.  
Percent Similarity: 35.3%      Conservative: 26  
Best Local Similarity: 26.2%      Mismatches: 107  
Query Match: 5.6%      Indels: 78  
RESULT 1118  
ID AAD30794 standard; DNA; 1614 BP.  
DE Hansenula polymorpha GPI cell wall anchor protein gene, HpGas1.  
PN WO200212509-A1.  
PD 14-FEB-2002.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
Percent Similarity: 36.4%      Conservative: 62  
Best Local Similarity: 23.1%      Mismatches: 173  
Query Match: 5.6%      Indels: 127  
RESULT 1119  
ID AAQ29277 standard; DNA; 1709 BP.  
DE Encodes secreted form of H23-ETA antigen.  
PN WO9207000-A1.  
PD 30-APR-1992.  
PA (TRGE ) TRANSGENE SA.  
Percent Similarity: 35.3%      Conservative: 29  
Best Local Similarity: 25.2%      Mismatches: 107  
Query Match: 5.6%      Indels: 78  
RESULT 1120  
ID ABK64853 standard; DNA; 1830 BP.  
DE Human benign prostatic hyperplasia gene #748.  
PN WO200212440-A2.  
PD 14-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
PA (NISB ) JAPAN TOBACCO INC.  
Percent Similarity: 38.2%      Conservative: 47  
Best Local Similarity: 24.8%      Mismatches: 133  
Query Match: 5.6%      Indels: 86  
RESULT 1121  
ID ACL28401 standard; cDNA; 2469 BP.  
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:2357.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 33.9%      Conservative: 43  
Best Local Similarity: 21.7%      Mismatches: 114  
Query Match: 5.6%      Indels: 119  
RESULT 1122  
ID AAF30055 standard; cDNA; 2482 BP.

DE Human cDNA encoding PRO256.  
PN WO200105972-A1.  
PD 25-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1123  
ID AAD16721 standard; cDNA; 2482 BP.  
DE Human hepatocyte growth factor activator inhibitor, PRO256 cDNA.  
PN WO200159100-A2.  
PD 16-AUG-2001.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1124  
ID ABK40259 standard; cDNA; 2482 BP.  
DE cDNA encoding human PRO256 polypeptide.  
PN WO200153486-A1.  
PD 26-JUL-2001.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1125  
ID ABL88092 standard; cDNA; 2482 BP.  
DE Human PRO256 cDNA sequence SEQ ID NO:41.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1126  
ID ABK69965 standard; DNA; 2482 BP.  
DE cDNA encoding human Pro peptide #5.  
PN WO200224888-A2.  
PD 28-MAR-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1127  
ID ABL95581 standard; cDNA; 2482 BP.  
DE Human angiogenesis related cDNA PRO256 SEQ ID NO: 41.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1128  
ID ADA01277 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003068779-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.





Query Match: 5.6% Indels: 173  
RESULT 1145  
ID ADD11290 standard; cDNA; 2482 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #21.  
PN US2003105013-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1146  
ID ADD37083 standard; cDNA; 2482 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #21.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1147  
ID ADE04873 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003068778-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1148  
ID ADE11179 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003073191-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1149  
ID ADD88110 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003082733-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1150  
ID ADD95405 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003064473-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1151  
ID ADE06335 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003073195-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1152  
ID ADE38110 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003119120-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173

RESULT 1153  
ID ADD88226 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003073189-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1154  
ID ADD90807 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003073188-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1155  
ID ADF99362 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003078401-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1156  
ID ADG06455 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003077742-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1157  
ID ADG05406 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003077741-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1158  
ID ADG82407 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003077744-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1159  
ID ADJ37292 standard; cDNA; 2482 BP.  
DE Human tumour therapy associated PRO256 cDNA.  
PN US2003211096-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1160  
ID ADE51660 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003104560-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
RESULT 1161

ID ADE51776 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003104561-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1162  
ID ADE37634 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003104564-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1163  
ID ADE37518 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003104565-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1164  
ID ADD95289 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003138901-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1165  
ID ADE37989 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003104566-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1166  
ID ADE76078 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003124665-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1167  
ID ADE39401 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003119117-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1168  
ID ADE04205 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003096364-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1169  
ID ADE39802 standard; cDNA; 2482 BP.

DE Human PRO polynucleotide #5.  
PN US2003138896-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1170  
ID ADE19667 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003138903-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1171  
ID ADE77245 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003124666-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1172  
ID ADE65353 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003119116-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1173  
ID ADE75962 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003124663-A1.  
PD 03-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1174  
ID ADE37873 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003119119-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1175  
ID ADE64483 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003119114-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1176  
ID ADE41291 standard; cDNA; 2482 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #21.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%      Conservative: 54  
Best Local Similarity: 20.8%      Mismatches: 143  
Query Match: 5.6%      Indels: 173  
RESULT 1177  
ID ADE38818 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.

PN	US2003096363-A1.				
PD	22-MAY-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	32.3%			Conservative:	54
Best Local Similarity:	20.8%			Mismatches:	143
Query Match:	5.6%			Indels:	173
RESULT 1178					
ID	ADE51892 standard; cDNA; 2482 BP.				
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO256.				
PN	US2003104562-A1.				
PD	05-JUN-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	32.3%			Conservative:	54
Best Local Similarity:	20.8%			Mismatches:	143
Query Match:	5.6%			Indels:	173
RESULT 1179					
ID	ADD90923 standard; cDNA; 2482 BP.				
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO256.				
PN	US2003138902-A1.				
PD	24-JUL-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	32.3%			Conservative:	54
Best Local Similarity:	20.8%			Mismatches:	143
Query Match:	5.6%			Indels:	173
RESULT 1180					
ID	ADE38702 standard; cDNA; 2482 BP.				
DE	Human PRO polynucleotide #5.				
PN	US2003108996-A1.				
PD	12-JUN-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	32.3%			Conservative:	54
Best Local Similarity:	20.8%			Mismatches:	143
Query Match:	5.6%			Indels:	173
RESULT 1181					
ID	ADE37402 standard; cDNA; 2482 BP.				
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO256.				
PN	US2003104563-A1.				
PD	05-JUN-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	32.3%			Conservative:	54
Best Local Similarity:	20.8%			Mismatches:	143
Query Match:	5.6%			Indels:	173
RESULT 1182					
ID	ADE06219 standard; cDNA; 2482 BP.				
DE	Human PRO polynucleotide #5.				
PN	US2003138898-A1.				
PD	24-JUL-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	32.3%			Conservative:	54
Best Local Similarity:	20.8%			Mismatches:	143
Query Match:	5.6%			Indels:	173
RESULT 1183					
ID	ADD90078 standard; cDNA; 2482 BP.				
DE	Human cDNA encoding secreted/transmembrane polypeptide PRO256.				
PN	US2003138904-A1.				
PD	24-JUL-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	32.3%			Conservative:	54
Best Local Similarity:	20.8%			Mismatches:	143
Query Match:	5.6%			Indels:	173
RESULT 1184					
ID	ADE38586 standard; cDNA; 2482 BP.				
DE	Human PRO polynucleotide #5.				
PN	US2003119086-A1.				
PD	26-JUN-2003.				
PA	(GETH ) GENENTECH INC.				
Percent Similarity:	32.3%			Conservative:	54
Best Local Similarity:	20.8%			Mismatches:	143
Query Match:	5.6%			Indels:	173
RESULT 1185					
ID	ADE39517 standard; cDNA; 2482 BP.				
DE	Human PRO polynucleotide #5.				
PN	US2003119118-A1.				

PD 26-JUN-2003.	PA (GETH ) GENENTECH INC.	Conservative: 54
Percent Similarity: 32.3%		Mismatches: 143
Best Local Similarity: 20.8%		Indels: 173
Query Match: 5.6%		
RESULT 1186		
ID ADD89122 standard; cDNA; 2482 BP.		
DE Human PRO polynucleotide #5.		
PN US2003138897-A1.		
PD 24-JUL-2003.		
PA (GETH ) GENENTECH INC.		
Percent Similarity: 32.3%	Conservative: 54	
Best Local Similarity: 20.8%	Mismatches: 143	
Query Match: 5.6%	Indels: 173	
RESULT 1187		
ID ADD88889 standard; cDNA; 2482 BP.		
DE Human PRO polynucleotide #5.		
PN US2003138899-A1.		
PD 24-JUL-2003.		
PA (GETH ) GENENTECH INC.		
Percent Similarity: 32.3%	Conservative: 54	
Best Local Similarity: 20.8%	Mismatches: 143	
Query Match: 5.6%	Indels: 173	
RESULT 1188		
ID ADE19783 standard; cDNA; 2482 BP.		
DE Human PRO polynucleotide #5.		
PN US2003138900-A1.		
PD 24-JUL-2003.		
PA (GETH ) GENENTECH INC.		
Percent Similarity: 32.3%	Conservative: 54	
Best Local Similarity: 20.8%	Mismatches: 143	
Query Match: 5.6%	Indels: 173	
RESULT 1189		
ID ADE77361 standard; cDNA; 2482 BP.		
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.		
PN US2003124667-A1.		
PD 03-JUL-2003.		
PA (GETH ) GENENTECH INC.		
Percent Similarity: 32.3%	Conservative: 54	
Best Local Similarity: 20.8%	Mismatches: 143	
Query Match: 5.6%	Indels: 173	
RESULT 1190		
ID ADE5237 standard; cDNA; 2482 BP.		
DE Human PRO polynucleotide #5.		
PN US2003119113-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Percent Similarity: 32.3%	Conservative: 54	
Best Local Similarity: 20.8%	Mismatches: 143	
Query Match: 5.6%	Indels: 173	
RESULT 1191		
ID ADE3285 standard; cDNA; 2482 BP.		
DE Human PRO polynucleotide #5.		
PN US2003119115-A1.		
PD 26-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Percent Similarity: 32.3%	Conservative: 54	
Best Local Similarity: 20.8%	Mismatches: 143	
Query Match: 5.6%	Indels: 173	
RESULT 1192		
ID ADE38470 standard; cDNA; 2482 BP.		
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.		
PN US2003104559-A1.		
PD 05-JUN-2003.		
PA (GETH ) GENENTECH INC.		
Percent Similarity: 32.3%	Conservative: 54	
Best Local Similarity: 20.8%	Mismatches: 143	
Query Match: 5.6%	Indels: 173	
RESULT 1193		
ID ADG11023 standard; cDNA; 2482 BP.		
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.		
PN US2003170809-A1.		
PD 11-SEP-2003.		
PA (GETH ) GENENTECH INC.		
Percent Similarity: 32.3%	Conservative: 54	
Best Local Similarity: 20.8%	Mismatches: 143	
Query Match: 5.6%	Indels: 173	





Best Local Similarity: 20.8% Mismatches: 143  
Query Match: Indels: 173  
RESULT 1210  
ID ADH49412 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119127-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1211  
ID ADH51876 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119125-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1212  
ID ADH49731 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119128-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1213  
ID ADH52332 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119130-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1214  
ID ADH43474 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #21.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1215  
ID ADH52448 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119129-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1216  
ID ADH58445 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119121-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1217  
ID ADH51760 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119126-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173

Query Match: 5.6% Indels: 173  
RESULT 1218  
ID ADH58321 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119122-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1219  
ID ADI13518 standard; cDNA; 2482 BP.  
DE Novel human secreted and transmembrane protein PRO256 cDNA.  
PN US2003119131-A1.  
PD 26-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1220  
ID ADK00774 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #5.  
PN US2003186373-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1221  
ID ADL08515 standard; cDNA; 2482 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO256.  
PN US2003186372-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1222  
ID ADK82819 standard; cDNA; 2482 BP.  
DE Human PRO polynucleotide #21.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1223  
ID AEF57691 standard; cDNA; 2482 BP.  
DE Human secreted protein PRO256/UNQ223, cDNA.  
PN WO2005112619-A2.  
PD 01-DEC-2005.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1224  
ID AEG75175 standard; cDNA; 2482 BP.  
DE Human PRO256 cDNA clone, DNA35880-1160.  
PN US2006073579-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173  
Query Match:  
RESULT 1225  
ID AEG74390 standard; cDNA; 2482 BP.  
DE Human PRO256 encoding cDNA SEQ ID NO:9.  
PN US2006073553-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Conservative: 54  
Mismatches: 143  
Indels: 173

Query Match: 5.6% Indels: 173  
RESULT 1226  
ID AEG73262 standard; cDNA; 2482 BP.  
DE Human PRO256 cDNA clone, DNA35880-1160.  
PN US2006073551-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Indels: 173  
Conservative: 54  
Mismatch: 143  
Indel: 173  
RESULT 1227  
ID AEG74506 standard; cDNA; 2482 BP.  
DE Human PRO256 encoding cDNA SEQ ID NO:9.  
PN US2006073552-A1.  
PD 06-APR-2006.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Indels: 173  
Conservative: 54  
Mismatch: 143  
Indel: 173  
RESULT 1228  
ID ADT19106 standard; cDNA; 2552 BP.  
DE Plant cDNA, Seq ID 4432.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Percent Similarity: 42.2%  
Best Local Similarity: 29.5%  
Query Match: 5.6%  
Indels: 28  
Conservative: 22  
Mismatch: 72  
Indel: 28  
RESULT 1229  
ID ADP81020 standard; DNA; 2679 BP.  
DE Human ovarian specific gene, SEQ ID NO 54.  
PN WO2004053079-A2.  
PD 24-JUN-2004.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Indels: 173  
Conservative: 54  
Mismatch: 143  
Indel: 173  
RESULT 1230  
ID AAT02504 standard; DNA; 2717 BP.  
DE Pectin-lyase-I gene expression system.  
PN EP683228-A2.  
PD 22-NOV-1995.  
PA (CIBA ) CIBA GEIGY AG.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERWALTUNGS GMBH.  
Percent Similarity: 34.0%  
Best Local Similarity: 22.4%  
Query Match: 5.6%  
Indels: 154  
Conservative: 56  
Mismatch: 165  
Indel: 154  
RESULT 1231  
ID ADZ03663 standard; cDNA; 2946 BP.  
DE PRG4-Lub:1 cDNA construct.  
PN WO2005016130-A2.  
PD 24-FEB-2005.  
PA (AMHP ) WYETH.  
Percent Similarity: 38.7%  
Best Local Similarity: 24.0%  
Query Match: 5.6%  
Indels: 96  
Conservative: 55  
Mismatch: 135  
Indel: 96  
RESULT 1232  
ID ACL28243 standard; cDNA; 2958 BP.  
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:2199.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 37.0%  
Best Local Similarity: 22.0%  
Query Match: 5.6%  
Indels: 118  
Conservative: 65  
Mismatch: 155  
Indel: 118  
RESULT 1233  
ID ABD32539 standard; cDNA; 2969 BP.  
DE Mouse cancer-associated cDNA MR7-023.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Percent Similarity: 42.1%  
Conservative: 29

Best Local Similarity: 27.2%  
Query Match: 5.6%  
Indels: 85  
Mismatch: 28  
RESULT 1234  
ID ADP81021 standard; DNA; 3125 BP.  
DE Human ovarian specific gene, SEQ ID NO 55.  
PN WO2004053079-A2.  
PD 24-JUN-2004.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 32.3%  
Best Local Similarity: 20.8%  
Query Match: 5.6%  
Indels: 173  
Conservative: 54  
Mismatch: 143  
Indel: 173  
RESULT 1235  
ID ADS48485 standard; cDNA; 3309 BP.  
DE Bacterial polynucleotide #3228.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 38.9%  
Best Local Similarity: 23.2%  
Query Match: 5.6%  
Indels: 96  
Conservative: 61  
Mismatch: 142  
Indel: 96  
RESULT 1236  
ID AEF99566 standard; cDNA; 3891 BP.  
DE C. botulinum BONT/A modified open reading frame, SEQ ID NO:53.  
PN WO2006017749-A2.  
PD 16-FEB-2006.  
PA (ALLR ) ALLERGAN INC.  
Percent Similarity: 35.6%  
Best Local Similarity: 21.6%  
Query Match: 5.6%  
Indels: 109  
Conservative: 55  
Mismatch: 144  
Indel: 109  
RESULT 1237  
ID ABL33102 standard; DNA; 7758 BP.  
DE Human immune system associated gene SEQ ID NO: 1075.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Percent Similarity: 44.6%  
Best Local Similarity: 33.1%  
Query Match: 5.6%  
Indels: 18  
Conservative: 16  
Mismatch: 59  
Indel: 18  
RESULT 1238  
ID ADZ03662 standard; DNA; 8049 BP.  
DE Vector Ptmcd2 with PRG4-Lub:1 cDNA construct.  
PN WO2005016130-A2.  
PD 24-FEB-2005.  
PA (AMHP ) WYETH.  
Percent Similarity: 38.7%  
Best Local Similarity: 24.0%  
Query Match: 5.6%  
Indels: 96  
Conservative: 55  
Mismatch: 135  
Indel: 96  
RESULT 1239  
ID AAK72613 standard; DNA; 8298 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27425.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 42.1%  
Best Local Similarity: 30.8%  
Query Match: 5.6%  
Indels: 6  
Conservative: 15  
Mismatch: 71  
Indel: 6  
RESULT 1240  
ID AAD08215 standard; DNA; 114793 BP.  
DE Human genome from BAC clone, hbml68.  
PN WO200142434-A1.  
PD 14-JUN-2001.  
PA (MERI ) MERCK & CO INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 26.6%  
Query Match: 5.6%  
Indels: 40  
Conservative: 25  
Mismatch: 78  
Indel: 40  
RESULT 1241  
ID ADD17541 standard; DNA; 578 BP.  
DE DNA (SeqID 1609) that confers an altered visual phenotype in plants.  
PN WO2003020741-A1.

PD 13-MAR-2003.  
PA (DOWC ) DOW CHEM CO.  
Percent Similarity: 42.7%  
Best Local Similarity: 27.1%  
Query Match: 5.5%  
RESULT 1242  
ID ADK52960 standard; DNA; 578 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #343.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC ) DOW CHEM CO.  
Percent Similarity: 42.7%  
Best Local Similarity: 27.1%  
Query Match: 5.5%  
RESULT 1243  
ID ADX28417 standard; cDNA; 818 BP.  
DE Plant full length insert polynucleotide seqid 11237.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Percent Similarity: 39.9%  
Best Local Similarity: 27.3%  
Query Match: 5.5%  
RESULT 1244  
ID AEI30716 standard; DNA; 982 BP.  
DE Soybean polymorphic locus, SEQ ID 3350.  
PN US2006135758-A1.  
PD 22-JUN-2006.  
PA (WUKK/) WU K.  
Percent Similarity: 39.9%  
Best Local Similarity: 27.3%  
Query Match: 5.5%  
RESULT 1245  
ID AAF12769 standard; cDNA; 1042 BP.  
DE Aspergillus oryzae EST SEQ ID NO:5292.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
Percent Similarity: 36.8%  
Best Local Similarity: 23.5%  
Query Match: 5.5%  
RESULT 1246  
ID ADU56810 standard; cDNA; 1042 BP.  
DE Aspergillus oryzae strain A1560/strain AL-1 EST, SEQ ID NO:5292.  
PN US2004229367-A1.  
PD 18-NOV-2004.  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES INC AS.  
Percent Similarity: 36.8%  
Best Local Similarity: 23.5%  
Query Match: 5.5%  
RESULT 1247  
ID ADZ94813 standard; cDNA; 1042 BP.  
DE Aspergillus oryzae expressed sequence tag cDNA SEQ ID NO 5292.  
PN US6902887-B1.  
PD 07-JUN-2005.  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES AS.  
Percent Similarity: 36.8%  
Best Local Similarity: 23.5%  
Query Match: 5.5%  
RESULT 1248  
ID AEI58414 standard; cDNA; 1348 BP.  
DE Zea mays coding sequence, SEQ ID NO: 2881.  
PN US2006143729-A1.

PD 29-JUN-2006.  
PA (CERE-) CERES INC.  
Percent Similarity: 37.6%  
Best Local Similarity: 24.1%  
Query Match: 5.5%  
RESULT 1249  
ID ADT47341 standard; cDNA; 1428 BP.  
DE Bacterial polynucleotide #22092.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 39.7%  
Best Local Similarity: 25.5%  
Query Match: 5.5%  
RESULT 1250  
ID ABS67721 standard; cDNA; 1555 BP.  
DE DNA encoding primate LP282.  
PN WO200263009-A2.  
PD 15-AUG-2002.  
PA (ELIL ) LILLY & CO ELI.  
Percent Similarity: 35.3%  
Best Local Similarity: 22.1%  
Query Match: 5.5%  
RESULT 1251  
ID ADT46663 standard; cDNA; 1638 BP.  
DE Bacterial polynucleotide #21414.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Percent Similarity: 40.0%  
Best Local Similarity: 25.2%  
Query Match: 5.5%  
RESULT 1252  
ID ADK60090 standard; DNA; 1640 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #7473.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC ) DOW CHEM CO.  
PA (DOWC ) DOW AGROSCIENCES LLC.  
Percent Similarity: 37.1%  
Best Local Similarity: 21.3%  
Query Match: 5.5%  
RESULT 1253  
ID AAA64661 standard; cDNA; 2126 BP.  
DE cDNA encoding TBP associated factor (TAFII68).  
PN WO200050595-A2.  
PD 31-AUG-2000.  
PA (GOUT/) GOUT I.  
PA (RODN/) RODNIN N.  
PA (FILO/) FILOMENKO V.  
PA (MATS/) MATSUKA G.  
PA (SCAN/) SCANLAN M.  
PA (OLDL/) OLD L.  
PA (BILY/) BILYNSKY B.  
Percent Similarity: 42.6%  
Best Local Similarity: 23.4%  
Query Match: 5.5%  
RESULT 1254  
ID ADB62594 standard; cDNA; 2335 BP.  
DE Human cDNA encoding clone HLUNG20083480.  
PN EF1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 41.5%  
Conservative: 49

Best Local Similarity: 24.6% Mismatches: 111  
Query Match: 5.5% Indels: 59  
RESULT 1255  
ID AEA15398 standard; cDNA; 2352 BP.  
DE Human polynucleotide #95.  
PN WO2005047534-A2.  
PD 26-MAY-2005.  
PA (FARB ) BAYER HEALTHCARE AG.  
Percent Similarity: 36.6% Conservative: 49  
Best Local Similarity: 22.7% Mismatches: 146  
Query Match: 5.5% Indels: 78  
RESULT 1256  
ID AAI59413 standard; cDNA; 2421 BP.  
DE Human polynucleotide SEQ ID NO 1616.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 32.8% Conservative: 33  
Best Local Similarity: 24.2% Mismatches: 135  
Query Match: 5.5% Indels: 124  
RESULT 1257  
ID ACC59980 standard; cDNA; 2526 BP.  
DE Human PMM-22 encoding cDNA SEQ ID NO:53.  
PN WO2003025131-A2.  
PD 27-MAR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 35.3% Conservative: 58  
Best Local Similarity: 22.1% Mismatches: 174  
Query Match: 5.5% Indels: 111  
RESULT 1258  
ID AAT12337 standard; DNA; 3004 BP.  
DE A. cellulolyticus E1 endoglucanase gene.  
PN WO9602551-A1.  
PD 01-FEB-1996.  
PA (MIDE ) MIDWEST RES INST.  
Percent Similarity: 36.6% Conservative: 37  
Best Local Similarity: 23.8% Mismatches: 115  
Query Match: 5.5% Indels: 69  
RESULT 1259  
ID AAZ55924 standard; DNA; 3004 BP.  
DE Acidothermus cellulolyticus E1 endoglucanase gene.  
PN CA2226898-A1.  
PD 25-SEP-1999.  
PA (MIDE ) MIDWEST RES INST.  
Percent Similarity: 36.6% Conservative: 37  
Best Local Similarity: 23.8% Mismatches: 115  
Query Match: 5.5% Indels: 69  
RESULT 1260  
ID ABK86729 standard; cDNA; 3004 BP.  
DE A. cellulolyticus cellulase E1 beta-1,4-endoglucanase precursor cDNA, e1.  
PN WO200234926-A2.  
PD 02-MAY-2002.  
PA (UNMS ) UNIV MICHIGAN STATE.  
Percent Similarity: 36.6% Conservative: 37  
Best Local Similarity: 23.8% Mismatches: 115  
Query Match: 5.5% Indels: 69  
RESULT 1261  
ID ADU48443 standard; DNA; 3004 BP.  
DE Acidothermus cellulolyticus endoglucanase E1 DNA.  
PN US6818803-B1.  
PD 16-NOV-2004.  
PA (WISC ) WISCONSIN ALUMNI RES FOUND.  
Percent Similarity: 36.6% Conservative: 37  
Best Local Similarity: 23.8% Mismatches: 115  
Query Match: 5.5% Indels: 69  
RESULT 1262  
ID ABX63016 standard; cDNA; 3125 BP.  
DE Human cDNA #16 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND/) BANDMAN O.  
Percent Similarity: 41.5% Conservative: 49  
Best Local Similarity: 24.6% Mismatches: 111

Query Match: 5.5% Indels: 59  
RESULT 1263  
ID AAI61199 standard; cDNA; 3138 BP.  
DE Human polynucleotide SEQ ID NO 5188.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 32.8% Conservative: 33  
Best Local Similarity: 24.2% Mismatches: 135  
Query Match: 5.5% Indels: 124  
RESULT 1264  
ID AAQ22202 standard; DNA; 3306 BP.  
DE A. chrysogenum phosphoglycerate kinase.  
PN EP474273-A.  
PD 11-MAR-1992.  
PA (ASAH ) ASahi KASEI KOGYO KK.  
Percent Similarity: 38.2% Conservative: 52  
Best Local Similarity: 22.2% Mismatches: 113  
Query Match: 5.5% Indels: 89  
RESULT 1265  
ID AAQ23005 standard; DNA; 3306 BP.  
DE Phosphoglycerate kinase gene (incl. promoter).  
PN JP04058891-A.  
PD 25-FEB-1992.  
PA (ASAH ) ASahi CHEM IND CO LTD.  
Percent Similarity: 38.2% Conservative: 52  
Best Local Similarity: 22.2% Mismatches: 113  
Query Match: 5.5% Indels: 89  
RESULT 1266  
ID AAD51687 standard; cDNA; 3840 BP.  
DE Human nucleic acid associated protein (NAAP)-13 encoding cDNA.  
PN WO200299115-A2.  
PD 12-DEC-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 41.5% Conservative: 49  
Best Local Similarity: 24.6% Mismatches: 111  
Query Match: 5.5% Indels: 59  
RESULT 1267  
ID AEL55888 standard; cDNA; 3967 BP.  
DE Mouse MKIAA1930 coding sequence, SEQ ID NO: 349.  
PN US2006216722-A1.  
PD 28-SEP-2006.  
PA (BETS/) BETSHOLTZ C.  
PA (TRYG/) TRYGGVASON K.  
PA (TAKE/) TAKEMOTO M.  
PA (HELL/) HE L.  
PA (PATR/) PATRAKKAS J.  
Percent Similarity: 35.6% Conservative: 59  
Best Local Similarity: 20.9% Mismatches: 138  
Query Match: 5.5% Indels: 122  
RESULT 1268  
ID ADE71196 standard; DNA; 4815 BP.  
DE Novel human protein coding sequence #12.  
PN JP2002345493-A.  
PD 03-DEC-2002.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
Percent Similarity: 41.2% Conservative: 48  
Best Local Similarity: 24.6% Mismatches: 112  
Query Match: 5.5% Indels: 59  
RESULT 1269  
ID ADV97761 standard; cDNA; 6432 BP.  
DE cDNA sequence encoding a murine protein kinase Seq 81.  
PN WO2005000200-A2.  
PD 06-JAN-2005.  
PA (SUGE-) SUGEN INC.  
Percent Similarity: 33.9% Conservative: 31  
Best Local Similarity: 23.9% Mismatches: 126  
Query Match: 5.5% Indels: 80  
RESULT 1270  
ID AAS54978 standard; DNA; 7035 BP.  
DE Staphylococcus aureus DNA for cellular proliferation protein #1290.  
PN WO200170955-A2.



PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.1%  
 Best Local Similarity: 20.6%  
 Query Match: 5.5%  
 RESULT 1271  
 ID AEH96869 standard; cDNA; 7035 BP.  
 DE Human cancer associated cDNA SEQ ID NO 162.  
 PN WO2006033664-A1.  
 PD 30-MAR-2006.  
 PA (AVAL-) AVALON PHARM.  
 Percent Similarity: 35.8%  
 Best Local Similarity: 22.4%  
 Query Match: 5.5%  
 RESULT 1272  
 ID AED50861 standard; DNA; 11040 BP.  
 DE S. cellulosum strain So ce 307 jerangolid biosynthetic cluster jerB gene.  
 PN US2005233369-A1.  
 PD 20-OCT-2005.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Percent Similarity: 32.3%  
 Best Local Similarity: 21.2%  
 Query Match: 5.5%  
 RESULT 1273  
 ID AEH56305 standard; DNA; 11517 BP.  
 DE Enterobacter cloacae protein coding sequence - SEQ ID 4475.  
 PN US7041814-B1.  
 PD 09-MAY-2006.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.8%  
 Best Local Similarity: 24.1%  
 Query Match: 5.5%  
 RESULT 1274  
 ID ABL03868 standard; cDNA; 31562 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6086.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 30.8%  
 Best Local Similarity: 21.8%  
 Query Match: 5.5%  
 RESULT 1275  
 ID AED50859 standard; DNA; 67323 BP.  
 DE S. cellulosum strain So ce 307 jerangolid biosynthetic gene cluster.  
 PN US2005233369-A1.  
 PD 20-OCT-2005.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Percent Similarity: 32.3%  
 Best Local Similarity: 21.2%  
 Query Match: 5.5%  
 RESULT 1276  
 ID ABV75557 standard; DNA; 75236 BP.  
 DE Saccharopolyspora butenyl-spinosyn biosynthetic gene cluster 1.  
 PN WO200279477-A2.  
 PD 10-OCT-2002.  
 PA (DOWC ) DOW AGROSCIENCES LLC.  
 Percent Similarity: 37.4%  
 Best Local Similarity: 21.2%  
 Query Match: 5.5%  
 RESULT 1277  
 Percent Similarity: 36.0%  
 Best Local Similarity: 24.5%  
 Query Match: 5.5%  
 RESULT 1278  
 Percent Similarity: 33.8%  
 Best Local Similarity: 19.5%  
 Query Match: 5.5%  
 RESULT 1279  
 ID AAI24837 standard; DNA; 531 BP.  
 DE Probe #14770 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.

Percent Similarity: 45.4%  
 Best Local Similarity: 27.0%  
 Query Match: 5.5%  
 RESULT 1280  
 ID ABA70232 standard; DNA; 531 BP.  
 DE Human foetal liver single exon nucleic acid probe #18537.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 45.4%  
 Best Local Similarity: 27.0%  
 Query Match: 5.5%  
 RESULT 1281  
 ID AAI50362 standard; DNA; 531 BP.  
 DE Probe #19048 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 45.4%  
 Best Local Similarity: 27.0%  
 Query Match: 5.5%  
 RESULT 1282  
 ID ABA36961 standard; DNA; 531 BP.  
 DE Probe #15427 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 45.4%  
 Best Local Similarity: 27.0%  
 Query Match: 5.5%  
 RESULT 1283  
 ID AAK44363 standard; DNA; 531 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 18920.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 45.4%  
 Best Local Similarity: 27.0%  
 Query Match: 5.5%  
 RESULT 1284  
 ID AAK18458 standard; DNA; 531 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 18449.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 45.4%  
 Best Local Similarity: 27.0%  
 Query Match: 5.5%  
 RESULT 1285  
 ID ABS44020 standard; DNA; 531 BP.  
 DE Human liver single exon probe, SEQ ID No 19010.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 45.4%  
 Best Local Similarity: 27.0%  
 Query Match: 5.5%  
 RESULT 1286  
 ID ABS18599 standard; DNA; 531 BP.  
 DE Human genome-derived single exon probe ORF from lung SEQ ID No 18590.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Percent Similarity: 45.4%  
 Best Local Similarity: 27.0%  
 Query Match: 5.5%  
 RESULT 1287  
 ID AAQ12218 standard; DNA; 836 BP.  
 DE SMUC-41 intestinal mucin cDNA clone.  
 PN WO9108217-A.  
 PD 13-JUN-1991.  
 PA (REGC ) UNIV CALIFORNIA.  
 Percent Similarity: 35.2%  
 Conservative: 30  
 Mismatches: 77  
 Indels: 13

Best Local Similarity: 23.3% Mismatches: 108  
Query Match: 5.5% Indels: 87  
RESULT 1288  
ID ADX15294 standard; cDNA; 846 BP.  
DE Plant full length insert polynucleotide seqid 9869.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Percent Similarity: 41.1% Conservative: 28  
Best Local Similarity: 25.9% Mismatches: 72  
Query Match: 5.5% Indels: 37  
RESULT 1289  
ID ADX14720 standard; cDNA; 862 BP.  
DE Plant full length insert polynucleotide seqid 9295.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Percent Similarity: 41.1% Conservative: 28  
Best Local Similarity: 25.9% Mismatches: 72  
Query Match: 5.5% Indels: 37  
RESULT 1290  
ID ADT17667 standard; cDNA; 864 BP.  
DE Plant cDNA, Seq ID 2993.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Percent Similarity: 40.3% Conservative: 30  
Best Local Similarity: 26.7% Mismatches: 78  
Query Match: 5.5% Indels: 55  
RESULT 1291  
ID AEI30715 standard; DNA; 930 BP.  
DE Soybean polymorphic locus, SEQ ID 3349.  
PN US2006135758-A1.  
PD 22-JUN-2006.  
PA (WUKK/) WU K.  
Percent Similarity: 41.1% Conservative: 28  
Best Local Similarity: 25.9% Mismatches: 72  
Query Match: 5.5% Indels: 37  
RESULT 1292  
ID AAF12775 standard; cDNA; 1347 BP.  
DE Aspergillus oryzae EST SEQ ID NO:5298.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.  
Percent Similarity: 36.0% Conservative: 23  
Best Local Similarity: 24.6% Mismatches: 66  
Query Match: 5.5% Indels: 64  
RESULT 1293  
ID ADU56816 standard; cDNA; 1347 BP.  
DE Aspergillus oryzae strain strain A1560/strain AL-1 EST, SEQ ID NO:5298.  
PN US2004229367-A1.  
PD 18-NOV-2004.  
PA (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES INC AS.  
Percent Similarity: 36.0% Conservative: 23  
Best Local Similarity: 24.6% Mismatches: 66  
Query Match: 5.5% Indels: 64  
RESULT 1294  
ID ADZ94819 standard; cDNA; 1347 BP.  
DE Aspergillus oryzae expressed sequence tag cDNA SEQ ID NO 5298.  
PN US6902887-B1.  
PD 07-JUN-2005.

PA (NOVO ) NOVOZYMES BIOTECH INC.  
PA (NOVO ) NOVOZYMES AS.  
Percent Similarity: 36.0% Conservative: 23  
Best Local Similarity: 24.6% Mismatches: 66  
Query Match: 5.5% Indels: 64  
RESULT 1295  
ID ADA69781 standard; DNA; 1650 BP.  
DE Rice gene, SEQ ID 3104.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 36.6% Conservative: 48  
Best Local Similarity: 24.0% Mismatches: 152  
Query Match: 5.5% Indels: 92  
RESULT 1296  
ID ADI57686 standard; cDNA; 1712 BP.  
DE Human breast specific nucleic acid (BSNA) #57.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 30.2% Conservative: 40  
Best Local Similarity: 21.3% Mismatches: 134  
Query Match: 5.5% Indels: 178  
RESULT 1297  
ID ADI57673 standard; cDNA; 1755 BP.  
DE Human breast specific nucleic acid (BSNA) #44.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 32.6% Conservative: 37  
Best Local Similarity: 22.6% Mismatches: 124  
Query Match: 5.5% Indels: 124  
RESULT 1298  
ID ADI57672 standard; cDNA; 1918 BP.  
DE Human breast specific nucleic acid (BSNA) #43.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 32.6% Conservative: 37  
Best Local Similarity: 22.6% Mismatches: 124  
Query Match: 5.5% Indels: 124  
RESULT 1299  
ID ABL04769 standard; cDNA; 2241 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 8789.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 37.6% Conservative: 39  
Best Local Similarity: 24.0% Mismatches: 131  
Query Match: 5.5% Indels: 48  
RESULT 1300  
ID ACH89449 standard; DNA; 2329 BP.  
DE Human genome derived single exon probe #22644.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Percent Similarity: 35.8% Conservative: 50  
Best Local Similarity: 22.8% Mismatches: 152  
Query Match: 5.5% Indels: 96  
RESULT 1301  
ID ACA92438 standard; DNA; 2352 BP.  
DE DNA encoding human PMMM-23.  
PN WO2003031939-A2.  
PD 17-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 32.7% Conservative: 54  
Best Local Similarity: 20.5% Mismatches: 130  
Query Match: 5.5% Indels: 169  
RESULT 1302  
ID ABL04347 standard; cDNA; 3188 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7523.

PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 33.9%  
Best Local Similarity: 21.7%  
Query Match: 5.5%  
Conservative: 50  
Mismatches: 159  
Indels: 112  
RESULT 1303  
ID ADO67427 standard; cDNA; 3538 BP.  
DE Novel human cDNA sequence #2400.  
PN EPI440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 41.9%  
Best Local Similarity: 24.8%  
Query Match: 5.5%  
Conservative: 36  
Mismatches: 89  
Indels: 33  
RESULT 1304  
ID ADI28073 standard; cDNA; 4111 BP.  
DE ECMCAD gene clone 553744CBL.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 26.7%  
Query Match: 5.5%  
Conservative: 35  
Mismatches: 81  
Indels: 85  
RESULT 1305  
ID ADK65923 standard; DNA; 4447 BP.  
DE Y lipolytica isocitrate lyase vector fragment #1.  
PN WO2004009828-A1.  
PD 29-JAN-2004.  
PA (UYDR ) UNIV DRESDEN TECH.  
Percent Similarity: 35.2%  
Best Local Similarity: 23.8%  
Query Match: 5.5%  
Conservative: 49  
Mismatches: 154  
Indels: 125  
RESULT 1306  
ID ABZ11844 standard; cDNA; 4573 BP.  
DE Human polynucleotide SEQ ID NO 726.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 36.7%  
Best Local Similarity: 23.3%  
Query Match: 5.5%  
Conservative: 50  
Mismatches: 160  
Indels: 77  
RESULT 1307  
ID ADP55703 standard; cDNA; 4839 BP.  
DE Human PRO cDNA sequence SEQ ID NO:1679.  
PN WO2004039956-A2.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 39.6%  
Best Local Similarity: 26.7%  
Query Match: 5.5%  
Conservative: 35  
Mismatches: 81  
Indels: 85  
RESULT 1308  
ID ABL04768 standard; cDNA; 4864 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 8786.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 37.6%  
Best Local Similarity: 24.0%  
Query Match: 5.5%  
Conservative: 39  
Mismatches: 131  
Indels: 48  
RESULT 1309  
ID ADM44362 standard; cDNA; 5323 BP.  
DE Novel human arginine-rich protein cDNA #726.  
PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Percent Similarity: 36.7%  
Best Local Similarity: 23.3%  
Query Match: 5.5%  
Conservative: 50  
Mismatches: 160  
Indels: 77  
RESULT 1310  
ID ABL25205 standard; DNA; 5931 BP.

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27088.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 31.0%  
Best Local Similarity: 21.5%  
Query Match: 5.5%  
Conservative: 40  
Mismatches: 127  
Indels: 162  
RESULT 1311  
ID ABL25204 standard; DNA; 7931 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27085.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 31.0%  
Best Local Similarity: 21.5%  
Query Match: 5.5%  
Conservative: 40  
Mismatches: 127  
Indels: 162  
RESULT 1312  
ID ADO80813 standard; DNA; 9163 BP.  
DE Porcine enterotoxigenic E coli resistance gene contig 132.  
PN WO2004048606-A2.  
PD 10-JUN-2004.  
PA (KGLV-) DEN KGL VETERINAER OG LANDBOHOJSKOLE.  
Percent Similarity: 35.7%  
Best Local Similarity: 23.8%  
Query Match: 5.5%  
Conservative: 40  
Mismatches: 116  
Indels: 100  
RESULT 1313  
ID ADK65925 standard; DNA; 9300 BP.  
DE Y lipolytica isocitrate lyase vector fragment #3.  
PN WO2004009828-A1.  
PD 29-JAN-2004.  
PA (UYDR ) UNIV DRESDEN TECH.  
Percent Similarity: 35.2%  
Best Local Similarity: 23.8%  
Query Match: 5.5%  
Conservative: 49  
Mismatches: 154  
Indels: 125  
RESULT 1314  
ID ADK65924 standard; DNA; 10056 BP.  
DE Y lipolytica isocitrate lyase vector fragment #2.  
PN WO2004009828-A1.  
PD 29-JAN-2004.  
PA (UYDR ) UNIV DRESDEN TECH.  
Percent Similarity: 35.2%  
Best Local Similarity: 23.8%  
Query Match: 5.5%  
Conservative: 49  
Mismatches: 154  
Indels: 125  
RESULT 1315  
ID ACC00398 standard; cDNA; 10569 BP.  
DE Human cell adhesion and extracellular matrix protein, CADECM-7, DNA.  
PN WO2003027230-A2.  
PD 03-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 41.0%  
Best Local Similarity: 24.5%  
Query Match: 5.5%  
Conservative: 62  
Mismatches: 147  
Indels: 78  
RESULT 1316  
ID ADW42645 standard; DNA; 31967 BP.  
DE Simian adenovirus 18 polynucleotide.  
PN WO2005001103-A2.  
PD 06-JAN-2005.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Percent Similarity: 34.1%  
Best Local Similarity: 22.7%  
Query Match: 5.5%  
Conservative: 48  
Mismatches: 155  
Indels: 124  
RESULT 1317  
ID ABL18214 standard; DNA; 34712 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 6115.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 35.2%  
Best Local Similarity: 22.2%  
Query Match: 5.5%  
Conservative: 52  
Mismatches: 147  
Indels: 115  
RESULT 1318  
ID ADM43175 standard; DNA; 35167 BP.  
DE Wild-type adenovirus serotype 24 nucleotide sequence SEQ ID NO:5.

PN WO2004018627-A2.  
PD 04-MAR-2004.  
PA (MERI ) MERCK & CO INC.  
Percent Similarity: 37.0%  
Best Local Similarity: 24.8%  
Query Match: 5.5%  
Conservative: 47  
Mismatches: 133  
Indels: 112  
RESULT 1319  
ID ADS00140 standard; DNA; 35167 BP.  
DE Wild-type human adenovirus serotype 24 DNA SEQ ID NO:1.  
PN WO2004083418-A1.  
PD 30-SEP-2004.  
PA (MERI ) MERCK & CO INC.  
Percent Similarity: 37.0%  
Best Local Similarity: 24.8%  
Query Match: 5.5%  
Conservative: 47  
Mismatches: 133  
Indels: 112  
RESULT 1320  
ID ABL03070 standard; cDNA; 35664 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3692.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 35.2%  
Best Local Similarity: 22.2%  
Query Match: 5.5%  
Conservative: 52  
Mismatches: 147  
Indels: 115  
RESULT 1321  
Percent Similarity: 37.9%  
Best Local Similarity: 23.5%  
Query Match: 5.5%  
Conservative: 45  
Mismatches: 128  
Indels: 65  
RESULT 1322  
ID AAF74218 standard; DNA; 1029 BP.  
DE DNA encoding environmental stress tolerant protein SEQ ID 63.  
PN WO200106006-A1.  
PD 25-JAN-2001.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
Percent Similarity: 46.9%  
Best Local Similarity: 30.0%  
Query Match: 5.5%  
Conservative: 22  
Mismatches: 48  
Indels: 21  
RESULT 1323  
ID ABQ80360 standard; cDNA; 1095 BP.  
DE A. fumigatus AfPGU3 cDNA.  
PN WO2003012071-A2.  
PD 13-FEB-2003.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 45.0%  
Best Local Similarity: 27.2%  
Query Match: 5.5%  
Conservative: 34  
Mismatches: 74  
Indels: 32  
RESULT 1324  
ID ABQ80359 standard; DNA; 1149 BP.  
DE A. fumigatus AfPGU3 DNA.  
PN WO2003012071-A2.  
PD 13-FEB-2003.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 45.0%  
Best Local Similarity: 27.2%  
Query Match: 5.5%  
Conservative: 34  
Mismatches: 74  
Indels: 32  
RESULT 1325  
ID AED40647 standard; cDNA; 1509 BP.  
DE Aspergillus fumigatus UnkAG cDNA.  
PN WO2005095975-A2.  
PD 13-OCT-2005.  
PA (FTWO-) F2G LTD.  
Percent Similarity: 39.6%  
Best Local Similarity: 25.6%  
Query Match: 5.5%  
Conservative: 44  
Mismatches: 104  
Indels: 90  
RESULT 1326  
ID AEC32076 standard; DNA; 1683 BP.  
DE Human CG57008-11 DNA, SEQ ID NO: 21.  
PN US2005197292-A1.  
PD 08-SEP-2005.  
PA (SMIT/) SMITHSON G.  
PA (MESR/) MESRI M.  
PA (STAR/) STARLING G.  
Percent Similarity: 35.4%  
Conservative: 42

Best Local Similarity: 22.8%  
Query Match: 5.5%  
Mismatches: 140  
Indels: 76  
RESULT 1327  
ID AEI88252 standard; cDNA; 1725 BP.  
DE cDNA encoding glucoamylase enzyme, SEQ ID NO:6.  
PN WO2006069289-A2.  
PD 29-JUN-2006.  
PA (NOVO ) NOVOZYMES NORTH AMERICA INC.  
PA (NOVO ) NOVOZYMES AS.  
Percent Similarity: 36.6%  
Best Local Similarity: 23.7%  
Query Match: 5.5%  
Conservative: 41  
Mismatches: 143  
Indels: 59  
RESULT 1328  
ID ABL02055 standard; cDNA; 1888 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 647.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Percent Similarity: 34.4%  
Best Local Similarity: 20.6%  
Query Match: 5.5%  
Conservative: 76  
Mismatches: 190  
Indels: 172  
RESULT 1329  
ID AEB44131 standard; DNA; 2000 BP.  
DE Lipid acyltransferase coding sequence, SEQ ID 66.  
PN US2005142647-A1.  
PD 30-JUN-2005.  
PA (WASS/) WASSELL P.  
PA (SOEJ/) SOE J B.  
PA (MIKK/) MIKKESEN J D.  
PA (KRIS/) KRISTENSEN A C J.  
Percent Similarity: 33.8%  
Best Local Similarity: 22.1%  
Query Match: 5.5%  
Conservative: 47  
Mismatches: 169  
Indels: 96  
RESULT 1330  
ID AEB28348 standard; DNA; 2000 BP.  
DE Glycolipid acyltransferase DNA #20.  
PN WO2005066347-A1.  
PD 21-JUL-2005.  
PA (DANI-) DANISCO AS.  
Percent Similarity: 33.8%  
Best Local Similarity: 22.1%  
Query Match: 5.5%  
Conservative: 47  
Mismatches: 169  
Indels: 96  
RESULT 1331  
ID AEF62840 standard; cDNA; 2000 BP.  
DE Lipid acyltransferase coding sequence #4.  
PN WO2006008508-A1.  
PD 26-JAN-2006.  
PA (DANI-) DANISCO AS.  
Percent Similarity: 33.8%  
Best Local Similarity: 22.1%  
Query Match: 5.5%  
Conservative: 47  
Mismatches: 169  
Indels: 96  
RESULT 1332  
ID AEF43084 standard; DNA; 2000 BP.  
DE Galactolipase gene SEQ ID NO:13.  
PN WO2006008653-A2.  
PD 26-JAN-2006.  
PA (DANI-) DANISCO AS.  
Percent Similarity: 33.8%  
Best Local Similarity: 22.1%  
Query Match: 5.5%  
Conservative: 47  
Mismatches: 169  
Indels: 96  
RESULT 1333  
ID AAS21319 standard; cDNA; 2164 BP.  
DE Human cDNA sequence encoding for PRO4322 polypeptide.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1334  
ID AAS15365 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO4322 polypeptide.  
PN WO200166740-A2.





Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1351  
ID ADA47529 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1352  
ID ADA67324 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1353  
ID ADB30331 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1354  
ID ADA85627 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1355  
ID ADA96839 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1356  
ID ADA79143 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1357  
ID ADA87282 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1358  
ID ADB16484 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Conservative: 33  
Mismatches: 135  
Indels: 124

Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1359  
ID ADA91576 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1360  
ID ADB14639 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1361  
ID ADB18600 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1362  
ID ADA93815 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1363  
ID ADB19711 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1364  
ID ADB13023 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1365  
ID ACD98499 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1366  
ID ADA74277 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1367  
ID ADB16484 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Conservative: 33  
Mismatches: 135  
Indels: 124

Query Match: 5.5% Indels: 124  
RESULT 1367  
ID ADB24510 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1368  
ID ADA82034 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1369  
ID ADA74997 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1370  
ID ADA85075 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1371  
ID ADA84523 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1372  
ID ADB29779 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1373  
ID ADA80307 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1374  
ID ADA75549 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124

RESULT 1375  
ID ADA46774 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1376  
ID ADB25070 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1377  
ID ADA93246 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1378  
ID ADB26596 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1379  
ID ADB30883 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1380  
ID ABT44622 standard; cDNA; 2164 BP.  
DE Human PRO4322 cDNA.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1381  
ID ADA60811 standard; cDNA; 2164 BP.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1382  
ID ADB23958 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1383  
ID ADB23958 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124

ID ADA96287 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1384

ID ADA80859 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1385

ID ADA95735 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1386

ID ADB26044 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1387

ID ADB21529 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1388

ID ACD82289 standard; cDNA; 2164 BP.  
DE Human secreted/transmembrane polypeptide PRO 4322 cDNA.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1389

ID ADA77308 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1390

ID ADB18048 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1391

ID ADA86731 standard; cDNA; 2164 BP.

DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1392

ID ADA87834 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1393

ID ADA46222 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1394

ID ADB28252 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1395

ID ADB28804 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1396

ID ADA76756 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1397

ID ADA88386 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1398

ID ADA97391 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1399

ID ADB27148 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.





Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1416  
ID ADB90175 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1417  
ID ADB39276 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1418  
ID ADB78200 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1419  
ID ADB87266 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #114.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1420  
ID ADB84848 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #114.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1421  
ID ADB46899 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1422  
ID ADB83963 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1423  
ID ADB86506 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Mismatches: 135  
Indels: 124

Query Match: 5.5%  
Indels: 124  
RESULT 1424  
ID ADB73118 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1425  
ID ADB77111 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1426  
ID ADB34268 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1427  
ID ADB35372 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1428  
ID ADB33716 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1429  
ID ADB34820 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1430  
ID ADB35924 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide SEQ ID NO 151.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1431  
ID ADB46319 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124

RESULT 1432  
ID ADC36956 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #114.  
PN US2003088065-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1433  
ID ADC21946 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #114.  
PN US2003096969-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1434  
ID ADC50192 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1435  
ID ADC71739 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1436  
ID ADC59718 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1437  
ID ADC49977 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003088064-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1438  
ID ADC49176 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1439  
ID ADC49693 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1440  
ID ADC58854 standard; cDNA; 2164 BP.

ID ADC47554 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1441  
ID ADC52725 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID151.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1442  
ID ADC57079 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID151.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1443  
ID ADC60270 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1444  
ID ADC50745 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1445  
ID ADC65272 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1446  
ID ADC54370 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID151.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1447  
ID ADC53331 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID151.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1448  
ID ADC58854 standard; cDNA; 2164 BP.

DE Novel human secreted and transmembrane protein cDNA Seq ID151.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1449  
ID ADC55732 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID151.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1450  
ID ADC58302 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID151.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1451  
ID ADC47299 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1452  
ID ADD02976 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1453  
ID ADC89968 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1454  
ID ADC69387 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1455  
ID ADC48276 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1456  
ID ADD09805 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.

PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1457  
ID ADC78174 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003096972-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1458  
ID ADD04380 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1459  
ID ADD06409 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003073816-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1460  
ID ADC80336 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1461  
ID ADD10843 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1462  
ID ADC47724 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1463  
ID ADC77928 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003088066-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
Conservative: 33  
Mismatches: 135  
Indels: 124  
RESULT 1464  
ID ADC79784 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003087358-A1.



PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1465  
ID ADD09253 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1466  
ID ADD50891 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003105291-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1467  
ID ADD40966 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1468  
ID ADD52105 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1469  
ID ADD51137 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003105290-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1470  
ID ADD52845 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1471  
ID ADD53397 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1472  
ID ADD51553 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003194779-A1.  
PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1473  
ID ADD02352 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1474  
ID ADD50618 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #114.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1475  
ID ADD01786 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1476  
ID ADD53968 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1477  
ID ADD50372 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #114.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1478  
ID ADD51383 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1479  
ID ADD92285 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%  
Best Local Similarity: 24.2%  
Query Match: 5.5%  
RESULT 1480  
ID ADD91181 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.

Conservative: 33  
Mismatch: 135  
Indels: 124

Conservative: 33  
Mismatch: 135  
Indels: 124

Conservative: 33  
Mismatch: 135  
Indels: 124

Conservative: 33  
Mismatch: 135  
Indels: 124

Conservative: 33  
Mismatch: 135  
Indels: 124

Conservative: 33  
Mismatch: 135  
Indels: 124

Conservative: 33  
Mismatch: 135  
Indels: 124

Conservative: 33  
Mismatch: 135  
Indels: 124

Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1481  
ID ADE03795 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1482  
ID ADE32092 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1483  
ID ADE22024 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1484  
ID ADD79248 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1485  
ID ADE41784 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1486  
ID ADE17601 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1487  
ID ADD91733 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1488  
ID ADE33196 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33

Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1489  
ID ADE33748 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1490  
ID ADD79800 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1491  
ID ADD92837 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1492  
ID ADE19257 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1493  
ID ADE18705 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1494  
ID ADE42901 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1495  
ID ADD95690 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1496  
ID ADE22576 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33  
Best Local Similarity: 24.2%      Mismatches: 135  
Query Match: 5.5%      Indels: 124  
RESULT 1497  
ID ADE33196 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8%      Conservative: 33

Query Match: 5.5% Indels: 124  
RESULT 1497  
ID ADD78694 standard; cDNA; 2164 BP.  
DE cDNA encoding human PRO polypeptide #76.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8% Conservative: 33  
Best Local Similarity: 24.2% Mismatches: 135  
Query Match: 5.5% Indels: 124  
RESULT 1498  
ID ADE32644 standard; cDNA; 2164 BP.  
DE Novel human secreted and transmembrane protein PRO4322 cDNA.  
PN US2003194766-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8% Conservative: 33  
Best Local Similarity: 24.2% Mismatches: 135  
Query Match: 5.5% Indels: 124  
RESULT 1499  
ID ADE42336 standard; cDNA; 2164 BP.  
DE Human PRO polynucleotide #76.  
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Percent Similarity: 32.8% Conservative: 33  
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PA (GETH ) GENENTECH INC.  
Percent Similarity: 32.8% Conservative: 33  
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GenCore version 6.2.1  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 20, 2007, 00:48:25 ; Search time 461 Seconds

(without alignments)  
3502.271 Million cell updates/sec

Title: US-09-944-929-83  
Perfect score: 2211  
Sequence: 1 MFFGGEGSLTYTLVICFLT.....LRRKYSRLDYLINGIYVDI 431

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2211	100.0	2284	3	US-09-990-444-514
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					Sequence 82, Appl
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					Sequence 514, Appl
					Sequence 82, Appl

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8	2211	100.0	2284	3	US-09-997-333-514	Sequence 514, Appl
9	2211	100.0	2284	3	US-09-992-598-514	Sequence 514, Appl
10	2211	100.0	2284	4	US-09-989-735-514	Sequence 514, Appl
11	2211	100.0	2284	5	US-09-989-726-514	Sequence 514, Appl
12	2211	100.0	2284	5	US-09-944-884-82	Sequence 82, Appl
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15	2211	100.0	2284	5	US-09-997-349-514	Sequence 514, Appl
16	2211	100.0	2284	5	US-09-997-653-514	Sequence 514, Appl
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22	2211	100.0	2284	5	US-09-989-733-514	Sequence 514, Appl
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36	242	10.9	295	5	US-10-793-479-9897	Sequence 9897, Ap
37	196.5	8.9	1826	3	US-09-774-528-230	Sequence 230, App
38	196.5	8.9	1826	3	US-10-120-988-230	Sequence 230, App
39	195.5	8.8	1932	5	US-10-185-047A-8	Sequence 8, Appli
40	194.5	8.8	1642	3	US-09-489-847-70	Sequence 70, Appl
41	188	8.5	1661	5	US-10-123-292-223	Sequence 223, App
42	188	8.5	1661	5	US-10-152-398-223	Sequence 223, App
43	188	8.5	1661	5	US-10-123-907-223	Sequence 223, App
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65	164	7.4	14246	5	US-10-704-781-1	Sequence 1, Appli
66	160.5	7.3	1638	3	US-09-799-451-412	Sequence 412, App
67	160	7.2	10174	5	US-10-171-311-82	Sequence 82, Appl
68	157	7.1	16562	3	US-09-949-016-13892	Sequence 13892, A
69	155.5	7.0	5403	5	US-09-745-008-33	Sequence 33, Appl
70	155	7.0	2922	5	US-10-108-260A-1446	Sequence 1446, Ap
71	152	6.9	1297	3	US-09-976-594-950	Sequence 950, App
72	150.5	6.8	929	5	US-10-703-032-2917	Sequence 2917, Ap
73	150.5	6.8	150223	5	US-10-624-149A-1	Sequence 1, Appli
74	148	6.7	2032	3	US-09-241-581B-5	Sequence 5, Appli
75	148	6.7	2032	3	US-08-265-428-5	Sequence 5, Appli
76	148	6.7	2032	5	US-08-765-108-5	Sequence 5, Appli
77	148	6.7	2032	8	PCT-US95-07721-5	Sequence 5, Appli
78	148	6.7	2563	5	US-10-703-032-2953	Sequence 2953, Ap
79	147.5	6.7	1236	5	US-10-077-584-3	Sequence 3, Appli



80	146	6.6	1159	5	US-10-703-032-2886	Sequence 2886, Ap	153	133	6.0	3228	3	US-09-487-558B-109	Sequence 109, App
C 81	146	6.6	767677	3	US-09-949-016-12147	Sequence 12147, A	154	132.5	6.0	617	5	US-10-703-032-77253	Sequence 77253, A
C 82	146	6.6	767677	3	US-09-949-016-17361	Sequence 17361, A	155	132.5	6.0	792	5	US-10-703-032-2920	Sequence 2920, Ap
C 83	145.5	6.6	2114	3	US-09-370-838-158	Sequence 158, App	156	132.5	6.0	6852	3	US-10-172-502-3	Sequence 3, Appli
C 84	145.5	6.6	2114	3	US-09-854-133-158	Sequence 158, App	157	132	6.0	532	5	US-10-703-032-98728	Sequence 98728, A
C 85	145	6.6	1088	5	US-10-703-032-103747	Sequence 103747,	158	132	6.0	585	5	US-10-703-032-77269	Sequence 77269, A
C 86	145	6.6	9636	2	US-08-323-170B-1	Sequence 1, Appli	159	132	6.0	613	5	US-10-703-032-105228	Sequence 105228,
C 87	145	6.6	9636	3	US-08-954-441-1	Sequence 1, Appli	160	132	6.0	615	5	US-10-703-032-65933	Sequence 65933, A
88	144.5	6.5	2156	5	US-10-451-467A-167	Sequence 167, App	161	132	6.0	814	5	US-10-703-032-4517	Sequence 4517, Ap
89	144.5	6.5	3423	3	US-09-614-221A-91	Sequence 91, Appl	162	132	6.0	1230	5	US-10-703-032-2320	Sequence 2320, Ap
C 90	143	6.5	720	5	US-10-703-032-14434	Sequence 14434, A	163	132	6.0	2455	3	US-09-103-429A-1	Sequence 1, Appli
C 91	142	6.4	12685	3	US-09-479-467A-3	Sequence 3, Appli	164	132	6.0	2455	3	US-09-294-663-1	Sequence 1, Appli
C 92	142	6.4	12685	3	US-09-655-160-3	Sequence 3, Appli	165	132	6.0	2821	3	US-09-103-429A-2	Sequence 2, Appli
93	141.5	6.4	3486	3	US-09-614-221A-292	Sequence 292, App	166	132	6.0	2821	3	US-09-294-663-2	Sequence 2, Appli
94	140.5	6.4	1490	5	US-10-703-032-8641	Sequence 8641, Ap	167	132	6.0	5511	3	US-08-928-361B-2	Sequence 2, Appli
95	139.5	6.3	1795	3	US-09-197-970B-6	Sequence 6, Appli	168	132	6.0	5511	3	US-09-588-995A-2	Sequence 2, Appli
96	139	6.3	657	5	US-10-703-032-35646	Sequence 35646, A	169	132	6.0	7334	3	US-08-928-361B-1	Sequence 1, Appli
97	139	6.3	867	3	US-09-216-393B-340	Sequence 340, App	170	132	6.0	7334	3	US-09-588-995A-1	Sequence 1, Appli
98	139	6.3	867	3	US-09-216-393B-342	Sequence 342, App	171	131.5	5.9	688	5	US-10-703-032-74240	Sequence 74240, A
99	139	6.3	867	5	US-10-321-856-340	Sequence 340, App	172	131	5.9	993	5	US-10-703-032-30891	Sequence 30891, A
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105	138.5	6.3	3159	3	US-09-437-054A-7	Sequence 7, Appli	C 178	130.5	5.9	1086	2	US-08-415-751-28	Sequence 28, Appl
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114	138.5	6.3	5318	3	US-08-928-361B-3	Sequence 3, Appli	C 187	129.5	5.9	640	5	US-10-703-032-103787	Sequence 103787,
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116	138	6.2	585	5	US-10-703-032-72752	Sequence 72752, A	189	129.5	5.9	754	5	US-10-703-032-76137	Sequence 76137, A
117	138	6.2	828	5	US-10-703-032-2946	Sequence 2946, Ap	190	129.5	5.9	812	5	US-10-703-032-76025	Sequence 76025, A
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119	136.5	6.2	1512	3	US-09-487-558B-423	Sequence 423, App	192	129.5	5.9	955	5	US-10-703-032-14354	Sequence 14354, A
120	136	6.2	1587	5	US-10-703-032-2948	Sequence 2948, Ap	C 193	129.5	5.9	1099	3	US-08-956-171B-825	Sequence 825, App
121	136	6.2	1905	5	US-10-455-719-150	Sequence 150, App	C 194	129.5	5.9	1099	3	US-08-781-986A-825	Sequence 825, App
122	136	6.2	2150	2	US-08-861-464-13	Sequence 13, Appl	C 195	129	5.8	756	5	US-10-703-032-103062	Sequence 103062,
123	136	6.2	2150	2	US-08-396-001-13	Sequence 13, Appl	196	129	5.8	1815	5	US-09-758-269-13	Sequence 13, Appl
124	136	6.2	2150	3	US-09-323-433A-13	Sequence 13, Appl	197	129	5.8	4725	5	US-10-041-018-147	Sequence 147, App
125	136	6.2	2150	3	US-09-826-752-13	Sequence 13, Appl	198	128.5	5.8	698	5	US-10-703-032-72864	Sequence 72864, A
126	136	6.2	2188	5	US-10-455-719-25	Sequence 25, Appl	199	128.5	5.8	704	5	US-10-703-032-68202	Sequence 68202, A
127	136	6.2	3015	5	US-09-373-658C-37	Sequence 37, Appl	200	128.5	5.8	927	5	US-10-703-032-2928	Sequence 2928, Ap
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130	135.5	6.1	878	5	US-10-703-032-8646	Sequence 8646, Ap	203	128	5.8	767677	3	US-09-949-016-12147	Sequence 12147, A
131	135.5	6.1	2139	5	US-10-455-719-76	Sequence 76, Appl	204	128	5.8	767677	3	US-09-949-016-17361	Sequence 17361, A
132	135.5	6.1	2256646	5	US-10-470-565-1	Sequence 1, Appli	205	128	5.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
133	135	6.1	619	5	US-10-703-032-68308	Sequence 68308, A	206	128	5.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
134	135	6.1	784	5	US-10-703-032-8057	Sequence 8057, Ap	207	127.5	5.8	730	5	US-10-703-032-66048	Sequence 66048, A
135	135	6.1	1132	5	US-10-703-032-2923	Sequence 2923, Ap	208	127.5	5.8	750	5	US-10-703-032-76120	Sequence 76120, A
136	135	6.1	1140	3	US-09-023-173-4	Sequence 4, Appli	209	127.5	5.8	798	5	US-10-703-032-76198	Sequence 76198, A
137	135	6.1	2481	3	US-09-248-796A-3204	Sequence 3204, Ap	210	127.5	5.8	841	5	US-10-703-032-76195	Sequence 76195, A
138	134.5	6.1	1923	3	US-09-687-538B-1	Sequence 1, Appli	211	127.5	5.8	849	5	US-10-703-032-66037	Sequence 66037, A
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141	134	6.1	1038	5	US-10-703-032-30847	Sequence 30847, A	214	127.5	5.8	30690	3	US-09-914-286-1	Sequence 1, Appli
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148	133	6.0	1542	3	US-08-685-558A-8	Sequence 8, Appli	221	127	5.7	7542	3	US-10-153-921-3	Sequence 3, Appli
149	133	6.0	1542	3	US-09-765-449-8	Sequence 8, Appli	222	127	5.7	7542	3	US-10-669-689-3	Sequence 3, Appli
150	133	6.0	1671	3	US-09-614-221A-554	Sequence 554, App	223	126.5	5.7	541	5	US-10-703-032-98533	Sequence 98533, A
151	133	6.0	1671	3	US-09-487-558B-425	Sequence 425, App	224	126.5	5.7	610	5	US-10-703-032-76118	Sequence 76118, A
152	133	6.0	2398	3	US-09-949-016-4313	Sequence 4313, Ap	225	126.5	5.7	640	5	US-10-703-032-103754	Sequence 103754,

226	126.5	5.7	671	5	US-10-703-032-72883	Sequence 72883, A	299	124.5	5.6	1425	3	US-09-408-257-2	Sequence 2, Appli
227	126.5	5.7	696	5	US-10-703-032-77250	Sequence 77250, A	300	124.5	5.6	1485	3	US-09-248-796A-2443	Sequence 2443, Ap
228	126.5	5.7	701	5	US-10-703-032-76101	Sequence 76101, A	301	124.5	5.6	2175	3	US-09-605-703B-653	Sequence 653, App
229	126.5	5.7	709	5	US-10-703-032-77228	Sequence 77228, A	302	124.5	5.6	2175	3	US-09-605-703B-655	Sequence 655, App
230	126.5	5.7	729	5	US-10-703-032-76085	Sequence 76085, A	303	124.5	5.6	4116	3	US-09-949-016-2584	Sequence 2584, Ap
231	126.5	5.7	809	5	US-10-703-032-8622	Sequence 8622, Ap	304	124.5	5.6	4116	3	US-09-949-016-2585	Sequence 2585, Ap
232	126.5	5.7	840	5	US-10-703-032-2309	Sequence 2309, Ap	305	124	5.6	546	5	US-10-703-032-98536	Sequence 98536, A
233	126.5	5.7	913	2	US-08-217-327-3	Sequence 3, Appli	306	124	5.6	549	5	US-10-703-032-65470	Sequence 65470, A
234	126.5	5.7	913	2	US-07-885-970A-3	Sequence 3, Appli	307	124	5.6	607	5	US-10-703-032-2869	Sequence 2869, Ap
235	126.5	5.7	913	2	US-08-298-687A-3	Sequence 3, Appli	308	124	5.6	697	5	US-10-703-032-72759	Sequence 72759, A
236	126.5	5.7	913	2	US-08-530-797-2	Sequence 2, Appli	309	124	5.6	698	5	US-10-703-032-72891	Sequence 72891, A
237	126.5	5.7	913	2	US-08-298-829-3	Sequence 3, Appli	310	124	5.6	699	5	US-10-703-032-72817	Sequence 72817, A
238	126.5	5.7	913	2	US-08-787-335-2	Sequence 2, Appli	311	124	5.6	704	5	US-10-703-032-72893	Sequence 72893, A
239	126.5	5.7	1232	5	US-10-703-032-2323	Sequence 2323, Ap	312	124	5.6	711	5	US-10-703-032-71945	Sequence 71945, A
240	126.5	5.7	6699	3	US-09-949-016-1059	Sequence 1059, Ap	313	124	5.6	711	5	US-10-703-032-72762	Sequence 72762, A
241	126.5	5.7	12381	5	US-09-743-162A-1	Sequence 1, Appli	314	124	5.6	736	5	US-10-703-032-8574	Sequence 8574, Ap
242	126	5.7	490	5	US-10-703-032-105236	Sequence 105236,	c 315	124	5.6	1411	5	US-10-703-032-8660	Sequence 8660, Ap
243	126	5.7	506	5	US-10-703-032-66050	Sequence 66050, A	316	124	5.6	2821	3	US-10-104-047-527	Sequence 527, App
244	126	5.7	673	5	US-10-703-032-77238	Sequence 77238, A	317	124	5.6	3604	3	US-09-799-451-287	Sequence 287, App
245	126	5.7	695	5	US-10-703-032-77259	Sequence 77259, A	318	124	5.6	5580	3	US-09-614-221A-536	Sequence 536, App
246	126	5.7	708	5	US-10-703-032-74073	Sequence 74073, A	319	124	5.6	18364	5	US-10-243-243C-7	Sequence 7, Appli
247	126	5.7	1021	3	US-09-533-559-745	Sequence 745, App	c 320	124	5.6	24459	3	US-09-902-540-5004	Sequence 5004, Ap
248	126	5.7	1021	5	US-10-653-047-745	Sequence 745, App	321	124	5.6	32241	3	US-09-902-540-1247	Sequence 1247, Ap
249	126	5.7	1059	3	US-09-902-540-7326	Sequence 7326, Ap	322	123.5	5.6	1109	5	US-10-703-032-8589	Sequence 8589, Ap
250	126	5.7	1059	5	US-10-703-032-4477	Sequence 4477, Ap	323	123.5	5.6	2754	2	US-08-270-076A-10	Sequence 10, Appl
251	126	5.7	1079	3	US-09-145-916-4	Sequence 4, Appli	324	123.5	5.6	99748	3	US-09-949-016-11990	Sequence 11990, A
252	126	5.7	1079	5	US-10-352-839A-4	Sequence 4, Appli	325	123.5	5.6	99749	3	US-09-949-016-16518	Sequence 16518, A
c 253	126	5.7	1446	3	US-09-533-559-4423	Sequence 4423, Ap	326	123	5.6	529	5	US-10-703-032-98703	Sequence 98703, A
c 254	126	5.7	1446	5	US-10-653-047-4423	Sequence 4423, Ap	327	123	5.6	540	5	US-10-703-032-105245	Sequence 105245,
255	126	5.7	1824	5	US-10-703-032-8718	Sequence 8718, Ap	328	123	5.6	563	5	US-10-703-032-66047	Sequence 66047, A
256	126	5.7	2093	2	US-08-287-001A-1	Sequence 1, Appli	329	123	5.6	630	5	US-10-703-032-66027	Sequence 66027, A
257	126	5.7	2093	8	PCT-US95-09941-1	Sequence 1, Appli	330	123	5.6	631	5	US-10-703-032-102987	Sequence 102987,
258	126	5.7	2256	4	US-10-094-749-676	Sequence 676, App	331	123	5.6	794	5	US-10-703-032-4515	Sequence 4515, Ap
259	126	5.7	3366	5	US-10-455-719-89	Sequence 89, Appl	332	123	5.6	844	5	US-10-333-951-5	Sequence 5, Appli
c 260	126	5.7	4039	3	US-09-902-540-696	Sequence 696, App	333	123	5.6	1614	5	US-10-703-032-66032	Sequence 66032, A
261	126	5.7	7577	3	US-09-637-048C-3	Sequence 3, Appli	334	123	5.6	2482	3	US-09-742-201-1	Sequence 1, Appli
262	126	5.7	7577	3	US-10-435-835-3	Sequence 3, Appli	335	123	5.6	2482	5	US-10-223-081-41	Sequence 41, Appl
263	126	5.7	7621	3	US-09-637-048C-6	Sequence 6, Appli	336	123	5.6	2482	5	US-10-223-087-41	Sequence 41, Appl
264	126	5.7	7621	3	US-10-435-835-6	Sequence 6, Appli	337	123	5.6	2482	5	US-10-223-082-41	Sequence 41, Appl
c 265	126	5.7	2256646	5	US-10-470-565-1	Sequence 1, Appli	338	123	5.6	2482	5	US-10-223-084-41	Sequence 41, Appl
266	125.5	5.7	508	5	US-10-703-032-66059	Sequence 66059, A	339	123	5.6	2482	5	US-10-245-913-9	Sequence 9, Appli
267	125.5	5.7	595	5	US-10-703-032-105461	Sequence 105461,	340	123	5.6	2482	5	US-10-245-752-9	Sequence 9, Appli
268	125.5	5.7	619	5	US-10-703-032-65542	Sequence 65542, A	341	123	5.6	2482	5	US-10-242-095-9	Sequence 9, Appli
269	125.5	5.7	669	5	US-10-703-032-76099	Sequence 76099, A	342	123	5.6	2482	5	US-10-242-652-9	Sequence 9, Appli
270	125.5	5.7	968	5	US-10-703-032-2322	Sequence 2322, Ap	343	123	5.6	2482	5	US-10-223-090-41	Sequence 41, Appl
271	125.5	5.7	1372	5	US-10-703-032-2315	Sequence 2315, Ap	344	123	5.6	2717	2	US-07-723-002C-1	Sequence 1, Appli
272	125.5	5.7	1860	3	US-09-894-844-65	Sequence 65, Appl	345	123	5.6	3069	5	US-10-703-032-14250	Sequence 14250, A
273	125.5	5.7	1917	3	US-09-248-796A-4647	Sequence 4647, Ap	c 346	123	5.6	38239	3	US-09-949-016-12348	Sequence 12348, A
274	125.5	5.7	2717	5	US-10-451-467A-237	Sequence 237, App	c 347	123	5.6	38252	3	US-09-949-016-13570	Sequence 13570, A
275	125	5.7	499	5	US-10-703-032-103635	Sequence 103635,	348	123	5.6	114793	3	US-10-148-806-3	Sequence 3, Appli
276	125	5.7	812	5	US-10-703-032-102939	Sequence 102939,	349	122.5	5.5	640	5	US-10-703-032-103774	Sequence 103774,
277	125	5.7	1293	2	US-08-924-440-1	Sequence 1, Appli	350	122.5	5.5	649	5	US-10-703-032-36211	Sequence 36211, A
c 278	125	5.7	1430	3	US-09-976-594-878	Sequence 878, App	351	122.5	5.5	669	5	US-10-703-032-72854	Sequence 72854, A
279	125	5.7	1463	3	US-09-533-559-11	Sequence 11, Appl	352	122.5	5.5	762	5	US-10-703-032-76086	Sequence 76086, A
280	125	5.7	1463	5	US-10-653-047-11	Sequence 11, Appl	353	122.5	5.5	1042	3	US-09-533-559-5292	Sequence 5292, Ap
281	125	5.7	2142	3	US-09-614-221A-331	Sequence 331, App	354	122.5	5.5	1042	5	US-10-653-047-5292	Sequence 5292, Ap
282	125	5.7	2142	3	US-09-487-558B-407	Sequence 407, App	355	122.5	5.5	1170	5	US-10-703-032-2319	Sequence 2319, Ap
283	125	5.7	2337	5	US-10-333-951-9	Sequence 9, Appli	356	122.5	5.5	2335	3	US-10-104-047-748	Sequence 748, App
c 284	125	5.7	2835	3	US-09-134-001C-1515	Sequence 1515, Ap	357	122.5	5.5	3004	2	US-08-276-213-6	Sequence 6, Appli
c 285	125	5.7	3561	3	US-09-134-001C-1685	Sequence 1685, Ap	358	122.5	5.5	3004	3	US-09-373-272-8	Sequence 8, Appli
c 286	125	5.7	3561	5	US-09-450-969-1309	Sequence 1309, Ap	359	122.5	5.5	3004	5	US-09-981-900B-4	Sequence 4, Appli
c 287	125	5.7	3561	3	US-10-724-972B-1309	Sequence 1309, Ap	360	122.5	5.5	3306	2	US-08-261-206A-71	Sequence 71, Appl
288	125	5.7	4983	3	US-09-270-767-12587	Sequence 12587, A	361	122.5	5.5	11517	5	US-09-252-691C-4475	Sequence 4475, Ap
289	125	5.7	4998	3	US-09-501-171-5	Sequence 5, Appli	362	122.5	5.5	189268	5	US-10-021-698A-697	Sequence 697, App
290	125	5.7	6414	3	US-09-134-001C-1626	Sequence 1626, Ap	363	122.5	5.5	1082144	4	US-09-531-120-211	Sequence 211, App
291	125	5.7	6414	5	US-09-450-969-1179	Sequence 1179, Ap	364	122	5.5	733	5	US-10-703-032-102930	Sequence 102930,
292	125	5.7	6414	5	US-10-724-972B-1179	Sequence 1179, Ap	365	122	5.5	954	3	US-09-248-796A-3469	Sequence 3469, Ap
c 293	125	5.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli	366	122	5.5	954	3	US-10-703-032-2317	Sequence 2317, Ap
c 294	125	5.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli	367	122	5.5	1267	5	US-10-703-032-2954	Sequence 2954, Ap
295	124.5	5.6	506	5	US-10-703-032-72742	Sequence 72742, A	368	122	5.5	1347	3	US-09-533-559-5298	Sequence 5298, Ap
296	124.5	5.6	940	5	US-10-703-032-74343	Sequence 74343, A	369	122	5.5	1347	5	US-10-653-047-5298	Sequence 5298, Ap
297	124.5	5.6	1425	2	US-08-578-551-2	Sequence 2, Appli	370	122	5.5	3936	5	US-10-455-719-143	Sequence 143, App
298	124.5	5.6	1425	2	US-09-190-982-2	Sequence 2, Appli	371	122	5.5	5323	3	US-09-799-451-726	Sequence 726, App

372	121.5	5.5	503	5	US-10-703-032-72922	Sequence 72922, A	445	120.5	5.5	1124	2	US-09-190-982-1	Sequence 1, Appli
373	121.5	5.5	548	5	US-10-703-032-72014	Sequence 72014, A	446	120.5	5.5	1124	3	US-09-408-257-1	Sequence 1, Appli
374	121.5	5.5	589	5	US-10-703-032-72737	Sequence 72737, A	447	120.5	5.5	1672	5	US-10-703-032-135	Sequence 135, App
375	121.5	5.5	606	5	US-10-703-032-104098	Sequence 104098,	448	120.5	5.5	3510	3	US-09-487-558B-105	Sequence 105, App
376	121.5	5.5	1029	5	US-10-031-331C-63	Sequence 63, Appl	449	120.5	5.5	3711	3	US-09-769-787-321	Sequence 321, App
377	121.5	5.5	2164	5	US-10-123-292-151	Sequence 151, App	450	120.5	5.5	5397	5	US-09-619-049-1472	Sequence 1472, Ap
378	121.5	5.5	2164	5	US-10-152-398-151	Sequence 151, App	451	120	5.4	544	5	US-10-703-032-98600	Sequence 98600, A
379	121.5	5.5	2164	5	US-10-123-907-151	Sequence 151, App	452	120	5.4	650	5	US-10-703-032-103871	Sequence 103871,
380	121.5	5.5	2164	5	US-10-147-512-151	Sequence 151, App	453	120	5.4	1823	3	US-09-620-312D-1012	Sequence 1012, Ap
381	121.5	5.5	2164	5	US-10-147-485-151	Sequence 151, App	454	120	5.4	1857	3	US-09-248-796A-5170	Sequence 5170, Ap
382	121.5	5.5	2164	5	US-10-124-814-151	Sequence 151, App	455	120	5.4	2669	5	US-09-983-531A-19	Sequence 19, Appl
383	121.5	5.5	2164	5	US-10-124-822-151	Sequence 151, App	456	120	5.4	3337	5	US-10-617-217A-169	Sequence 169, App
384	121.5	5.5	2164	5	US-10-219-074-227	Sequence 227, App	457	120	5.4	3457	3	US-09-799-451-869	Sequence 869, App
385	121.5	5.5	2164	5	US-10-227-873-227	Sequence 227, App	458	120	5.4	9645	5	US-09-522-699A-1	Sequence 1, Appli
386	121.5	5.5	2164	5	US-10-131-833A-151	Sequence 151, App	C 459	120	5.4	31422	3	US-09-914-286-2	Sequence 2, Appli
387	121.5	5.5	2164	5	US-10-218-849-227	Sequence 151, App	C 460	120	5.4	35100	3	US-09-782-378A-26	Sequence 2, Appli
388	121.5	5.5	2164	5	US-10-142-419-151	Sequence 151, App	461	120	5.4	145597	5	US-10-624-149A-2	Sequence 105467,
389	121.5	5.5	2164	5	US-10-216-168-227	Sequence 227, App	462	119.5	5.4	484	5	US-10-703-032-105467	Sequence 74309, A
390	121.5	5.5	2164	5	US-10-152-375-151	Sequence 151, App	463	119.5	5.4	523	5	US-10-703-032-74309	Sequence 66014, A
391	121.5	5.5	2164	5	US-10-131-818A-151	Sequence 151, App	464	119.5	5.4	819	5	US-10-703-032-66014	Sequence 6039, Ap
392	121.5	5.5	2164	5	US-10-145-873-151	Sequence 151, App	465	119.5	5.4	990	3	US-09-248-796A-6039	Sequence 4617, Ap
393	121.5	5.5	2164	5	US-10-152-395-151	Sequence 151, App	466	119.5	5.4	1149	3	US-09-248-796A-4617	Sequence 125, App
394	121.5	5.5	2164	5	US-10-131-822A-151	Sequence 151, App	C 467	119.5	5.4	1700	3	US-09-533-559-125	Sequence 125, App
395	121.5	5.5	2164	5	US-10-142-763-151	Sequence 151, App	C 468	119.5	5.4	1700	5	US-10-653-047-125	Sequence 125, App
396	121.5	5.5	2164	5	US-10-128-694A-151	Sequence 151, App	469	119.5	5.4	1804	3	US-10-029-517-17	Sequence 17, Appl
397	121.5	5.5	2164	5	US-10-123-213-151	Sequence 151, App	470	119.5	5.4	2017	5	US-10-703-032-17664	Sequence 17664, A
398	121.5	5.5	2164	5	US-10-123-909-151	Sequence 151, App	471	119.5	5.4	2747	3	US-09-620-312D-19	Sequence 19, Appl
399	121.5	5.5	2164	5	US-10-131-826A-151	Sequence 151, App	472	119.5	5.4	3108	5	US-10-210-120-59	Sequence 59, Appl
400	121.5	5.5	2164	5	US-10-147-513-151	Sequence 151, App	473	119.5	5.4	3110	3	US-09-023-655-1072	Sequence 1072, Ap
401	121.5	5.5	2164	5	US-10-121-043-151	Sequence 151, App	474	119.5	5.4	3132	2	US-08-224-482-3	Sequence 3, Appli
402	121.5	5.5	2164	5	US-10-139-980-151	Sequence 151, App	475	119.5	5.4	3132	3	US-09-205-921-1	Sequence 1, Appli
403	121.5	5.5	2901	3	US-09-487-558B-371	Sequence 371, App	476	119.5	5.4	3132	3	US-09-300-958A-32	Sequence 32, Appl
404	121.5	5.5	3401	5	US-10-451-467A-51	Sequence 51, Appl	477	119.5	5.4	3132	3	US-09-702-705-320	Sequence 320, App
405	121.5	5.5	4184	3	US-09-949-016-4495	Sequence 4495, Ap	478	119.5	5.4	3132	3	US-09-736-457-320	Sequence 320, App
406	121.5	5.5	5649	3	US-09-902-540-735	Sequence 735, App	479	119.5	5.4	3132	3	US-09-614-124B-320	Sequence 320, App
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409	121.5	5.5	12191	3	US-09-949-016-16237	Sequence 16237, A	482	119.5	5.4	3132	3	US-09-658-824-320	Sequence 320, App
410	121.5	5.5	85692	5	US-10-461-194B-1	Sequence 1, Appli	483	119.5	5.4	3132	3	US-10-017-754-320	Sequence 320, App
411	121	5.5	539	5	US-10-703-032-77283	Sequence 77283, A	484	119.5	5.4	3132	3	US-09-651-563-320	Sequence 320, App
412	121	5.5	551	5	US-10-703-032-77245	Sequence 77245, A	485	119.5	5.4	3132	3	US-09-519-642-320	Sequence 320, App
413	121	5.5	571	5	US-10-703-032-97726	Sequence 97726, A	486	119.5	5.4	3132	4	US-09-648-389A-6	Sequence 6, Appli
414	121	5.5	576	5	US-10-703-032-77257	Sequence 77257, A	487	119.5	5.4	3132	4	US-09-880-107-3721	Sequence 3721, Ap
415	121	5.5	648	5	US-10-703-032-103019	Sequence 103019,	488	119.5	5.4	3137	3	US-09-949-016-5863	Sequence 5863, Ap
416	121	5.5	854	5	US-10-703-032-57737	Sequence 57737, A	489	119.5	5.4	4035	3	US-09-919-039-147	Sequence 147, App
417	121	5.5	1048	3	US-09-533-559-6603	Sequence 6603, Ap	490	119.5	5.4	6340	5	US-10-325-899-9210	Sequence 9210, Ap
418	121	5.5	1048	5	US-10-653-047-6603	Sequence 6603, Ap	491	119.5	5.4	6590	4	US-09-648-389A-4	Sequence 4, Appli
419	121	5.5	1119	5	US-10-333-951-8	Sequence 8, Appli	492	119.5	5.4	6940	4	US-09-880-107-1724	Sequence 1724, Ap
C 420	121	5.5	1176	5	US-10-703-032-8924	Sequence 8924, Ap	493	119.5	5.4	7825	3	US-09-949-016-17605	Sequence 17605, A
421	121	5.5	1859	3	US-08-894-818B-15	Sequence 15, Appl	494	119.5	5.4	8030	3	US-09-902-540-857	Sequence 857, App
422	121	5.5	1859	3	US-09-841-553-15	Sequence 15, Appl	C 495	119.5	5.4	57280	3	US-09-949-016-11796	Sequence 11796, A
423	121	5.5	1984	2	US-07-885-970A-25	Sequence 25, Appl	C 496	119.5	5.4	57280	3	US-09-949-016-12843	Sequence 12843, A
424	121	5.5	1985	2	US-08-298-687A-25	Sequence 25, Appl	C 497	119.5	5.4	57280	3	US-09-949-016-12844	Sequence 12844, A
425	121	5.5	1985	2	US-08-298-829-25	Sequence 25, Appl	C 498	119.5	5.4	57280	3	US-09-949-016-12846	Sequence 12846, A
426	121	5.5	2145	5	US-10-455-719-151	Sequence 151, App	C 499	119.5	5.4	57280	3	US-09-949-016-13542	Sequence 13542, A
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433	121	5.5	5891	5	US-10-451-467A-137	Sequence 137, App	C 506	119.5	5.4	57280	3	US-09-949-016-14636	Sequence 14636, A
434	121	5.5	6713	3	US-09-949-016-642	Sequence 642, App	C 507	119.5	5.4	57280	3	US-09-949-016-14637	Sequence 14637, A
435	121	5.5	9700	3	US-09-698-295-9	Sequence 9, Appli	C 508	119.5	5.4	57280	3	US-09-949-016-14638	Sequence 14638, A
436	121	5.5	9700	5	US-10-754-342-9	Sequence 9, Appli	C 509	119.5	5.4	57280	3	US-09-949-016-14639	Sequence 14639, A
437	121	5.5	9865	3	US-09-698-295-2	Sequence 2, Appli	C 510	119.5	5.4	57280	3	US-09-949-016-14640	Sequence 14640, A
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587	118	5.3	1417	5	US-10-703-032-2940	Sequence 2940, Ap	660	118	5.3	2436	5	US-10-063-523-99	Sequence 99, Appl
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773 116 5.2 1437 5 US-10-703-032-17223 Sequence 17223, A  
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792 116 5.2 37968 5 US-10-455-719-19 Sequence 19, Appl  
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812	115.5	5.2	3016	5	US-10-231-913-15	Sequence 15, Appl	885	114	5.2	2113	5	US-10-653-047-297	Sequence 297, App
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C 816	115.5	5.2	3337	3	US-08-719-821C-1	Sequence 1, Appli	889	114	5.2	2508	5	US-09-783-931C-1	Sequence 1, Appli
817	115.5	5.2	3343	3	US-10-029-517-102	Sequence 102, App	890	114	5.2	2517	2	US-07-906-930E-1	Sequence 1, Appli
C 818	115.5	5.2	12311	3	US-08-750-717-1	Sequence 1, Appli	891	114	5.2	2643	3	US-09-949-002-213	Sequence 213, App
819	115.5	5.2	17083	5	US-10-475-970-4	Sequence 4, Appli	892	114	5.2	2883	3	US-08-981-392-3	Sequence 3, Appli
C 820	115.5	5.2	17580	3	US-09-949-016-16055	Sequence 16055, A	893	114	5.2	2883	3	US-09-908-322-3	Sequence 3, Appli
C 821	115.5	5.2	36519	3	US-08-923-137-2	Sequence 2, Appli	894	114	5.2	2883	5	US-09-783-931C-3	Sequence 3, Appli
C 822	115.5	5.2	39154	3	US-09-949-016-12384	Sequence 12384, A	895	114	5.2	3183	5	US-10-108-260A-445	Sequence 445, App
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C 824	115.5	5.2	39443	3	US-09-949-016-14326	Sequence 14326, A	897	114	5.2	7541	3	US-09-637-048C-4	Sequence 4, Appli
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839	115	5.2	1197	3	US-09-252-991A-920	Sequence 920, App	912	113.5	5.1	645	3	US-09-533-559-5595	Sequence 5595, Ap
840	115	5.2	1533	3	US-09-248-796A-4410	Sequence 4410, Ap	913	113.5	5.1	645	5	US-10-653-047-5595	Sequence 5595, Ap
841	115	5.2	1608	3	US-09-292-225-20	Sequence 20, Appl	914	113.5	5.1	838	5	US-10-703-032-62878	Sequence 62878, A
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C 844	115	5.2	1608	5	US-09-662-293-22	Sequence 22, Appl	C 917	113.5	5.1	1380	3	US-09-620-312D-59	Sequence 59, Appl
845	115	5.2	1644	5	US-10-703-032-8673	Sequence 8673, Ap	C 918	113.5	5.1	2328	3	US-09-252-991A-5729	Sequence 5729, Ap
846	115	5.2	1662	3	US-09-949-016-2911	Sequence 2911, Ap	919	113.5	5.1	4015	5	US-10-426-776-45	Sequence 45, Appl
847	115	5.2	1665	3	US-09-292-225-17	Sequence 17, Appl	920	113.5	5.1	4230	3	US-09-252-991A-5711	Sequence 5711, Ap
C 848	115	5.2	1665	3	US-09-292-225-19	Sequence 19, Appl	921	113.5	5.1	4941	3	US-09-252-991A-5741	Sequence 5741, Ap
C 849	115	5.2	1665	5	US-09-662-293-17	Sequence 17, Appl	922	113.5	5.1	8147	3	US-09-514-247A-9	Sequence 9, Appli
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851	115	5.2	1752	3	US-09-292-225-14	Sequence 14, Appl	924	113.5	5.1	42000	5	US-10-159-257C-1	Sequence 1, Appli
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858	115	5.2	2912	3	US-10-132-350-1	Sequence 1, Appli	C 931	113	5.1	648	3	US-09-248-796A-7888	Sequence 2888, Ap
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869	114.5	5.2	1575	3	US-09-605-703B-1467	Sequence 1467, Ap	942	113	5.1	1721	3	US-10-029-517-3	Sequence 3, Appli
870	114.5	5.2	1839	3	US-09-248-796A-3174	Sequence 3174, Ap	943	113	5.1	1721	5	US-10-171-311-155	Sequence 155, App
C 871	114.5	5.2	2489	3	US-09-141-047-7	Sequence 7, Appli	944	113	5.1	1721	5	US-10-342-887-775	Sequence 775, App
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873	114.5	5.2	4975	5	US-10-475-970-27	Sequence 27, Appl	946	113	5.1	2070	3	US-09-949-016-5494	Sequence 5494, Ap
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875	114	5.2	434	5	US-10-703-032-97962	Sequence 97962, A	948	113	5.1	2070	3	US-09-949-016-5496	Sequence 5496, Ap
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878	114	5.2	713	5	US-10-703-032-102975	Sequence 102975, A	951	113	5.1	2179	7	US-09-925-065A-683197	Sequence 683197, A
879	114	5.2	763	5	US-10-703-032-57846	Sequence 57846, A	952	113	5.1	2247	3	US-08-760-615-5	Sequence 5, Appli
880	114	5.2	863	5	US-10-703-032-24597	Sequence 24597, A	953	113	5.1	2297	3	US-09-797-039-1	Sequence 1, Appli
881	114	5.2	951	3	US-09-248-796A-12352	Sequence 12352, A	954	113	5.1	2297	5	US-10-170-789-1	Sequence 1, Appli
882	114	5.2	1007	5	US-10-703-032-2313	Sequence 2313, Ap	955	113	5.1	2409	3	US-09-533-559-282	Sequence 282, App





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1103	111.5	5.0	1809	3	US-10-012-064A-71	Sequence 71, Appl	1176	111	5.0	6195	3	US-09-854-856-25	Sequence 25, Appl
1104	111.5	5.0	1809	4	US-10-015-392A-71	Sequence 71, Appl	1177	111	5.0	6195	3	US-10-010-720-25	Sequence 25, Appl
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1106	111.5	5.0	1809	5	US-10-015-386A-71	Sequence 71, Appl	1179	111	5.0	6231	3	US-10-010-720-45	Sequence 45, Appl
1107	111.5	5.0	1809	5	US-10-012-121A-71	Sequence 71, Appl	1180	111	5.0	6279	3	US-09-854-856-9	Sequence 9, Appl
1108	111.5	5.0	1809	5	US-10-006-485A-71	Sequence 71, Appl	1181	111	5.0	6279	3	US-10-010-720-9	Sequence 9, Appl
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1112	111.5	5.0	1809	5	US-10-015-519A-71	Sequence 71, Appl	1185	111	5.0	6411	3	US-10-010-720-13	Sequence 13, Appl
1113	111.5	5.0	1809	5	US-10-015-715A-71	Sequence 71, Appl	1186	111	5.0	6426	3	US-09-854-856-55	Sequence 55, Appl
1114	111.5	5.0	1809	5	US-10-007-236A-71	Sequence 71, Appl	1187	111	5.0	6426	3	US-10-010-720-55	Sequence 55, Appl
1115	111.5	5.0	1809	5	US-10-012-149A-71	Sequence 71, Appl	1188	111	5.0	6474	3	US-09-854-856-51	Sequence 51, Appl
1116	111.5	5.0	1809	5	US-10-007-194A-71	Sequence 71, Appl	1189	111	5.0	6474	3	US-10-010-720-51	Sequence 51, Appl
1117	111.5	5.0	1809	5	US-10-013-910A-71	Sequence 71, Appl	1190	111	5.0	6510	3	US-09-854-856-39	Sequence 39, Appl
1118	111.5	5.0	1809	5	US-10-006-117A-71	Sequence 71, Appl	1191	111	5.0	6510	3	US-10-010-720-39	Sequence 39, Appl
1119	111.5	5.0	1809	5	US-10-015-480A-71	Sequence 71, Appl	1192	111	5.0	6558	3	US-09-854-856-35	Sequence 35, Appl
1120	111.5	5.0	1809	5	US-10-006-172A-71	Sequence 71, Appl	1193	111	5.0	6558	3	US-10-010-720-35	Sequence 35, Appl
1121	111.5	5.0	1809	5	US-10-015-395A-71	Sequence 71, Appl	1194	111	5.0	6606	3	US-09-854-856-23	Sequence 23, Appl
1122	111.5	5.0	1809	5	US-10-183-001-251	Sequence 251, App	1195	111	5.0	6606	3	US-10-010-720-23	Sequence 23, Appl
1123	111.5	5.0	1809	5	US-10-015-610A-71	Sequence 71, Appl	1196	111	5.0	6654	3	US-09-854-856-19	Sequence 19, Appl
1124	111.5	5.0	1809	5	US-10-180-998-251	Sequence 251, App	1197	111	5.0	6654	3	US-10-010-720-19	Sequence 19, Appl
1125	111.5	5.0	1809	5	US-10-201-769-251	Sequence 251, App	1198	111	5.0	6690	3	US-09-854-856-7	Sequence 7, Appl
1126	111.5	5.0	1809	5	US-10-006-130A-71	Sequence 71, Appl	1199	111	5.0	6690	3	US-10-010-720-7	Sequence 7, Appl
1127	111.5	5.0	1809	5	US-10-174-576-251	Sequence 251, App	1200	111	5.0	6738	3	US-09-854-856-3	Sequence 3, Appl
1128	111.5	5.0	1809	5	US-10-174-581-251	Sequence 251, App	1201	111	5.0	6738	3	US-10-010-720-3	Sequence 3, Appl
1129	111.5	5.0	1809	5	US-10-015-869A-71	Sequence 71, Appl	1202	111	5.0	6885	3	US-09-854-856-49	Sequence 49, Appl
1130	111.5	5.0	1809	5	US-10-207-916-251	Sequence 251, App	1203	111	5.0	6885	3	US-10-010-720-49	Sequence 49, Appl
1131	111.5	5.0	1809	5	US-10-174-583-251	Sequence 251, App	1204	111	5.0	6969	3	US-09-854-856-33	Sequence 33, Appl
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1449 107.5 4.9 1279 3 US-09-686-583B-7 Sequence 7, Appli  
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1453 107.5 4.9 1359 3 US-09-686-583B-14 Sequence 14, Appl  
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1455 107.5 4.9 1359 5 US-10-401-324A-14 Sequence 14, Appl  
c1456 107.5 4.9 1359 5 US-10-401-324A-15 Sequence 15, Appl  
1457 107.5 4.9 1360 5 US-10-703-032-20818 Sequence 20818, A  
1458 107.5 4.9 1465 3 US-09-686-583B-11 Sequence 11, Appl  
c1459 107.5 4.9 1465 3 US-09-686-583B-13 Sequence 13, Appl  
1460 107.5 4.9 1465 5 US-10-401-324A-11 Sequence 11, Appl  
c1461 107.5 4.9 1465 5 US-10-401-324A-13 Sequence 13, Appl  
1462 107.5 4.9 1828 3 US-09-902-540-3724 Sequence 3724, Ap  
c1463 107.5 4.9 2477 3 US-09-902-540-1971 Sequence 1971, Ap  
1464 107.5 4.9 3306 3 US-09-081-385-10 Sequence 10, Appl  
1465 107.5 4.9 3306 3 US-09-752-639-10 Sequence 10, Appl  
1466 107.5 4.9 3306 3 US-09-712-813-10 Sequence 10, Appl

1467 107.5 4.9 3306 3 US-09-700-354A-10 Sequence 10, Appl  
1468 107.5 4.9 4312 3 US-10-104-047-468 Sequence 468, App  
1469 107.5 4.9 4466 3 US-09-410-551B-20 Sequence 20, Appl  
1470 107.5 4.9 4466 3 US-09-940-316B-20 Sequence 20, Appl  
1471 107.5 4.9 4478 3 US-09-410-551B-16 Sequence 16, Appl  
1472 107.5 4.9 4478 3 US-09-940-316B-16 Sequence 16, Appl  
1473 107.5 4.9 4547 3 US-09-410-551B-22 Sequence 22, Appl  
1474 107.5 4.9 4547 3 US-09-940-316B-22 Sequence 22, Appl  
1475 107.5 4.9 4571 3 US-09-410-551B-18 Sequence 18, Appl  
1476 107.5 4.9 4571 3 US-09-940-316B-18 Sequence 18, Appl  
1477 107.5 4.9 6463 3 US-09-332-063-1 Sequence 1, Appli  
1478 107.5 4.9 6897 5 US-10-455-719-8 Sequence 8, Appli  
c1479 107.5 4.9 10096 3 US-09-902-540-935 Sequence 935, App  
1480 107.5 4.9 12173 3 US-09-902-540-1022 Sequence 1022, Ap  
1481 107.5 4.9 16423 3 US-09-902-540-1120 Sequence 1120, Ap  
1482 107.5 4.9 36535 5 US-10-494-364A-9 Sequence 9, Appli  
1483 107.5 4.9 60785 3 US-09-949-016-12774 Sequence 12774, A  
1484 107.5 4.9 60785 3 US-09-949-016-15665 Sequence 15665, A  
c1485 107.5 4.9 83617 3 US-09-949-016-12254 Sequence 12254, A  
1486 107 4.8 650 5 US-10-703-032-103837 Sequence 103837,  
1487 107 4.8 665 5 US-10-703-032-74149 Sequence 74149, A  
1488 107 4.8 702 5 US-10-703-032-76154 Sequence 76154, A  
c1489 107 4.8 768 5 US-09-938-842A-812 Sequence 812, App  
1490 107 4.8 900 3 US-10-101-464A-282 Sequence 282, App  
c1491 107 4.8 965 5 US-10-666-642-1435 Sequence 1435, Ap  
c1492 107 4.8 965 5 US-10-225-066A-1085 Sequence 1085, Ap  
1493 107 4.8 1119 5 US-10-630-880-11 Sequence 11, Appl  
1494 107 4.8 1155 3 US-09-354-231B-9 Sequence 9, Appli  
1495 107 4.8 1155 3 US-09-128-602B-9 Sequence 9, Appli  
1496 107 4.8 1155 3 US-09-128-602B-11 Sequence 11, Appl  
1497 107 4.8 1155 3 US-09-995-297-9 Sequence 9, Appli  
1498 107 4.8 1155 3 US-09-995-297-11 Sequence 11, Appl  
1499 107 4.8 1155 3 US-09-771-904A-9 Sequence 9, Appli  
1500 107 4.8 1155 4 US-09-771-904A-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-866-028-82

; Sequence 82, Application US/09866028

; Patent No. 6642360

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein,David

; APPLICANT: Eaton,Dan

; APPLICANT: Ferrara,Napoleone

; APPLICANT: Filvaroff,Ellen

; APPLICANT: Gerritsen,Mary

; APPLICANT: Goddard,Audrey

; APPLICANT: Godowski,Paul

; APPLICANT: Grimaldi,Christopher

; APPLICANT: Gurney,Austin

; APPLICANT: Hillan,Kenneth

; APPLICANT: Kljavin,Ivar

; APPLICANT: Napier,Mary

; APPLICANT: Roy,Margaret

; APPLICANT: Tumas,Daniel

; APPLICANT: Wood,William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548PlC1

; CURRENT APPLICATION NUMBER: US/09/866,028

; CURRENT FILING DATE: 2001-05-25

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 82

; LENGTH: 2284

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-866-028-82

Alignment Scores:

Pred. No.:	1.82e-216	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0
US-09-944-929-83 (1-431) x US-09-866-028-82 (1-2284)			
QY	1	MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleCysPheLeuThr	20
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QY	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp	40
Db	286	CTAAGGCTGTCTGCTAGTCAGATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGAC	345
QY	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60
Db	346	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA	405
QY	61	GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80
Db	406	GAAGACTGCATTAAATCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC	465
QY	81	LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys	100
Db	466	TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCCACTGCTACCTATTTTCTGT	525
QY	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120
Db	526	CCCAACGAGGAAGCCCTGTCATTGAAACACAGCAAAAGGACTTATGAGTTACAGGATAAT	585
QY	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140
Db	586	ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCCAAGAGTTACCCCAAGAGATTCT	645
QY	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160
Db	646	CTCTTACATGGCCAAATTTTCAACAGCAGTCACTCCCTTAGCCCATCATCACACAGATTAT	705
QY	161	SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp	180
Db	706	TCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTTCTCAGAAGTTTGGATCCTCAGAT	765
QY	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200
Db	766	CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCACTCTTGCTTTATAAGGAA	825
QY	201	LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220
Db	826	AAAGGCCATTCTCAGAGTTCCAAATTTCTCTGTATCAAGAAATAGCTCATCTGCTGCCT	885
QY	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240
Db	886	GAAAATGTGAGTGGCTCCCGACTACGGTGCGAGTTGCTTCTCCACATACCACCTCGGCT	945
QY	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260
Db	946	ACTCCAAAGCCCGCCACCCTTTTACCACCAATGCTTTCAGTGACACCTTCTGGGACTTCC	1005
QY	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280
Db	1006	CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACTGTCACTTCTCAGCTTCCCAACG	1065
QY	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
Db	1066	ACCCTCATTTCTACAGTTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA	1125
QY	301	AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320
Db	1126	GCAGTTCTGACTACCACTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA	1185

QY	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
Db	1186	CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCCTACTGCA	1245
QY	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg	360
Db	1246	CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGTAGG	1305
QY	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1306	GAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCCAGAAATCAGTACGGCCTTCCA	1365
QY	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1366	TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTTCTGTTGATAGGC	1425
QY	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgLysArgTyrSerArgLeu	420
Db	1426	CTCGTCTCTCTGGGTAGAATCCTTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTG	1485
QY	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
Db	1486	GATTATTGATCAATGGGATCTATGTGGACATC	1518
RESULT 2			
US-09-944-457-82			
; Sequence 82, Application US/09944457			
; Patent No. 6734288			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin			
; APPLICANT: Botstein, David			
; APPLICANT: Eaton, Dan			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gerritsen, Mary			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul			
; APPLICANT: Grimaldi, Christopher			
; APPLICANT: Gurney, Austin			
; APPLICANT: Hillan, Kenneth			
; APPLICANT: Kljavin, Ivar			
; APPLICANT: Napier, Mary			
; APPLICANT: Roy, Margaret			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Wood, William			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: ACIDS ENCODING THE SAME			
; FILE REFERENCE: P2548P1C1			
; CURRENT APPLICATION NUMBER: US/09/944,457			
; CURRENT FILING DATE: 2001-09-26			
; PRIOR APPLICATION NUMBER: 09/866,028			
; PRIOR FILING DATE: 2001-05-25			
; PRIOR APPLICATION NUMBER: 60/067,411			
; PRIOR FILING DATE: December 3, 1997			
; PRIOR APPLICATION NUMBER: 60/069,334			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069335			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069,278			
; PRIOR FILING DATE: December 11, 1997			
; PRIOR APPLICATION NUMBER: 60/069,425			
; PRIOR FILING DATE: December 12, 1997			
; PRIOR APPLICATION NUMBER: 60/069,696			
; PRIOR FILING DATE: December 16, 1997			
; PRIOR APPLICATION NUMBER: 60/069,694			
; PRIOR FILING DATE: December 16, 1997			
; PRIOR APPLICATION NUMBER: 60/069,702			
; PRIOR FILING DATE: December 16, 1997			
; PRIOR APPLICATION NUMBER: 60/069,870			
; PRIOR FILING DATE: December 17, 1997			
; PRIOR APPLICATION NUMBER: 60/069,873			
; PRIOR FILING DATE: December 17, 1997			
; PRIOR APPLICATION NUMBER: 60/068,017			



;  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. 6734288ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 82  
; LENGTH: 2284  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-944-457-82

Alignment Scores:  
Pred. No.: 1.82e-216 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

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Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValValIleAasp 40  
Db 286 CTAAGGCTGTCTGTAGTCAGAAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGAC 345  
Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
Db 346 ATCCAGTCATCTCTTTCTAAGGGAAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405  
Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465  
Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTCTGT 525  
Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
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Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
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Db 646 CTCTTACATGGCCAAATTTTCACAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705  
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Db 706 TCAAAGCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAAGTTTGGATCCTCAGAT 765  
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGTCCAGCTCCTTGTCTATAAGGAA 825  
Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
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Db 886 GAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACACCTCGGCT 945  
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCCAAAGCCGCCACCCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACCTGTCACTTCTCAGCCTCCCACG 1065  
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Qy 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1126 GCAGTTCTGACTACCACCTTTTCAGGCACCTACGGACTCGAAGGCGAGCTTAGAAACCAT 1185  
Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db 1186 CCGTTTACAGAAATCTCCAACCTTAACCTTGAACACACAGGGAATGTGTATAACCTACTGCA 1245  
Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGTAGG 1305  
Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
Db 1306 GAGGCCAGTCCAGGCAGTTTCTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCCA 1365



Qy	381	PheGluLysTrpLeuLeuIleGlySerLeuPheGlyValLeuPheLeuValIleGly	400
Db	1366	TTTTAAAAATGGCTTCTTATCGGGTCCCTGTCTTTGGTGTCCTGTTCCTGGTGATAGGC	1425
Qy	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu	420
Db	1426	CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG	1485
Qy	421	AspTyrLeuIleAsnGlyIleTyrValAspile	431
Db	1486	GATTATTGATCAATGGGATCTATGTGGACATC	1518

### RESULT 3

US-09-945-584-82

; Sequence 82, Application US/09945584

; Patent No. 6908993

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/945,584

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/067,411

; PRIOR FILING DATE: December 3, 1997

; PRIOR APPLICATION NUMBER: 60/069,334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997

; PRIOR APPLICATION NUMBER: 60/069,696

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,702

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,870

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/069,873

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017

; PRIOR FILING DATE: December 18, 1997

; PRIOR APPLICATION NUMBER: 60/070,440

; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/074,092

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/075,945

; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112,850

; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 60/113,296

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; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6908993ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-945-584-82

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Alignment Scores:

Pred. No.:	1.82e-216	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-944-929-83 (1-431) x US-09-945-584-82 (1-2284)

Qy		1	MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr	20
Dd		226	ATGTCTTCGGGGAGAGAAGGAGCTTGACTTACACTTTGGTAATAATTGCCTCCCTGACA	285
Qy		21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysserLeuGluAspValValileAasp	40
Dd		286	CTAAGGCGTGCTGTCTAGTCAGAAATGCCCTCAAAAAGAGTCTAGAAGATGTTGTTCATTGAC	345
Qy		41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValtyrThrSerThrGln	60
Dd		346	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCCGTATATACTTCAACTCAA	405
Qy		61	GluASPcysiIeasnserCysSserthrLysasniIeserglyaspLysalaCysasn	80
Dd		406	GAAGACTGCATTAAATCTTGCTGTTTCAACAAAAAACATATCATGGGGACAAGCATGTAAAC	465

QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTCCTGT 525

QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
Db 526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
Db 586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCAAGAGTTACCCCGAAGATTCT 645

QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
Db 646 CTCTTACATGGCCAATTTTCACAGCAGTCACTCCCTAGCCCATCATCACACAGATTAT 705

QY 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTCTCAGAAAGTTTGGATCCTCAGAT 765

QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACTATTAAAGATGGATGAAGCAAGTGCCTCAGCTCCTTGCTTATAAGGAA 825

QY 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 826 AAAGGCCATTCTCAGAGTTTCACAATTTTCCTCTGTATCAAGAAATAGCTCATCTGTGCCT 885

QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCCAAAGCCCGCACCTTCTACCCACCAATGCTCAGTGACACCTTCTGGGACTTCC 1005

QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACCACACAGCTCCACCTGTAACTGTAACCACTGTCACTTCTCAGCCTCCACG 1065

QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGGGCTACACTCCAAGCAATGGCTACAACA 1125

QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1126 GCAGTTCTGACTACCACTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCAT 1185

QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db 1186 CCGTTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCTTACTGCA 1245

QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGlyArg 360  
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QY 361 GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
Db 1306 GAGGCCAGTCCAGCAGTTCTCTCCAGGGCAGTGTCCAGAAATCAGTACGGCCTTCCA 1365

QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
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QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
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QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518

RESULT 4  
US-09-991-181-514  
; Sequence 514, Application US/09991181  
; Patent No. 6913919  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C53  
; CURRENT APPLICATION NUMBER: US/09/991,181  
; CURRENT FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
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; PRIOR APPLICATION NUMBER: 60/083322  
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;	PRIOR FILING DATE: 1998-07-01
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;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091544
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;	PRIOR APPLICATION NUMBER: 60/091519
;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091626
;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091633
;	PRIOR FILING DATE: 1998-07-02
;	PRIOR APPLICATION NUMBER: 60/091978
;	PRIOR FILING DATE: 1998-07-07
;	PRIOR APPLICATION NUMBER: 60/091982
;	PRIOR FILING DATE: 1998-07-07
;	PRIOR APPLICATION NUMBER: 60/092182
;	PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	1.82e-216	Length:	2284
Score:	2211.00	Matches:	431
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-944-929-83 (1-431) x US-09-991-181-514 (1-2284)

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QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40

Db 286 CTAAGCGTGTCTGCTAGTCAGAAATTCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGAC 345

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Db 346 ATCCAGTCATCTCTTTCTAAGGAATCAGAGGCAATGAGCCGTATATACTTTCAACTCAA 405

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Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCAAGCTCTTGCTTATAAGGAA 825

Qy 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
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Db 826 AAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

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Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
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Db 946 ACTCCAAAGCCCGCCACCCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

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Db 1126 GCAGTTCTGACTACCACTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCAT 1185

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Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGTGGAGGTAGG 1305

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RESULT 5

US-09-944-944-82  
; Sequence 82, Application US/09944944  
; Patent No. 6929947  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,944  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
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; PRIOR FILING DATE: February 25, 1998  
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; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999



; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. 6929947ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
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; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 82
; LENGTH: 2284
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-944-82

Alignment Scores:
Pred. No.: 1.82e-216 Length: 2284
Score: 2211.00 Matches: 431
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-09-944-929-83 (1-431) x US-09-944-944-82 (1-2284)

QY 1 MetPheGlyGlyGlySerLeuThrThrThrLeuValIleCysPheLeuThr 20
Db 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCTTGACA 285
QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40
Db 286 CTAAGGCTGCTGCTAGTCAGAATTGCCTCAAAAAGAGCTAGAAAGATGTTGTCATTGAC 345
QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60
Db 346 ATCCAGTCATCTCTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATATACTTCAACTCAA 405
QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
Db 406 GAAGACTGCATTAATCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465
QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100

Db 466 TTGATGATCTTCGACACTCGAAAAACAGTAGACAAACCAACTGCTACCTATTTTCTGT 525
QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
Db 526 CCAACGAGGAGAGCCTGTCCATTGAAACACGCAAAAGGACTTATGAGTTACAGGATAATT 585
QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140
Db 586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAAGATTACCCCGAGGAAGATTCT 645
QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160
Db 646 CTCTTACATGGCCAAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACACAGATTAT 705
QY 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
Db 706 TCAAAGCCCAACGATATCTCATGGAGAGACACACTTCTCAGAAAGTTTGGATCCTCAGAT 765
QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTCCCAGCTCCTTGTCTTATAAGGAA 825
QY 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220
Db 826 AAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885
QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaAlaSerProHisThrThrSerAla 240
Db 886 GAAAATGTGAGTGGCTCCAGCTACGGTGGAGTGTCTTCTCCACATACCACTCGGCT 945
QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
Db 946 ACTCCAAAGCCCGCACCTTCTTACCCACCAATGCTTCTCAGTGACACCTTCTGGGACTTCC 1005
QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
Db 1006 CAGCCACAGCTGGCCACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCACG 1065
QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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Db 1246 CTTTCTATGTCAATGTGGAGTCTTCCACTATGATAAAACTGCTTCTCTGGGAAGGTAGG 1305
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Db 1366 TTTGAAAAATGGCTTCTTATCGGTCCCTGCTCTTGTGTCTTGTGTCTTGTGTGTGTGTGT 1425
QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
Db 1426 CTCGTCTCTCTGGGTAGAATCCTTTCCGGAATCACTCCGAGGAAACGTTACTCAAGACTG 1485
QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
Db 1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518

RESULT 6

US-09-990-444-514

; Sequence 514, Application US/09990444

; Patent No. 6930170  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C19  
; CURRENT APPLICATION NUMBER: US/09/990,444  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
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; PRIOR APPLICATION NUMBER: 60/087607  
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; PRIOR FILING DATE: 1998-06-23  
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; PRIOR APPLICATION NUMBER: 60/091360  
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; PRIOR FILING DATE: 1998-07-01  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
;  
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 1.82e-216 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-09-944-929-83 (1-431) x US-09-990-444-514 (1-2284)

Qy 1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleCysPheLeuThr 20  
Db 226 ATGTTCTCGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTGGCTTCCTGACA 285  
Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40  
Db 286 CTAAGGCTGTCTGCTAGTCAGATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345  
Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60

Db 346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCGTATATACTTCAACTCAA 405  
Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAGACTGTCATTAATTCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 465  
Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCCAACTGCTACCTATTTTCTGT 525  
Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
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Qy 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
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Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCCAAAGCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
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RESULT 7

US-09-945-587-82

; Sequence 82, Application US/09945587

; Patent No. 6936254

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/945,587

; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/067,411

; PRIOR FILING DATE: December 3, 1997

; PRIOR APPLICATION NUMBER: 60/069,334

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069335

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278

; PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997

; PRIOR APPLICATION NUMBER: 60/069,696

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,702

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,870

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/069,873

; PRIOR FILING DATE: December 17, 1997

; PRIOR APPLICATION NUMBER: 60/068,017

; PRIOR FILING DATE: December 18, 1997

; PRIOR APPLICATION NUMBER: 60/070,440

; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/074,092

; PRIOR FILING DATE: February 9, 1998

; PRIOR APPLICATION NUMBER: 60/075,945

; PRIOR FILING DATE: February 25, 1998

; PRIOR APPLICATION NUMBER: 60/112,850

; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 60/113,296

; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 60/146,222

; PRIOR FILING DATE: July 28, 1999

; PRIOR APPLICATION NUMBER: PCT/US98/19330

; PRIOR FILING DATE: September 16, 1998

; PRIOR APPLICATION NUMBER: PCT/US98/25108

; PRIOR FILING DATE: December 1, 1998

; PRIOR APPLICATION NUMBER: 09/216,021

; PRIOR FILING DATE: December 16, 1998

; PRIOR APPLICATION NUMBER: 09/218,517

; PRIOR FILING DATE: December 22, 1998

; PRIOR APPLICATION NUMBER: 09/254,311

; PRIOR FILING DATE: March 3, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/12252

; PRIOR FILING DATE: June 22, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: September 15, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/28409

; PRIOR FILING DATE: No. 6936254ember 30, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: No. 6936254ember 30, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/28301

; PRIOR FILING DATE: December 1, 1999

; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: December 16, 1999

; PRIOR APPLICATION NUMBER: PCT/US00/03565

; PRIOR FILING DATE: February 11, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: February 22, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: March 2, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/08439

; PRIOR FILING DATE: March 30, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/14042

; PRIOR FILING DATE: May 22, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/20710

; PRIOR FILING DATE: July 28, 2000

; PRIOR APPLICATION NUMBER: PCT/US00/32678

; PRIOR FILING DATE: December 1, 2000

; PRIOR APPLICATION NUMBER: PCT/US01/06520

; PRIOR FILING DATE: February 28, 2001

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 82

; LENGTH: 2284

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-945-587-82

Alignment Scores:

Pred. No.:	1.82e-216	Length:	2284
Score:	2211.00	Matches:	431
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US-09-944-929-83 (1-431) x US-09-945-587-82 (1-2284)

Qy 1 MetPheGlyGlyGlySerLeuThrThrLeuValIleIleCysPheLeuThr 20  
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Db 226 ATGTTCTTCGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTGCTTCCTGACA 285

Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValIleAsp 40  
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Db 286 CTAAGGCTGCTGCTAGTCAGAAATGCCTCAAAAAGAGCTAGAGATGTTGTCAATTGAC 345

Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
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Db 346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405

Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
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Db 406 GAAGACTGCATTAATTCTTGTCTGTTCAACAAAAACATATCAGGGGGCAAGCATGTAAC 465

Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
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Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACCAACCCACTGCTACTATTTTCTGT 525

Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120



Db 526 CCCAACGAGGAAGCCTGTCCATTGAAACCCAGCAAAAGGACTTATGAGTTACAGGATAATT 585  
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Db 586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAGAGTTACCCAGGAAGATTCT 645  
Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
Db 646 CTCTTACATGGCCAAATTTTCAAGCAGTCACTCCCTAGCCCATCATCACAGATTAT 705  
Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCAAAGCCACCAGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765  
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGACTCCTTGTTATAAGGAA 825  
Qy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluAlaHisLeuLeuPro 220  
Db 826 AAAGGCCATTCTCAGAGTTTCAAAATTTTCTCTGTATCAAGAAATAGCTCATCTGCTGCCT 885  
Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAAATGTGAGTGGCTCCCGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945  
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCCAAGCCCGCCACCTTTTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCTGTCACTTCTCAGCCTCCACG 1065  
Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
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Db 1126 GCAGTTCTGACTACCACTTTCCAGCACCTACGGACTCGAAAGGCAGCTTAGAAACCAT 1185  
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Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
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RESULT 8

US-09-997-333-514  
; Sequence 514, Application US/09997333  
; Patent No. 6953836  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C27  
; CURRENT APPLICATION NUMBER: US/09/997,333  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

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Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60
Db	346	ATCCAGTCATCTCTTTCTAAGGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA	405

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RESULT 9

US-09-992-598-514

; Sequence 514, Application US/09992598

; Patent No. 6956108

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C20

; CURRENT APPLICATION NUMBER: US/09/992,598

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

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; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089653  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089801  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089907  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089908  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: 60/089947  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/089948  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/089952  
; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: 60/090246  
; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 60/090252  
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; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: 60/090349  
; PRIOR FILING DATE: 1998-06-23  
; PRIOR APPLICATION NUMBER: 60/090355  
; PRIOR FILING DATE: 1998-06-23  
; PRIOR APPLICATION NUMBER: 60/090429  
; PRIOR FILING DATE: 1998-06-24  
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; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090445  
; PRIOR FILING DATE: 1998-06-24  
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; PRIOR FILING DATE: 1998-06-26  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091544  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 1.82e-216 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-09-944-929-83 (1-431) x US-09-992-598-514 (1-2284)

Qy 1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20  
Db 226 ATGTTCTTCGGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTGCTTCTGACA 285



QY 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40  
Db 286 CTAAGGCTGTCTGTAGTCAGAAATTGCCTCAAAAAGAGTCTAGAGAGTGTGTCAATTGAC 345

QY 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
Db 346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATATACTTCAACTCAA 405

QY 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAGACTGCATTAAATTCTTGCTGTTCAACAAAAACATATACAGGGACAAAGCATGTAAAC 465

QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCCAACTGCTACCTATTTTCTGT 525

QY 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
Db 526 CCCAACGAGGAAGCCTGTCCATTGAAACCCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

QY 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
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QY 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
Db 646 CTCTTACATGGCCAAATTTTCAACAGCAGTCACCTCCCTAGCCCATCATCACAGATTAT 705

QY 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCAAAGCCCAACCGATATCTCATGGAGAGACACTTCTCAGAAAGTTTGGATCCTCAGAT 765

QY 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCCTTGCTTATAAGGAA 825

QY 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 826 AAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885

QY 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

QY 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

QY 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCACG 1065

QY 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1066 ACCCTCATTTCTACAGTTTTCACGGGCTCGGGCTACACTCCAAGCAATGGCTACAACA 1125

QY 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1126 GCAGTTCTGACTACACCTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCAT 1185

QY 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db 1186 CCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCCTACTGCA 1245

QY 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg 360  
Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGTAGG 1305

QY 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
Db 1306 GAGGCCAGTCCAGGCAAGTTCTCTCCAGGGCAGTGTTCAGAAATCAGTACGGCCCTTCCA 1365

QY 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
Db 1366 TTTGAAAAAATGGCTTCTTATCGGTCCTGCTCTTTGGTGTCTCTTCTGCTGATAGGC 1425

QY 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgLysArgTyrSerArgLeu 420  
Db 1426 CTCGTCCTCCTGGGTAGATCCTTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518

RESULT 10  
US-09-989-735-514  
; Sequence 514, Application US/09989735  
; Patent No. 6972185  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C61  
; CURRENT APPLICATION NUMBER: US/09/989,735  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
; PRIOR FILING DATE: 1998-05-28  
; PRIOR APPLICATION NUMBER: 60/087607  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087609  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; PRIOR APPLICATION NUMBER: 60/087827



Best Local Similarity: 100.0%				Mismatches: 0			
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Qy	1	MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr	20				
Db	226	ATGTTCTTCGGGGAGAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA	285				
Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp	40				
Db	286	CTAAGGCTGTCTGCTAGTCAGAATTGCCCTCAAAAAAGAGTCTAGAAGATGTTGTCAATTGAC	345				
Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60				
Db	346	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATATCTTCAACTCAA	405				
Qy	61	GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80				
Db	406	GAAGACTGCATTAAATTTCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAAC	465				
Qy	81	LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys	100				
Db	466	TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCCCACTGCTACCTATTTTCTGT	525				
Qy	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120				
Db	526	CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT	585				
Qy	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140				
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Qy	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160				
Db	646	CTCTTACATGGCCAAATTTTCAAGCAGTCACTCCCCTAGCCCCATCATCACAGATTAT	705				
Qy	161	SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp	180				
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Qy	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200				
Db	766	CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCCTTGCTTATAAGGAA	825				
Qy	201	LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220				
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Qy	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240				
Db	886	GAAAAATGTGAGTGGCTCCAGCTACGGTGCGAGTTGCTTCTCCACATACCACCTCGGCT	945				
Qy	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260				
Db	946	ACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC	1005				
Qy	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280				
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Db	1066	ACCCTCATTTCTACAGTTTTTTACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA	1125				
Qy	301	AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320				
Db	1126	GCAGTTCTGACTACCACTTTTACGGCACCTTACGGACTCGAAAGGCAGCTTAGAAACCAT	1185				
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Db	1306	GAGGCCAGTCCAGGCAGTTCTCTCCAGGCGCAGTGTCCAGAAAAATCAGTACGGCCTTCCA	1365
QY	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1366	TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCTGCTCCTGGTGATAGGC	1425
QY	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu	420
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QY	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
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; Sequence 514, Application US/09989726			
; Patent No. 7018811			
; GENERAL INFORMATION:			
; APPLICANT: Ashkenazi, Avi J.			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Napier, Mary A.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: P2730P1C60			
; CURRENT APPLICATION NUMBER: US/09/989,726			
; CURRENT FILING DATE: 2001-11-19			
; PRIOR APPLICATION NUMBER: 60/049787			
; PRIOR FILING DATE: 1997-06-16			
; PRIOR APPLICATION NUMBER: 60/062250			
; PRIOR FILING DATE: 1997-10-17			
; PRIOR APPLICATION NUMBER: 60/065186			
; PRIOR FILING DATE: 1997-11-12			
; PRIOR APPLICATION NUMBER: 60/065311			
; PRIOR FILING DATE: 1997-11-13			
; PRIOR APPLICATION NUMBER: 60/066770			
; PRIOR FILING DATE: 1997-11-24			
; PRIOR APPLICATION NUMBER: 60/075945			
; PRIOR FILING DATE: 1998-02-25			
; PRIOR APPLICATION NUMBER: 60/078910			
; PRIOR FILING DATE: 1998-03-20			
; PRIOR APPLICATION NUMBER: 60/083322			
; PRIOR FILING DATE: 1998-04-28			
; PRIOR APPLICATION NUMBER: 60/084600			
; PRIOR FILING DATE: 1998-05-07			





; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 1.82e-216 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 5 Gaps: 0

US-09-944-929-83 (1-431) x US-09-989-726-514 (1-2284)

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Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAasp 40  
Db 286 CTAAGGCTGTCTGCTAGTCAGAAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGAC 345  
Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
Db 346 ATCCAGTCATCTCTTTCTAAGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405  
Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAGACTGCATTATTTCTTGCTGTTCAACAAAAACATATACAGGGGACAAAGCATGTAAC 465  
Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCAACTGCTACCTATTTTCTGT 525  
Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
Db 526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585  
Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
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Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCAAAGCCCAACCGATATCTCATGGAGAGACACACTTTTCTCAGAAAGTTTGGATCCTCAGAT 765  
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCCTTGCTTATAAGGAA 825  
Qy 201 LysGlyHisSerGlnSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 826 AAAGGCCATTCTCAGAGTTTCAAAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCT 885  
Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAAAATGTGAGTGGCTCCAGCTACGGTGCGAGTTGCTTCTCCACATACCACTCGGCT 945  
Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCCAAAGCCCGCCACCTTTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005  
Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCAGTCTCACTTCTCAGCCTCCCAAG 1065  
Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300

Db 1066 ACCCTCATTTCTACAGTTTTTACACGGGCTGCGGTACACTCCAAGCAATGGCTACAACA 1125  
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Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
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Db 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTCTGGTGATAGGC 1425  
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Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518

RESULT 12

US-09-944-884-82  
; Sequence 82, Application US/09944884  
; Patent No. 7018837  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,884  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 82  
; LENGTH: 2284  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-944-884-82

Alignment Scores:  
Pred. No.: 1.82e-216 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 5 Gaps: 0

US-09-944-929-83 (1-431) x US-09-944-884-82 (1-2284)

Qy 1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleCysPheLeuThr 20  
Db 226 ATGTTCTCGGGGAGAGGAGCTTGACTTACACTTTGGTAATAATTGCTTCCTGACA 285

Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40  
Db 286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCAATGAC 345

Qy 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
Db 346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCGTATATACTTCAACTCAA 405

Qy 61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 406 GAAAGACTGCATTAAATCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC 465

Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 466 TTGATGATCTTCGACACTCGAAAAACAGTAGACAACCCAACTGCTACCTATTTTCTGT 525

Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
Db 526 CCCAAGGAGGAGCCCTGCTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585

Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
Db 586 ACAGATTTTCCATCTTTGACAGAAAATTTGCCAAGCCAAAGAGTTACCCAGGAAGATTCT 645

Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
Db 646 CTCTTACATGGCCAAATTTTCAAGCAGTCACCTCCCTTAGCCCCATCATCACAGATTAT 705

Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 706 TCAAGCCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765

Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuAlaTyrLysGlu 200  
Db 766 CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCAGCTCCTTGCTTATAAGGAA 825

Qy 201 LysGlyHisSerGlnSerSerGlnPheSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 826 AAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCGCT 885

Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240  
Db 886 GAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945

Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 946 ACTCCAAAGCCCGCCACCCTTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005

Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1006 CAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTCAGCCTCCACG 1065

Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1066 ACCCTCATTTCTACAGTTTTTACACGGGCTCGGGCTACACTCCAAGCAATGGCTACAACA 1125

Qy 301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185

Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db 1186 CCGTTTACAGAAATCTCCAACTTAACCTTTGAACACAGGGAATGTGTATAACCTTACTGCA 1245

Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGTAGG 1305

Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
Db 1306 GAGGCCAGTCCAGGCAGTTCTCTCCAGGCAGTGTTCAGAAAATCAGTACGGCCTTCCA 1365

Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
Db 1366 TTTGAAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTGTTCTGGTATAGGC 1425

Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420  
Db 1426 CTCGTCTCTCTGGGTAGAAATCCTTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485

Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518

RESULT 13

US-09-997-514-514  
; Sequence 514, Application US/099997514  
; Patent No. 7019116

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C46

; CURRENT APPLICATION NUMBER: US/09/997,514

; CURRENT FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600

; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/087106

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02



Alignment Scores:									
Pred. No.:	1.82e-216	Length:	2284						
Score:	2211.00	Matches:	431						
Percent Similarity:	100.0%	Conservative:	0						
Best Local Similarity:	100.0%	Mismatches:	0						
Query Match:	100.0%	Indels:	0						
DB:	5	Gaps:	0						
US-09-944-929-83 (1-431) x US-09-997-514-514 (1-2284)									
Qy	1	MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr	20						
Db	226	ATGTTCTTCGGGGAGAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA	285						
Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp	40						
Db	286	CTAAGGCTGCTCTGTAGTCAGAAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGAC	345						
Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60						
Db	346	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCCGTATATACTTCAACTCAA	405						
Qy	61	GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80						
Db	406	GAAGACTGCATTAATTTCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC	465						
Qy	81	LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrIleuPhePheCys	100						
Db	466	TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTCTGT	525						
Qy	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120						
Db	526	CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT	585						
Qy	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140						
Db	586	ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCCAAGAGTTACCCCGAGGAATTCT	645						
Qy	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160						
Db	646	CTCTTACATGGCCAAATTTTCAAGCAGTCACCTCCCTAGCCCATCATCACAGATTAT	705						
Qy	161	SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp	180						
Db	706	TCAAAGCCCAACCGATATCTCATGGAGAGACACACTTCTCAGAAAGTTTGGATCCTCAGAT	765						
Qy	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200						
Db	766	CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCACCTCCTGCTTATAAGGAA	825						
Qy	201	LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220						
Db	826	AAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAATAGCTCATCTGCTGCCT	885						
Qy	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240						
Db	886	GAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCGGCT	945						
Qy	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260						
Db	946	ACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAAGTACACCTTCTGGGACTTCC	1005						
Qy	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280						
Db	1006	CAGCCACAGCTGGCCACACACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCACG	1065						
Qy	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300						
Db	1066	ACCCTCATTTCTACAGTTTTCACCGGGCTCGGGCTACACTCCAAGCAATGGCTACAACA	1125						
Qy	301	AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320						

Qy	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
Db	1186	CCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTTACTGCA	1245
Qy	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTyrGluGlyArg	360
Db	1246	CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGTAGG	1305
Qy	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1306	GAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCAGAGAAATCAGTACGGCTTCCA	1365
Qy	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1366	TTTGAATAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCCTGGTATAGGC	1425
Qy	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu	420
Db	1426	CTCGTCTCTCTGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG	1485
Qy	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
Db	1486	GATTATTGATCAATGGGATCTATGTGGACATC	1518
RESULT 14			
US-09-989-728-514			
; Sequence 514, Application US/09989728			
; Patent No. 7029873			
; GENERAL INFORMATION:			
; APPLICANT: Ashkenazi, Avi J.			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan L.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Kljavin, Ivar J.			
; APPLICANT: Napier, Mary A.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			
; APPLICANT: Roy, Margaret Ann			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Williams, P. Mickey			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
; TITLE OF INVENTION: Acids Encoding the Same			
; FILE REFERENCE: P2730P1C72			
; CURRENT APPLICATION NUMBER: US/09/989,728			
; CURRENT FILING DATE: 2001-11-20			
; PRIOR APPLICATION NUMBER: 60/049787			
; PRIOR FILING DATE: 1997-06-16			
; PRIOR APPLICATION NUMBER: 60/062250			
; PRIOR FILING DATE: 1997-10-17			
; PRIOR APPLICATION NUMBER: 60/065186			
; PRIOR FILING DATE: 1997-11-12			
; PRIOR APPLICATION NUMBER: 60/065311			
; PRIOR FILING DATE: 1997-11-13			
; PRIOR APPLICATION NUMBER: 60/066770			
; PRIOR FILING DATE: 1997-11-24			
; PRIOR APPLICATION NUMBER: 60/075945			
; PRIOR FILING DATE: 1998-02-25			
; PRIOR APPLICATION NUMBER: 60/078910			

RESULT 14

US-09-989-728-514  
; Sequence 514, Application US/09989728  
; Patent No. 7029873  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C72  
; CURRENT APPLICATION NUMBER: US/09/989, 728  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910

Db 1126 GCAGTTCTGACTACCACCTTTTCAGGCACCTACGGACTCGAAAGGACGCTTAGAAACCATTA 1185  
Qy 321 PropheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db 1186 CCGTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCCTACTGCA 1245  
Qy 341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360  
Db 1246 CTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGGTAGG 1305  
Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
Db 1306 GAGGCCAGTCCAGGCAGTTCTCTCCAGGCAGTGTTCAGAAAAATCAGTACGGCCTTCCA 1365  
Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
Db 1366 TTTGAAAAAATGGCTTCTTATFCGGGTCCCTGCTCTTTGGTGTCTCTGTCTGGTGATAGGC 1425  
Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420  
Db 1426 CTCGTCTCTCTGGGTAGAAATCCTTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485  
Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
Db 1486 GATTATTGATCAATGGGATCTATGTGGACATC 1518



;	PRIOR APPLICATION NUMBER:	60/089599
;	PRIOR FILING DATE:	1998-06-17
;	PRIOR APPLICATION NUMBER:	60/089600
;	PRIOR FILING DATE:	1998-06-17
;	PRIOR APPLICATION NUMBER:	60/089653
;	PRIOR FILING DATE:	1998-06-17
;	PRIOR APPLICATION NUMBER:	60/089801
;	PRIOR FILING DATE:	1998-06-18
;	PRIOR APPLICATION NUMBER:	60/089907
;	PRIOR FILING DATE:	1998-06-18
;	PRIOR APPLICATION NUMBER:	60/089908
;	PRIOR FILING DATE:	1998-06-18
;	PRIOR APPLICATION NUMBER:	60/089947
;	PRIOR FILING DATE:	1998-06-19
;	PRIOR APPLICATION NUMBER:	60/089948
;	PRIOR FILING DATE:	1998-06-19
;	PRIOR APPLICATION NUMBER:	60/089952
;	PRIOR FILING DATE:	1998-06-19
;	PRIOR APPLICATION NUMBER:	60/090246
;	PRIOR FILING DATE:	1998-06-22
;	PRIOR APPLICATION NUMBER:	60/090252
;	PRIOR FILING DATE:	1998-06-22
;	PRIOR APPLICATION NUMBER:	60/090254
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;	PRIOR APPLICATION NUMBER:	60/090349
;	PRIOR FILING DATE:	1998-06-23
;	PRIOR APPLICATION NUMBER:	60/090355
;	PRIOR FILING DATE:	1998-06-23
;	PRIOR APPLICATION NUMBER:	60/090429
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090431
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090435
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090444
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090445
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090472
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090535
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090540
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090542
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090557
;	PRIOR FILING DATE:	1998-06-24
;	PRIOR APPLICATION NUMBER:	60/090676
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090678
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090690
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090694
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;	PRIOR APPLICATION NUMBER:	60/090695
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;	PRIOR APPLICATION NUMBER:	60/090696
;	PRIOR FILING DATE:	1998-06-25
;	PRIOR APPLICATION NUMBER:	60/090862
;	PRIOR FILING DATE:	1998-06-26
;	PRIOR APPLICATION NUMBER:	60/090863
;	PRIOR FILING DATE:	1998-06-26
;	PRIOR APPLICATION NUMBER:	60/091360
;	PRIOR FILING DATE:	1998-07-01
;	PRIOR APPLICATION NUMBER:	60/091478
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/091544
;	PRIOR FILING DATE:	1998-07-01
;	PRIOR APPLICATION NUMBER:	60/091519
;	PRIOR FILING DATE:	1998-07-02
;	PRIOR APPLICATION NUMBER:	60/091626

; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 1.82e-216 Length: 2284  
Score: 2211.00 Matches: 431  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 5 Gaps: 0

US-09-944-929-83 (1-431) x US-09-989-728-514 (1-2284)

QY	1	MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleCysPheLeuThr	20
Db	226	ATGTTCTTCGGGGAGAGGAGCTTGACTTACACTTTTGCTAATAATTGCTTCCTGACA	285
QY	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp	40
Db	286	CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCTATGAC	345
QY	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60
Db	346	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA	405
QY	61	GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80
Db	406	GAAAGACTGCATTAAATTCCTGTGTTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC	465
QY	81	LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys	100
Db	466	TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCAACTGCTACCTATTTTCTGT	525
QY	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120
Db	526	CCCAACGAGGAAGCCCTGCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT	585
QY	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140
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QY	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240
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QY	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280

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US-09-997-349-514  
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; Patent No. 7034106  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C37  
; CURRENT APPLICATION NUMBER: US/09/997,349  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17



;  
; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091544  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091626  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091633  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
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; PRIOR FILING DATE: 1998-07-09

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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94	2211	100.0	2284	8	US-10-429-667-82	Sequence 82, Appl
96	2211	100.0	2284	9	US-10-677-471-82	Sequence 82, Appl
97	2211	100.0	2284	9	US-10-677-669-82	Sequence 82, Appl
98	2211	100.0	2284	10	US-10-735-014-82	Sequence 82, Appl
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c 162	197	8.9	10346	16	US-10-100-683-12711	Sequence 12711, A	685	160.5	7.3	1134	23	US-11-371-354-56046	Sequence 56046, A
c 163	197	8.9	10346	23	US-11-001-793-12711	Sequence 12711, A	686	160.5	7.3	1638	9	US-10-302-172-412	Sequence 412, App
164	197	8.9	10615	23	US-11-033-056A-38342	Sequence 38342, A	687	160.5	7.3	2753	18	US-11-097-143-40007	Sequence 40007, A
165	196.5	8.9	1826	8	US-10-120-988-230	Sequence 230, App	688	160.5	7.3	22622	18	US-11-097-143-40006	Sequence 40006, A
166	195.5	8.8	1969	23	US-11-371-354-10439	Sequence 10439, A	689	160	7.2	5564	11	US-10-956-157-4662	Sequence 4662, Ap
c 167	195.5	8.8	2095	9	US-10-276-774-51	Sequence 51, Appl	690	160	7.2	6564	10	US-10-723-860-5185	Sequence 5185, Ap
168	194.5	8.8	1642	9	US-10-351-334-70	Sequence 70, Appl	691	160	7.2	7286	26	US-11-443-428A-304824	Sequence 304824,
169	194.5	8.8	1642	16	US-10-100-683-3775	Sequence 3775, Ap	692	160	7.2	7286	26	US-11-443-428A-304821	Sequence 304821,
170	194.5	8.8	1642	21	US-11-229-769-70	Sequence 70, Appl	693	160	7.2	7286	26	US-11-443-428A-304823	Sequence 304823,
171	194.5	8.8	1642	23	US-11-001-793-3775	Sequence 3775, Ap	694	160	7.2	8484	26	US-11-443-428A-304856	Sequence 304856,
172	194	8.8	1895	16	US-10-100-683-516	Sequence 516, App	695	160	7.2	8850	26	US-11-443-428A-304854	Sequence 304854,
173	194	8.8	1895	23	US-11-001-793-516	Sequence 516, App	696	160	7.2	8992	26	US-11-443-428A-304855	Sequence 304855,
174	188	8.5	478	3	US-09-918-995-32190	Sequence 32190, A	697	160	7.2	9081	26	US-11-443-428A-304851	Sequence 304851,
175	188	8.5	1350	23	US-11-371-354-632	Sequence 632, App	698	160	7.2	9138	26	US-11-443-428A-304850	Sequence 304850,
176	188	8.5	1350	23	US-11-371-354-4447	Sequence 4447, Ap	699	160	7.2	9175	26	US-11-443-428A-304816	Sequence 304816,
177	188	8.5	1350	23	US-11-371-354-57982	Sequence 57982, A	700	160	7.2	9344	26	US-11-443-428A-304849	Sequence 304849,
623	188	8.5	1661	10	US-10-931-886-223	Sequence 223, App	701	160	7.2	9408	26	US-11-443-428A-304819	Sequence 304819,
625	188	8.5	1661	11	US-10-955-952-223	Sequence 223, App	702	160	7.2	9424	26	US-11-443-428A-304815	Sequence 304815,
627	188	8.5	1661	12	US-10-973-115B-223	Sequence 223, App	703	160	7.2	9812	26	US-11-443-428A-304848	Sequence 304848,
631	188	8.5	1661	14	US-10-964-241-223	Sequence 223, App	704	160	7.2	9812	26	US-11-443-428A-304852	Sequence 304852,
632	188	8.5	1661	21	US-11-290-153-223	Sequence 223, App	705	160	7.2	10174	7	US-10-171-311-82	Sequence 82, Appl
633	186.5	8.4	2081	21	US-11-266-748A-74381	Sequence 74381, A	706	160	7.2	10174	16	US-10-567-867-471	Sequence 471, App
c 634	186.5	8.4	2081	21	US-11-266-748A-127192	Sequence 127192,	707	160	7.2	10174	23	US-11-510-530-82	Sequence 82, Appl
635	184.5	8.3	1153	26	US-11-443-428A-50583	Sequence 50583, A	708	160	7.2	10361	12	US-10-330-773-629	Sequence 629, App
636	178.5	8.1	1053	26	US-11-443-428A-50592	Sequence 50592, A	709	160	7.2	10361	14	US-10-540-898-629	Sequence 629, App
637	175	7.9	30542	11	US-10-737-082-74	Sequence 74, Appl	710	160	7.2	10383	26	US-11-582-861-12175	Sequence 12175, A
638	175	7.9	30542	11	US-10-765-790-74	Sequence 74, Appl	711	160	7.2	10586	26	US-11-443-428A-304813	Sequence 304813,
639	172.5	7.8	7587	26	US-11-443-428A-732416	Sequence 732416,	712	160	7.2	11275	26	US-11-443-428A-304820	Sequence 304820,
640	172.5	7.8	7588	26	US-11-443-428A-488748	Sequence 488748,	713	160	7.2	11315	26	US-11-443-428A-304812	Sequence 304812,
641	172.5	7.8	8521	26	US-11-443-428A-488746	Sequence 488746,	714	160	7.2	11400	26	US-11-443-428A-304853	Sequence 304853,
642	172.5	7.8	8679	26	US-11-443-428A-488744	Sequence 488744,	715	160	7.2	11446	26	US-11-443-428A-304817	Sequence 304817,
643	172.5	7.8	8959	26	US-11-443-428A-732412	Sequence 732412,	716	160	7.2	11464	26	US-11-443-428A-304818	Sequence 304818,
644	172.5	7.8	8960	26	US-11-443-428A-488737	Sequence 488737,	717	160	7.2	11509	26	US-11-443-428A-304814	Sequence 304814,
645	172.5	7.8	9625	26	US-11-443-428A-732415	Sequence 732415,	718	160	7.2	11510	26	US-11-443-428A-304845	Sequence 304845,
646	172.5	7.8	9626	26	US-11-443-428A-488742	Sequence 488742,	719	160	7.2	11563	26	US-11-443-428A-304847	Sequence 304847,
647	172.5	7.8	9811	26	US-11-443-428A-732414	Sequence 732414,	720	159	7.2	5451	26	US-11-443-428A-304828	Sequence 304828,
648	172.5	7.8	9812	26	US-11-443-428A-488741	Sequence 488741,	721	158.5	7.2	1604	9	US-10-312-352-66	Sequence 66, Appl
649	172.5	7.8	10042	26	US-11-443-428A-732413	Sequence 732413,	722	158.5	7.2	2346	26	US-11-443-428A-72983	Sequence 72983, A
650	172.5	7.8	10043	26	US-11-443-428A-488734	Sequence 488734,	723	158.5	7.2	2388	9	US-10-115-635-295	Sequence 295, App
651	172.5	7.8	15720	3	US-09-922-217-1058	Sequence 1058, Ap	724	157.5	7.1	1779	17	US-10-537-743-57	Sequence 57, Appl
652	172.5	7.8	15720	3	US-09-833-263-1058	Sequence 1058, Ap	725	157.5	7.1	1806	26	US-11-443-428A-50580	Sequence 50580, A
653	172.5	7.8	15720	3	US-09-873-367C-695	Sequence 695, App	726	157.5	7.1	2350	11	US-10-756-149-1514	Sequence 1514, Ap
654	172.5	7.8	15720	7	US-10-025-380-1058	Sequence 1058, Ap	727	157.5	7.1	2429	7	US-10-149-819-28	Sequence 28, Appl
655	172.5	7.8	15720	8	US-10-393-590-14	Sequence 14, Appl	728	157.5	7.1	4892	26	US-11-443-428A-73514	Sequence 73514, A
656	172.5	7.8	15720	8	US-10-393-567-14	Sequence 14, Appl	729	157	7.1	16562	16	US-10-940-774-13892	Sequence 13892, A
657	172.5	7.8	15720	8	US-10-394-087-13	Sequence 13, Appl	730	157	7.1	51879	16	US-10-990-328-94645	Sequence 94645, A
658	172.5	7.8	15720	8	US-10-394-087-14	Sequence 14, Appl	c 731	156	7.1	2300	18	US-11-097-143-39130	Sequence 39130, A
659	172.5	7.8	15720	9	US-10-734-564-54	Sequence 54, Appl	c 732	156	7.1	3161	18	US-11-097-143-39133	Sequence 39133, A
660	172.5	7.8	15720	11	US-10-843-641A-695	Sequence 695, App	c 733	156	7.1	745443	15	US-10-915-727-12213	Sequence 12213, A
661	172.5	7.8	15720	11	US-10-887-553A-340	Sequence 340, App	734	155.5	7.0	5403	3	US-09-745-008-33	Sequence 33, Appl
662	172.5	7.8	15720	14	US-10-700-439-85	Sequence 85, Appl	735	155.5	7.0	5403	22	US-11-365-743-33	Sequence 33, Appl
663	172.5	7.8	15720	14	US-10-541-749-36	Sequence 36, Appl	736	155	7.0	2922	8	US-10-108-260A-1446	Sequence 1446, Ap
664	172.5	7.8	15720	14	US-10-219-051B-10429	Sequence 10429, A	737	155	7.0	2922	21	US-11-293-697-1446	Sequence 1446, Ap
665	172.5	7.8	15720	14	US-10-219-051B-13788	Sequence 13788, A	738	154.5	7.0	6687	26	US-11-443-428A-637776	Sequence 637776,
666	172.5	7.8	15720	20	US-11-108-172-1058	Sequence 1058, Ap	739	154.5	7.0	7760	26	US-11-443-428A-637774	Sequence 637774,
667	172.5	7.8	15720	21	US-11-105-233-118	Sequence 118, App	740	154.5	7.0	9571	26	US-11-443-428A-637773	Sequence 637773,
668	172.5	7.8	15720	21	US-11-266-748A-56381	Sequence 56381, A	741	154.5	7.0	9690	26	US-11-443-428A-637769	Sequence 637769,
669	172.5	7.8	15730	26	US-11-443-428A-732409	Sequence 732409,	742	154.5	7.0	9730	26	US-11-443-428A-637770	Sequence 637770,
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c 673	169.5	7.7	1000	21	US-11-266-748A-341937	Sequence 341937,	746	154	7.0	127943	12	US-10-330-773-628	Sequence 628, App
674	169.5	7.7	1000	21	US-11-266-748A-401794	Sequence 401794,	747	154	7.0	127943	14	US-10-540-898-628	Sequence 628, App
c 675	169.5	7.7	1000	21	US-11-266-748A-472840	Sequence 472840,	c 748	153.5	6.9	4755	18	US-11-097-143-40483	Sequence 40483, A
676	167.5	7.6	1964	21	US-11-266-748A-369782	Sequence 369782,	749	153.5	6.9	149430	10	US-10-626-832-1	Sequence 1, Appli
677	167.5	7.6	1964	21	US-11-266-748A-389221	Sequence 389221,	750	152.5	6.9	6029	26	US-11-443-428A-731600	Sequence 731600,
c 678	167.5	7.6	1964	21	US-11-266-748A-453161	Sequence 453161,	751	152	6.9	1129	26	US-11-443-428A-71320	Sequence 71320, A
679	164	7.4	3437	26	US-11-443-428A-73516	Sequence 73516, A	752	152	6.9	1679	26	US-11-443-428A-125231	Sequence 125231,

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755	152	6.9	2658	26	US-11-443-428A-71847	Sequence 71847, A	828	145.5	6.6	7593	11	US-10-363-483A-4842	Sequence 4842, Ap
756	152	6.9	2791	26	US-11-443-428A-71850	Sequence 71850, A	C 829	145.5	6.6	15172	23	US-11-491-125A-67810	Sequence 67810, A
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758	152	6.9	5795	14	US-10-219-051B-8003	Sequence 8003, Ap	C 831	145	6.6	571	23	US-11-001-793-12709	Sequence 12709, A
759	152	6.9	5795	16	US-10-515-373-3291	Sequence 3291, Ap	C 832	145	6.6	1088	16	US-10-703-032-103747	Sequence 103747,
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761	152	6.9	5795	23	US-11-059-535-2295	Sequence 2295, Ap	834	145	6.6	3990	26	US-11-443-428A-73519	Sequence 73519, A
762	152	6.9	13555	3	US-09-764-891-7281	Sequence 7281, Ap	835	145	6.6	13631	18	US-11-097-143-27772	Sequence 27772, A
763	151.5	6.9	4829	18	US-11-097-143-17339	Sequence 17339, A	C 836	145	6.6	961710	16	US-10-990-328-94469	Sequence 94469, A
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765	151.5	6.9	57082	14	US-10-475-117-311	Sequence 311, App	838	144.5	6.5	2156	23	US-11-158-863-167	Sequence 167, App
C 766	151	6.8	1571	21	US-11-266-748A-15633	Sequence 15633, A	839	144.5	6.5	2630	25	US-11-433-832-44540	Sequence 44540, A
C 767	151	6.8	1571	21	US-11-266-748A-21283	Sequence 21283, A	840	144.5	6.5	3423	10	US-10-793-639-91	Sequence 91, Appl
C 768	151	6.8	1571	21	US-11-266-748A-65013	Sequence 65013, A	841	144.5	6.5	3642	26	US-11-443-428A-469360	Sequence 469360,
C 769	151	6.8	1571	21	US-11-266-748A-67869	Sequence 67869, A	842	144.5	6.5	4383	8	US-10-295-027-427	Sequence 427, App
770	151	6.8	5089	26	US-11-443-428A-73518	Sequence 73518, A	843	144.5	6.5	37292	16	US-10-990-328-94032	Sequence 94032, A
771	151	6.8	5929	18	US-11-097-143-6038	Sequence 6038, Ap	C 844	144.5	6.5	768043	23	US-11-033-056A-35581	Sequence 35581, A
C 772	151	6.8	11963	18	US-11-097-143-6037	Sequence 6037, Ap	C 845	144.5	6.5	768043	23	US-11-033-056A-36107	Sequence 36107, A
773	150.5	6.8	929	16	US-10-703-032-2917	Sequence 2917, Ap	C 846	144.5	6.5	768043	23	US-11-033-056A-36550	Sequence 36550, A
774	150.5	6.8	2583	21	US-11-292-431-2	Sequence 2, Appli	C 847	144.5	6.5	768043	23	US-11-033-056A-37683	Sequence 37683, A
775	150.5	6.8	3090	21	US-11-292-431-1	Sequence 1, Appli	C 848	144.5	6.5	788459	23	US-11-033-056A-37294	Sequence 37294, A
776	150.5	6.8	150223	9	US-10-624-149A-1	Sequence 1, Appli	849	144.5	6.5	924430	15	US-10-915-727-12216	Sequence 12216, A
777	150.5	6.8	150223	27	US-11-550-934-1	Sequence 1, Appli	850	144.5	6.5	1090936	15	US-10-915-727-12210	Sequence 12210, A
778	150	6.8	513	3	US-09-998-598-821	Sequence 821, App	C 851	144	6.5	2244	9	US-10-437-963-90584	Sequence 90584, A
C 779	150	6.8	513	3	US-09-998-598-1376	Sequence 1376, Ap	852	144	6.5	2558	13	US-10-449-902-26396	Sequence 26396, A
780	150	6.8	13014	25	US-11-066-316A-9888	Sequence 9888, Ap	853	143.5	6.5	1038	12	US-10-932-182A-166937	Sequence 166937,
781	150	6.8	38546	25	US-11-066-316A-380	Sequence 380, App	854	143.5	6.5	1038	21	US-11-217-529-166937	Sequence 166937,
782	150	6.8	38665	25	US-11-066-316A-379	Sequence 379, App	855	143.5	6.5	1851	12	US-10-932-182A-76890	Sequence 76890, A
783	150	6.8	39790	25	US-11-066-316A-382	Sequence 382, App	856	143.5	6.5	1851	21	US-11-217-529-76890	Sequence 76890, A
784	150	6.8	41958	25	US-11-066-316A-383	Sequence 383, App	857	143.5	6.5	2517	18	US-11-097-143-38435	Sequence 38435, A
785	150	6.8	43342	25	US-11-066-316A-384	Sequence 384, App	858	143.5	6.5	2607	18	US-11-097-143-21794	Sequence 21794, A
786	150	6.8	158834	25	US-11-066-316A-9976	Sequence 9976, Ap	C 859	143.5	6.5	5146	18	US-11-097-143-38434	Sequence 38434, A
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788	149	6.7	515	10	US-10-357-930-47904	Sequence 47904, A	C 861	143.5	6.5	7782	18	US-11-097-143-36208	Sequence 36208, A
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790	149	6.7	4911	12	US-10-932-182A-75783	Sequence 75783, A	863	143	6.5	889	25	US-11-433-832-13791	Sequence 13791, A
791	149	6.7	4911	21	US-11-217-529-75783	Sequence 75783, A	864	143	6.5	1543	21	US-11-266-748A-262390	Sequence 262390,
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795	148	6.7	1044	11	US-10-508-263-109	Sequence 109, App	C 868	143	6.5	2336	18	US-11-097-143-35734	Sequence 35734, A
C 796	148	6.7	1751	9	US-10-437-963-9763	Sequence 9763, Ap	869	143	6.5	2610	12	US-10-932-182A-81636	Sequence 81636, A
797	148	6.7	2220	26	US-11-443-428A-71848	Sequence 71848, A	870	143	6.5	2610	21	US-11-217-529-81636	Sequence 81636, A
798	148	6.7	2563	16	US-10-703-032-2953	Sequence 2953, Ap	871	143	6.5	3789	23	US-11-584-793-25	Sequence 25, Appl
C 799	148	6.7	2570	9	US-10-138-588-73	Sequence 73, Appl	872	143	6.5	3791	26	US-11-443-428A-533457	Sequence 533457,
C 800	148	6.7	2859	26	US-11-443-428A-477722	Sequence 477722,	873	143	6.5	1971884	22	US-11-184-236-70	Sequence 70, Appl
C 801	148	6.7	7417	18	US-11-097-143-21793	Sequence 21793, A	874	143	6.5	2540030	22	US-11-184-236-69	Sequence 69, Appl
802	148	6.7	31497	14	US-10-475-117-309	Sequence 309, App	875	143	6.5	4647455	14	US-10-641-321-205	Sequence 205, App
C 803	148	6.7	39746	18	US-11-097-143-17338	Sequence 17338, A	C 876	142.5	6.4	1190	9	US-10-437-963-87233	Sequence 87233, A
804	148	6.7	66765	9	US-10-715-066-4	Sequence 4, Appli	877	142.5	6.4	1461	9	US-10-437-963-14952	Sequence 14952, A
805	148	6.7	66765	13	US-10-544-944-2	Sequence 2, Appli	878	142.5	6.4	1843	13	US-10-449-902-12684	Sequence 12684, A
806	148	6.7	66765	14	US-10-475-117-314	Sequence 314, App	879	142.5	6.4	2918	13	US-10-449-902-12834	Sequence 12834, A
807	148	6.7	66765	21	US-11-266-748A-23729	Sequence 23729, A	880	142.5	6.4	5731	21	US-11-266-748A-32357	Sequence 32357, A
808	147.5	6.7	1236	7	US-10-077-584-3	Sequence 3, Appli	881	142	6.4	803	26	US-11-443-428A-580301	Sequence 580301,
809	147.5	6.7	1236	22	US-11-363-870-3	Sequence 3, Appli	882	142	6.4	2917	14	US-10-541-749-95	Sequence 95, Appl
810	147.5	6.7	1236	22	US-11-363-869-3	Sequence 3, Appli	883	142	6.4	2917	21	US-11-266-748A-59060	Sequence 59060, A
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812	147	6.6	1669	25	US-11-433-832-47155	Sequence 47155, A	885	141.5	6.4	803	9	US-10-767-701-19903	Sequence 19903, A
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815	146	6.6	2709	18	US-11-097-143-8609	Sequence 8609, Ap	888	141.5	6.4	3486	12	US-10-932-182A-191019	Sequence 191019,
C 816	146	6.6	230196	15	US-10-915-727-12204	Sequence 12204, A	889	141.5	6.4	3486	21	US-11-217-529-191019	Sequence 191019,
C 817	146	6.6	767677	16	US-10-940-774-12147	Sequence 12147, A	890	141	6.4	1226	10	US-10-425-115-20293	Sequence 20293, A
C 818	146	6.6	767677	16	US-10-940-774-17361	Sequence 17361, A	C 891	141	6.4	1501	6	US-09-815-264-11482	Sequence 11482, A
C 819	146	6.6	1048668	23	US-11-033-056A-36314	Sequence 36314, A	C 892	141	6.4	1501	27	US-11-595-983-11482	Sequence 11482, A
C 820	145.5	6.6	843	16	US-10-100-683-12710	Sequence 12710, A	893	141	6.4	1691	26	US-11-443-428A-631718	Sequence 631718,
C 821	145.5	6.6	843	23	US-11-001-793-12710	Sequence 12710, A	894	141	6.4	2130	13	US-10-449-902-28237	Sequence 28237, A
C 822	145.5	6.6	2114	3	US-09-738-973-158	Sequence 158, App	895	141	6.4	3191	26	US-11-443-428A-732419	Sequence 732419,
C 823	145.5	6.6	2114	3	US-09-854-133-158	Sequence 158, App	896	141	6.4	3377	26	US-11-443-428A-732418	Sequence 732418,
C 824	145.5	6.6	2114	7	US-10-144-649A-158	Sequence 158, App	897	141	6.4	3608	26	US-11-443-428A-732417	Sequence 732417,
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1048	135	6.1	58880	23	US-11-491-125A-6983	Sequence 6983, Ap	1121	133	6.0	2408	26	US-11-443-428A-383985	Sequence 383985,
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1070	134.5	6.1	3309400	14	US-10-805-394-1	Sequence 1, Appli	c1143	132.5	6.0	1501	27	US-11-595-983-34890	Sequence 34890, A
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1074	134	6.1	837	23	US-11-001-793-4762	Sequence 4762, Ap	1147	132.5	6.0	2528	26	US-11-443-428A-379726	Sequence 379726,
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1192	132	6.0	4475	26	US-11-443-428A-732425	Sequence 732425,	1265	131	5.9	32391	15	US-10-796-280-12262	Sequence 12262, A
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1195	132	6.0	4892	26	US-11-443-428A-488739	Sequence 488739,	c1268	131	5.9	138808	14	US-10-540-898-905	Sequence 905, App
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1209	131.5	5.9	2457	12	US-10-932-182A-1494	Sequence 1494, Ap	1282	130.5	5.9	1706	16	US-10-940-774-2380	Sequence 2380, Ap
1210	131.5	5.9	2457	21	US-11-217-529-1494	Sequence 1494, Ap	1283	130.5	5.9	1924	14	US-10-528-948-5	Sequence 5, Appli
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c1213	131.5	5.9	12279	9	US-10-363-616-80	Sequence 80, Appl	1286	130.5	5.9	2220	9	US-10-425-114-27723	Sequence 27723, A
c1214	131.5	5.9	523508	17	US-10-674-575-1480	Sequence 1480, Ap	1287	130.5	5.9	2220	23	US-11-520-715-27723	Sequence 27723, A
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1219	131	5.9	1295	21	US-11-266-748A-188416	Sequence 188416,	1292	130.5	5.9	3559	26	US-11-443-428A-497871	Sequence 497871,
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:

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-Q=/abss/ABSSWEB\_spool/US09944929/runat\_19092007\_175127\_26724/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_New -QFMT=fastap -SUFFIX=rnpbn -SIMRANGE=0.0005  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500 -DOCALIGN=200 -THR SCORE=pct  
-THR MAX=100 -THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=0  
-MINLEN=0 -MAXLEN=200000000 -MINDBSEQLEN=1 -HOST=ai3-01  
-USER=US09944929 @CGN 1 1 13 @runat\_19092007\_175127\_26724 -NCPU=6 -NO MMAP  
-NEG SCORES=0 -WAIT -LONGLOG -MINDIST=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

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2: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US06\_NEW\_PUB\_seq.\*  
3: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US07\_NEW\_PUB\_seq.\*  
4: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US08\_NEW\_PUB\_seq.\*  
5: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09\_NEW\_PUB\_seq.\*  
6: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/PCT\_NEW\_PUB\_seq.\*  
7: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11\_NEW\_PUB\_seq.\*  
8: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11\_NEW\_PUB\_seq.1.\*  
9: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US60\_NEW\_PUB\_seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	6.7	43816	8 US-11-699-229-58	Sequence 58, Appl
2	140.5	6.4	2544	8 US-11-713-768-79587	Sequence 79587, A
3	136.5	6.2	1061	8 US-11-514-704-5545	Sequence 5545, Ap
4	136.5	6.2	1923	8 US-11-544-679-14	Sequence 14, Appl
5	136.5	6.2	3637	8 US-11-544-679-13	Sequence 13, Appl
6	131.5	5.9	1425	8 US-11-713-768-5840	Sequence 5840, Ap
7	131	5.9	2903	8 US-11-514-704-17345	Sequence 17345, A
8	130	5.9	2443	8 US-11-514-704-13576	Sequence 13576, A
9	129.5	5.9	1297	8 US-11-713-768-9744	Sequence 9744, Ap
10	128.5	5.8	705	8 US-11-561-363-119	Sequence 119, App

11	128.5	5.8	1153	8 US-11-514-704-20175	Sequence 20175, A
12	127.5	5.8	1644	8 US-11-514-704-2455	Sequence 2455, Ap
13	127.5	5.8	2085	8 US-11-713-768-72372	Sequence 72372, A
14	127.5	5.8	2154	8 US-11-713-768-71163	Sequence 71163, A
15	127	5.7	1348	8 US-11-514-704-14352	Sequence 14352, A
16	126.5	5.7	1785	1 US-10-438-246-12882	Sequence 12882, A
17	126.5	5.7	2180	1 US-10-438-246-22240	Sequence 22240, A
18	126.5	5.7	3379	8 US-11-514-704-6220	Sequence 6220, Ap
19	125.5	5.7	1541	8 US-11-649-663A-5299	Sequence 5299, Ap
20	125	5.7	2818	1 US-10-562-377-156	Sequence 156, App
21	125	5.7	2964	1 US-10-438-246-12791	Sequence 12791, A
22	125	5.7	2964	1 US-10-438-246-22220	Sequence 22220, A
23	125	5.7	46030	8 US-11-257-477-1	Sequence 1, Appli
24	124.5	5.6	1209	8 US-11-649-663A-1609	Sequence 1609, Ap
25	124.5	5.6	1209	8 US-11-713-768-81597	Sequence 81597, A
26	124.5	5.6	3117	1 US-10-567-764-14	Sequence 14, Appl
27	124	5.6	2252	8 US-11-514-704-21629	Sequence 21629, A
28	123.5	5.6	4441	8 US-11-514-704-19034	Sequence 19034, A
29	123.5	5.6	117750	8 US-11-257-477-169	Sequence 169, App
30	123	5.6	2482	8 US-11-234-694-9	Sequence 9, Appli
31	123	5.6	2946	1 US-10-567-764-6	Sequence 6, Appli
32	123	5.6	2969	8 US-11-257-477-2	Sequence 2, Appli
33	123	5.6	8049	1 US-10-567-764-5	Sequence 5, Appli
34	122.5	5.5	857	1 US-10-438-246-47	Sequence 47, Appl
35	122.5	5.5	1348	8 US-11-649-663A-2881	Sequence 2881, Ap
36	122.5	5.5	3004	8 US-11-489-234-4	Sequence 4, Appli
37	122	5.5	4839	1 US-10-533-069-1679	Sequence 1679, Ap
38	121.5	5.5	2164	8 US-11-552-437-227	Sequence 227, App
39	121.5	5.5	2374	8 US-11-514-704-7147	Sequence 7147, Ap
40	121.5	5.5	3210	1 US-10-567-764-18	Sequence 18, Appl
41	121.5	5.5	3271	8 US-11-514-704-5311	Sequence 5311, Ap
42	120.5	5.5	2173	8 US-11-514-704-8202	Sequence 8202, Ap
43	120.5	5.5	2291	8 US-11-649-663A-5167	Sequence 5167, Ap
44	120	5.4	860	1 US-10-438-246-27138	Sequence 27138, A
45	120	5.4	945	8 US-11-514-704-2453	Sequence 2453, Ap
46	120	5.4	1328	8 US-11-713-768-61011	Sequence 61011, A
47	120	5.4	2410	8 US-11-514-704-12355	Sequence 12355, A
48	120	5.4	3303	1 US-10-567-764-22	Sequence 22, Appl
49	120	5.4	4443	8 US-11-713-768-71358	Sequence 71358, A
50	120	5.4	9645	1 US-10-565-068-95	Sequence 95, Appl
51	119.5	5.4	979	1 US-10-438-246-27134	Sequence 27134, A
52	119.5	5.4	1289	8 US-11-713-768-51143	Sequence 51143, A
53	119.5	5.4	3132	1 US-10-533-069-253	Sequence 253, App
54	119.5	5.4	3329	8 US-11-514-704-4838	Sequence 4838, Ap
55	119	5.4	1556	8 US-11-514-704-6219	Sequence 6219, Ap
56	119	5.4	3024	1 US-10-567-764-10	Sequence 10, Appl
57	119	5.4	5931	8 US-11-524-253-1	Sequence 1, Appli
58	118.5	5.4	2160	8 US-11-514-704-18123	Sequence 18123, A
59	118.5	5.4	2724	8 US-11-561-363-59	Sequence 59, Appl
60	118.5	5.4	5373	1 US-10-438-246-12713	Sequence 12713, A
61	118	5.3	1161	8 US-11-713-768-12766	Sequence 12766, A
62	118	5.3	4446	1 US-10-438-246-11631	Sequence 11631, A
63	117.5	5.3	795	8 US-11-713-768-111455	Sequence 111455,
64	117.5	5.3	2251	1 US-10-438-246-3982	Sequence 3982, Ap
65	117.5	5.3	3304	8 US-11-514-704-8575	Sequence 8575, Ap
66	117	5.3	821	8 US-11-713-768-63219	Sequence 63219, A
67	117	5.3	1480	8 US-11-514-704-4869	Sequence 4869, Ap
68	117	5.3	1682	1 US-10-593-213-5	Sequence 5, Appli
69	117	5.3	1922	8 US-11-649-663A-4329	Sequence 4329, Ap
70	117	5.3	3788	8 US-11-713-768-81415	Sequence 81415, A
71	116.5	5.3	1191	8 US-11-649-663A-1605	Sequence 1605, Ap
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73	116.5	5.3	1789	8 US-11-649-663A-4267	Sequence 4267, Ap
74	116.5	5.3	8041	8 US-11-514-704-14588	Sequence 14588, A
75	116	5.2	1106	8 US-11-713-768-64806	Sequence 64806, A
76	116	5.2	1512	8 US-11-514-704-17665	Sequence 17665, A
77	116	5.2	1752	8 US-11-713-768-6840	Sequence 6840, Ap
78	116	5.2	2304	8 US-11-514-704-16667	Sequence 16667, A
79	116	5.2	3862	8 US-11-514-704-1681	Sequence 1681, Ap
80	116	5.2	4473	8 US-11-514-704-733	Sequence 733, App
81	116	5.2	4829	8 US-11-514-704-97	Sequence 97, Appl
82	115.5	5.2	999	8 US-11-514-704-20177	Sequence 20177, A
83	115.5	5.2	1525	8 US-11-713-768-62162	Sequence 62162, A

84 115.5 5.2 2444 8 US-11-713-768-91589 Sequence 91589, A  
85 115.5 5.2 2444 8 US-11-713-768-95345 Sequence 95345, A  
86 115 5.2 1080 1 US-10-438-246-12618 Sequence 12618, A  
87 115 5.2 1308 8 US-11-514-704-11332 Sequence 11332, A  
88 115 5.2 1330 8 US-11-713-768-62336 Sequence 62336, A  
89 115 5.2 1360 8 US-11-649-663A-3535 Sequence 3535, Ap  
90 115 5.2 1636 8 US-11-514-704-20652 Sequence 20652, A  
91 115 5.2 2283 8 US-11-713-768-47906 Sequence 47906, A  
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93 115 5.2 10722 1 US-10-438-246-5243 Sequence 5243, Ap  
94 114.5 5.2 1069 8 US-11-514-704-20180 Sequence 20180, A  
95 114.5 5.2 1444 8 US-11-713-768-20232 Sequence 20232, A  
96 114.5 5.2 1457 1 US-10-438-246-21254 Sequence 21254, A  
97 114.5 5.2 2200 1 US-10-438-246-3973 Sequence 3973, Ap  
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99 114 5.2 936 8 US-11-713-768-51047 Sequence 51047, A  
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101 114 5.2 2329 8 US-11-713-768-97016 Sequence 97016, A  
102 114 5.2 2330 8 US-11-713-768-30481 Sequence 30481, A  
103 114 5.2 2330 8 US-11-713-768-34071 Sequence 34071, A  
104 114 5.2 2681 8 US-11-514-704-996 Sequence 996, App  
105 114 5.2 3073 8 US-11-514-704-21517 Sequence 21517, A  
106 114 5.2 10838 8 US-11-717-800-31 Sequence 31, Appl  
107 113.5 5.1 1490 8 US-11-713-768-62765 Sequence 62765, A  
108 113.5 5.1 1629 1 US-10-594-266-45 Sequence 45, Appl  
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112 113.5 5.1 4227 8 US-11-514-704-13683 Sequence 13683, A  
113 113.5 5.1 5372 8 US-11-514-704-15923 Sequence 15923, A  
114 113 5.1 1663 8 US-11-713-768-105811 Sequence 105811, A  
115 113 5.1 1665 8 US-11-713-768-30064 Sequence 30064, A  
116 113 5.1 1665 8 US-11-713-768-33654 Sequence 33654, A  
117 113 5.1 2046 8 US-11-713-768-73756 Sequence 73756, A  
118 113 5.1 2481 8 US-11-514-704-23281 Sequence 23281, A  
119 113 5.1 3200 1 US-10-533-069-301 Sequence 301, App  
120 113 5.1 9781 8 US-11-514-704-7075 Sequence 7075, Ap  
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123 112.5 5.1 1094 8 US-11-649-663A-1355 Sequence 1355, Ap  
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125 112.5 5.1 1335 1 US-10-438-246-3917 Sequence 3917, Ap  
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130 112.5 5.1 3153 8 US-11-514-704-3852 Sequence 3852, Ap  
131 112.5 5.1 3550 8 US-11-713-768-5508 Sequence 5508, Ap  
132 112.5 5.1 4375 8 US-11-514-704-24808 Sequence 24808, A  
133 112.5 5.1 5169 8 US-11-514-704-231 Sequence 231, App  
134 112.5 5.1 6065 8 US-11-625-795-12 Sequence 12, Appl  
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143 111.5 5.0 958 8 US-11-514-704-11966 Sequence 11966, A  
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145 111.5 5.0 1184 8 US-11-713-768-67723 Sequence 67723, A  
146 111.5 5.0 1392 8 US-11-713-768-67361 Sequence 67361, A  
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152 111.5 5.0 49175 8 US-11-257-477-4 Sequence 4, Appli  
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154 111 5.0 918 1 US-10-438-246-27137 Sequence 27137, A  
155 111 5.0 1071 8 US-11-514-704-997 Sequence 997, App  
156 111 5.0 1255 8 US-11-713-768-47047 Sequence 47047, A

157 111 5.0 1269 8 US-11-713-768-57665 Sequence 57665, A  
158 111 5.0 1384 8 US-11-514-704-21628 Sequence 21628, A  
159 111 5.0 1900 8 US-11-514-704-6528 Sequence 6528, Ap  
160 111 5.0 1993 8 US-11-514-704-7577 Sequence 7577, Ap  
161 111 5.0 2263 8 US-11-713-768-44996 Sequence 44996, A  
162 111 5.0 2263 8 US-11-713-768-46082 Sequence 46082, A  
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164 111 5.0 2699 8 US-11-514-704-16608 Sequence 16608, A  
165 111 5.0 3865 1 US-10-438-246-21018 Sequence 21018, A  
166 111 5.0 5382 8 US-11-514-704-22237 Sequence 22237, A  
167 111 5.0 10291 8 US-11-514-704-500 Sequence 500, App  
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171 110.5 5.0 1074 1 US-10-438-246-13172 Sequence 13172, A  
172 110.5 5.0 1249 8 US-11-713-768-57833 Sequence 57833, A  
173 110.5 5.0 1307 8 US-11-649-663A-4163 Sequence 4163, Ap  
174 110.5 5.0 1478 1 US-10-438-246-23517 Sequence 23517, A  
175 110.5 5.0 1818 8 US-11-713-768-1559 Sequence 1559, Ap  
176 110.5 5.0 1983 1 US-10-533-069-931 Sequence 931, App  
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178 110.5 5.0 2410 8 US-11-649-663A-3823 Sequence 3823, Ap  
179 110.5 5.0 2440 8 US-11-514-704-23345 Sequence 23345, A  
180 110.5 5.0 12649 8 US-11-717-800-12 Sequence 12, Appl  
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182 110 5.0 1455 1 US-10-438-246-13051 Sequence 13051, A  
183 110 5.0 1746 8 US-11-728-567-271 Sequence 271, App  
184 110 5.0 1776 8 US-11-713-768-45411 Sequence 45411, A  
185 110 5.0 1776 8 US-11-713-768-49806 Sequence 49806, A  
186 110 5.0 1855 8 US-11-514-704-5306 Sequence 5306, Ap  
187 110 5.0 2631 1 US-10-438-246-13632 Sequence 13632, A  
188 110 5.0 5759 8 US-11-514-704-9343 Sequence 9343, Ap  
189 109.5 5.0 1077 8 US-11-649-663A-3601 Sequence 3601, Ap  
190 109.5 5.0 1191 8 US-11-514-704-20639 Sequence 20639, A  
191 109.5 5.0 1255 1 US-10-438-246-28517 Sequence 28517, A  
192 109.5 5.0 1305 8 US-11-713-768-79864 Sequence 79864, A  
193 109.5 5.0 1367 8 US-11-514-704-2793 Sequence 2793, Ap  
194 109.5 5.0 1437 8 US-11-514-704-23684 Sequence 23684, A  
195 109.5 5.0 1606 8 US-11-514-704-18897 Sequence 18897, A  
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209 109 4.9 1908 8 US-11-514-704-12934 Sequence 12934, A  
210 109 4.9 2131 8 US-11-713-768-9713 Sequence 9713, Ap  
211 109 4.9 2372 8 US-11-713-768-14237 Sequence 14237, A  
212 109 4.9 2380 1 US-10-438-246-15533 Sequence 15533, A  
213 109 4.9 2380 1 US-10-438-246-23426 Sequence 23426, A  
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215 109 4.9 2978 8 US-11-514-704-15232 Sequence 15232, A  
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217 109 4.9 3981 1 US-10-438-246-21630 Sequence 21630, A  
218 109 4.9 5468 1 US-10-438-246-13823 Sequence 13823, A  
219 109 4.9 5468 1 US-10-438-246-22992 Sequence 22992, A  
220 108.5 4.9 894 8 US-11-649-663A-1891 Sequence 1891, Ap  
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224 108.5 4.9 957 8 US-11-713-768-91210 Sequence 91210, A  
225 108.5 4.9 957 8 US-11-713-768-94966 Sequence 94966, A  
226 108.5 4.9 1062 8 US-11-713-768-7227 Sequence 7227, Ap  
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228 108.5 4.9 1284 1 US-10-438-246-11720 Sequence 11720, A  
229 108.5 4.9 1318 1 US-10-438-246-21299 Sequence 21299, A

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C 231	108.5	4.9	1418	8	US-11-713-768-39032	Sequence 39032, A	304	106	4.8	2271	8	US-11-713-768-92836	Sequence 92836, A
232	108.5	4.9	1977	1	US-10-438-246-29387	Sequence 29387, A	305	106	4.8	2275	8	US-11-514-704-4071	Sequence 4071, Ap
233	108.5	4.9	4625	1	US-10-533-069-1028	Sequence 1028, Ap	306	106	4.8	2418	8	US-11-713-768-50710	Sequence 50710, A
234	108.5	4.9	6131	8	US-11-514-704-3190	Sequence 3190, Ap	307	106	4.8	2604	8	US-11-514-704-13361	Sequence 13361, A
235	108.5	4.9	6408	1	US-10-438-246-11810	Sequence 11810, A	308	106	4.8	3318	1	US-10-438-246-11282	Sequence 11282, A
236	108.5	4.9	6408	1	US-10-438-246-21380	Sequence 21380, A	309	106	4.8	3318	8	US-11-514-704-1842	Sequence 1842, Ap
237	108	4.9	742	8	US-11-514-704-22761	Sequence 22761, A	310	106	4.8	3372	1	US-10-438-246-21032	Sequence 21032, A
238	108	4.9	1911	8	US-11-514-704-1000	Sequence 1000, Ap	311	106	4.8	3516	8	US-11-365-630-9	Sequence 9, Appli
239	108	4.9	2142	1	US-10-438-246-12114	Sequence 12114, A	C 312	106	4.8	4102	1	US-10-562-377-138	Sequence 138, App
240	108	4.9	2142	1	US-10-438-246-21659	Sequence 21659, A	C 313	106	4.8	4240	8	US-11-514-704-22510	Sequence 22510, A
241	108	4.9	2293	8	US-11-514-704-3387	Sequence 3387, Ap	C 314	106	4.8	4561	8	US-11-514-704-23219	Sequence 23219, A
242	108	4.9	2853	8	US-11-514-704-9222	Sequence 9222, Ap	315	105.5	4.8	1068	1	US-10-438-246-13271	Sequence 13271, A
C 243	108	4.9	5091	1	US-10-438-246-12692	Sequence 12692, A	316	105.5	4.8	1280	8	US-11-514-704-23105	Sequence 23105, A
C 244	108	4.9	5091	1	US-10-438-246-22105	Sequence 22105, A	317	105.5	4.8	1312	1	US-10-438-246-953	Sequence 953, App
245	108	4.9	7598	8	US-11-514-704-10960	Sequence 10960, A	318	105.5	4.8	1388	8	US-11-514-704-9682	Sequence 9682, Ap
246	107.5	4.9	840	8	US-11-514-704-5518	Sequence 5518, Ap	C 319	105.5	4.8	1479	1	US-10-438-246-22489	Sequence 22489, A
247	107.5	4.9	878	8	US-11-514-704-6221	Sequence 6221, Ap	320	105.5	4.8	1498	8	US-11-514-704-6465	Sequence 6465, Ap
248	107.5	4.9	1060	8	US-11-713-768-107178	Sequence 107178, A	C 321	105.5	4.8	1605	8	US-11-713-768-22766	Sequence 22766, A
C 249	107.5	4.9	1065	8	US-11-713-768-63805	Sequence 63805, A	322	105.5	4.8	1958	8	US-11-713-768-8207	Sequence 8207, Ap
250	107.5	4.9	1113	1	US-10-438-246-13458	Sequence 13458, A	323	105.5	4.8	1958	8	US-11-713-768-15424	Sequence 15424, A
251	107.5	4.9	1338	8	US-11-713-768-60538	Sequence 60538, A	C 324	105.5	4.8	2963	8	US-11-514-704-24905	Sequence 24905, A
252	107.5	4.9	1470	1	US-10-438-246-4378	Sequence 4378, Ap	325	105.5	4.8	3459	8	US-11-514-704-6264	Sequence 6264, Ap
253	107.5	4.9	1507	1	US-10-438-246-22587	Sequence 22587, A	326	105	4.7	959	8	US-11-514-704-22439	Sequence 22439, A
254	107.5	4.9	1660	8	US-11-649-663A-2925	Sequence 2925, Ap	C 327	105	4.7	1082	8	US-11-514-704-22241	Sequence 22241, A
C 255	107.5	4.9	1854	1	US-10-438-246-508	Sequence 508, App	C 328	105	4.7	1163	8	US-11-713-768-103696	Sequence 103696, A
256	107.5	4.9	2297	8	US-11-514-704-18728	Sequence 18728, A	329	105	4.7	1191	8	US-11-649-663A-2165	Sequence 2165, Ap
C 257	107.5	4.9	2379	8	US-11-514-704-21485	Sequence 21485, A	330	105	4.7	1191	8	US-11-713-768-4665	Sequence 4665, Ap
258	107.5	4.9	2742	8	US-11-514-704-11612	Sequence 11612, A	C 331	105	4.7	1233	8	US-11-713-768-26301	Sequence 26301, A
259	107.5	4.9	2837	8	US-11-257-477-5	Sequence 5, Appli	332	105	4.7	1360	8	US-11-713-768-53291	Sequence 53291, A
260	107.5	4.9	2961	8	US-11-514-704-11394	Sequence 11394, A	333	105	4.7	1407	1	US-10-547-956-751	Sequence 751, App
C 261	107.5	4.9	3469	8	US-11-514-704-20883	Sequence 20883, A	334	105	4.7	1561	8	US-11-713-768-6855	Sequence 6855, Ap
262	107.5	4.9	3737	8	US-11-514-704-15165	Sequence 15165, A	335	105	4.7	1604	8	US-11-514-704-3626	Sequence 3626, Ap
C 263	107	4.8	965	8	US-11-728-567-1085	Sequence 1085, Ap	336	105	4.7	1636	1	US-10-438-246-4009	Sequence 4009, Ap
C 264	107	4.8	1029	8	US-11-649-663A-1923	Sequence 1923, Ap	337	105	4.7	1638	8	US-11-713-768-62310	Sequence 62310, A
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C 266	107	4.8	1029	8	US-11-713-768-93303	Sequence 93303, A	339	105	4.7	1678	8	US-11-713-768-17674	Sequence 17674, A
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C 269	107	4.8	1566	8	US-11-713-768-26022	Sequence 26022, A	342	105	4.7	1982	8	US-11-514-704-869	Sequence 869, App
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271	107	4.8	1809	8	US-11-713-768-96499	Sequence 96499, A	344	105	4.7	2085	8	US-11-514-704-16725	Sequence 16725, A
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C 273	107	4.8	1948	1	US-10-438-246-654	Sequence 654, App	346	105	4.7	2320	8	US-11-713-768-107648	Sequence 107648, A
274	107	4.8	2011	8	US-11-713-768-64205	Sequence 64205, A	347	105	4.7	3178	1	US-10-565-068-79	Sequence 79, Appl
275	107	4.8	2286	8	US-11-514-704-18779	Sequence 18779, A	348	105	4.7	3476	8	US-11-234-694-51	Sequence 51, Appl
276	107	4.8	3015	8	US-11-514-704-735	Sequence 735, App	349	105	4.7	3552	8	US-11-395-197-136	Sequence 136, App
277	107	4.8	3232	8	US-11-514-704-3625	Sequence 3625, Ap	350	105	4.7	3552	8	US-11-396-216-136	Sequence 136, App
278	107	4.8	3791	8	US-11-514-704-7761	Sequence 7761, Ap	351	105	4.7	5003	8	US-11-514-704-2758	Sequence 2758, Ap
279	106.5	4.8	789	8	US-11-713-768-7404	Sequence 7404, Ap	352	105	4.7	5350	1	US-10-533-069-2297	Sequence 2297, Ap
280	106.5	4.8	846	8	US-11-514-704-20178	Sequence 20178, A	C 353	105	4.7	6813	1	US-10-438-246-23229	Sequence 23229, A
281	106.5	4.8	962	1	US-10-438-246-29760	Sequence 29760, A	C 354	104.5	4.7	916	8	US-11-514-704-21055	Sequence 21055, A
282	106.5	4.8	1085	8	US-11-514-704-20179	Sequence 20179, A	C 355	104.5	4.7	1075	8	US-11-514-704-11356	Sequence 11356, A
283	106.5	4.8	1150	8	US-11-713-768-59072	Sequence 59072, A	356	104.5	4.7	1077	8	US-11-649-663A-1629	Sequence 1629, Ap
C 284	106.5	4.8	1176	1	US-10-438-246-364	Sequence 364, App	357	104.5	4.7	1077	8	US-11-713-768-82114	Sequence 82114, A
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286	106.5	4.8	1367	8	US-11-649-663A-4343	Sequence 4343, Ap	C 359	104.5	4.7	1172	1	US-10-438-246-4376	Sequence 4376, Ap
287	106.5	4.8	1594	8	US-11-713-768-60242	Sequence 60242, A	C 360	104.5	4.7	1266	8	US-11-713-768-2604	Sequence 2604, Ap
288	106.5	4.8	1726	1	US-10-438-246-4312	Sequence 4312, Ap	C 361	104.5	4.7	1484	8	US-11-713-768-43445	Sequence 43445, A
289	106.5	4.8	2207	8	US-11-514-704-1147	Sequence 1147, Ap	362	104.5	4.7	1599	8	US-11-713-768-65334	Sequence 65334, A
C 290	106.5	4.8	2235	1	US-10-438-246-13260	Sequence 13260, A	363	104.5	4.7	1819	8	US-11-514-704-16932	Sequence 16932, A
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C 292	106.5	4.8	3152	8	US-11-514-704-24322	Sequence 24322, A	365	104.5	4.7	2334	8	US-11-713-768-86885	Sequence 86885, A
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297	106	4.8	1450	8	US-11-514-704-12852	Sequence 12852, A	370	104.5	4.7	3722	8	US-11-514-704-2717	Sequence 2717, Ap
298	106	4.8	1566	8	US-11-514-704-10390	Sequence 10390, A	C 371	104.5	4.7	4314	8	US-11-514-704-22823	Sequence 22823, A
299	106	4.8	1798	8	US-11-514-704-17670	Sequence 17670, A	C 372	104.5	4.7	4437	1	US-10-438-246-12694	Sequence 12694, A
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381 104 4.7 1500 8 US-11-713-768-59255 Sequence 59255, A  
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410 103.5 4.7 2662 8 US-11-514-704-12334 Sequence 12334, A  
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8 2237 4.6 101.5 514 101.5 4.6 2237 8 US-11-514-704-17841 Sequence 17841, A  
8 2288 4.6 101.5 515 101.5 4.6 2288 8 US-11-514-704-19871 Sequence 19871, A  
8 2653 4.6 101.5 516 101.5 4.6 2653 8 US-11-514-704-11993 Sequence 11993, A  
1 2656 4.6 101.5 517 101.5 4.6 2656 1 US-10-438-246-1104 Sequence 1104, Ap  
8 2658 4.6 101.5 518 101.5 4.6 2658 8 US-11-514-704-6846 Sequence 6846, Ap  
8 2773 4.6 101.5 519 101.5 4.6 2773 8 US-11-649-663A-1465 Sequence 1465, Ap  
8 2773 4.6 101.5 520 101.5 4.6 2773 8 US-11-713-768-49006 Sequence 49006, A  
8 2791 4.6 101.5 521 101.5 4.6 2791 8 US-11-649-663A-2825 Sequence 2825, Ap





C 668	99.5	4.5	2260	1	US-10-438-246-12799	Sequence 12799, A	741	98.5	4.5	1194	1	US-10-554-789-7	Sequence 7, Appli
C 669	99.5	4.5	2377	8	US-11-514-704-7309	Sequence 7309, Ap	742	98.5	4.5	1298	8	US-11-514-704-18243	Sequence 18243, A
C 670	99.5	4.5	2378	1	US-10-438-246-22227	Sequence 22227, A	743	98.5	4.5	1306	8	US-11-713-768-68388	Sequence 68388, A
C 671	99.5	4.5	2409	1	US-10-438-246-15529	Sequence 15529, A	744	98.5	4.5	1359	8	US-11-514-704-18592	Sequence 18592, A
C 672	99.5	4.5	2409	1	US-10-438-246-23427	Sequence 23427, A	745	98.5	4.5	1374	8	US-11-713-768-62916	Sequence 62916, A
C 673	99.5	4.5	2489	8	US-11-514-704-5448	Sequence 5448, Ap	746	98.5	4.5	1436	8	US-11-649-663A-4393	Sequence 4393, Ap
C 674	99.5	4.5	2994	8	US-11-407-888-54	Sequence 54, Appl	747	98.5	4.5	1468	8	US-11-514-704-16599	Sequence 16599, A
C 675	99.5	4.5	3109	8	US-11-514-704-7417	Sequence 7417, Ap	748	98.5	4.5	1504	8	US-11-514-704-3608	Sequence 3608, Ap
C 676	99.5	4.5	3260	8	US-11-514-704-8459	Sequence 8459, Ap	C 749	98.5	4.5	1507	8	US-11-713-768-52831	Sequence 52831, A
C 677	99.5	4.5	3482	8	US-11-514-704-16158	Sequence 16158, A	750	98.5	4.5	1516	1	US-10-438-246-20968	Sequence 20968, A
C 678	99.5	4.5	4162	8	US-11-514-704-10	Sequence 10, Appl	751	98.5	4.5	1620	8	US-11-514-704-1616	Sequence 1616, Ap
C 679	99.5	4.5	4290	8	US-11-514-704-5407	Sequence 5407, Ap	C 752	98.5	4.5	1672	1	US-10-438-246-21326	Sequence 21326, A
C 680	99.5	4.5	6603	1	US-10-594-266-55	Sequence 55, Appl	753	98.5	4.5	1676	8	US-11-713-768-10252	Sequence 10252, A
C 681	99.5	4.5	7119	8	US-11-514-704-20569	Sequence 20569, A	754	98.5	4.5	1677	8	US-11-614-098-13	Sequence 13, Appl
C 682	99	4.5	837	8	US-11-561-363-53	Sequence 53, Appl	C 755	98.5	4.5	1692	1	US-10-438-246-28383	Sequence 28383, A
C 683	99	4.5	915	8	US-11-713-768-111259	Sequence 111259,	756	98.5	4.5	1757	1	US-10-438-246-21156	Sequence 21156, A
C 684	99	4.5	916	8	US-11-649-663A-947	Sequence 947, App	757	98.5	4.5	1767	8	US-11-713-768-59929	Sequence 59929, A
C 685	99	4.5	916	8	US-11-713-768-16344	Sequence 16344, A	C 758	98.5	4.5	1836	8	US-11-514-704-22177	Sequence 22177, A
C 686	99	4.5	976	1	US-10-438-246-28231	Sequence 28231, A	C 759	98.5	4.5	1854	1	US-10-547-956-17	Sequence 17, Appl
C 687	99	4.5	989	8	US-11-514-704-25032	Sequence 25032, A	760	98.5	4.5	1867	8	US-11-649-663A-3355	Sequence 3355, Ap
C 688	99	4.5	1036	1	US-10-438-246-11427	Sequence 11427, A	761	98.5	4.5	1909	8	US-11-649-663A-3777	Sequence 3777, Ap
C 689	99	4.5	1045	1	US-10-438-246-27141	Sequence 27141, A	762	98.5	4.5	1931	8	US-11-514-704-6529	Sequence 6529, Ap
C 690	99	4.5	1074	8	US-11-699-588-14	Sequence 14, Appl	763	98.5	4.5	1956	8	US-11-514-704-4783	Sequence 4783, Ap
C 691	99	4.5	1116	8	US-11-713-768-68953	Sequence 68953, A	764	98.5	4.5	2149	8	US-11-649-663A-271	Sequence 271, App
C 692	99	4.5	1157	8	US-11-713-768-6941	Sequence 6941, Ap	765	98.5	4.5	2159	8	US-11-514-704-943	Sequence 943, App
C 693	99	4.5	1173	1	US-10-438-246-11485	Sequence 11485, A	C 766	98.5	4.5	2313	8	US-11-514-704-390	Sequence 390, App
C 694	99	4.5	1178	8	US-11-649-663A-4045	Sequence 4045, Ap	767	98.5	4.5	2384	8	US-11-514-704-16088	Sequence 16088, A
C 695	99	4.5	1188	1	US-10-438-246-21120	Sequence 21120, A	768	98.5	4.5	2550	8	US-11-514-704-13928	Sequence 13928, A
C 696	99	4.5	1353	8	US-11-713-768-65219	Sequence 65219, A	769	98.5	4.5	2744	8	US-11-514-704-1358	Sequence 1358, Ap
C 697	99	4.5	1489	8	US-11-713-768-19277	Sequence 19277, A	770	98.5	4.5	3203	8	US-11-514-704-11302	Sequence 11302, A
C 698	99	4.5	1520	8	US-11-514-704-15285	Sequence 15285, A	771	98.5	4.5	3319	1	US-10-533-069-566	Sequence 566, App
C 699	99	4.5	1596	1	US-10-438-246-13222	Sequence 13222, A	C 772	98.5	4.5	4314	8	US-11-514-704-24321	Sequence 24321, A
C 700	99	4.5	1631	8	US-11-614-098-9	Sequence 9, Appli	773	98.5	4.5	4766	8	US-11-514-704-8137	Sequence 8137, Ap
C 701	99	4.5	1636	8	US-11-514-704-2451	Sequence 2451, Ap	774	98.5	4.5	4881	1	US-10-438-246-14505	Sequence 14505, A
C 702	99	4.5	1676	8	US-11-713-768-18691	Sequence 18691, A	775	98.5	4.5	5406	1	US-10-438-246-12260	Sequence 12260, A
C 703	99	4.5	1696	8	US-11-649-663A-629	Sequence 629, App	776	98.5	4.5	5622	1	US-10-438-246-12261	Sequence 12261, A
C 704	99	4.5	1696	8	US-11-713-768-7273	Sequence 7273, Ap	C 777	98.5	4.5	5941	1	US-10-438-246-21796	Sequence 21796, A
C 705	99	4.5	1741	8	US-11-649-663A-725	Sequence 725, App	C 778	98.5	4.5	6258	8	US-11-514-704-7695	Sequence 7695, Ap
C 706	99	4.5	1741	8	US-11-713-768-3093	Sequence 3093, Ap	C 779	98.5	4.5	6718	8	US-11-514-704-38	Sequence 38, Appl
C 707	99	4.5	1766	8	US-11-514-704-14695	Sequence 14695, A	780	98.5	4.5	6718	8	US-11-514-704-21252	Sequence 21252, A
C 708	99	4.5	1849	8	US-11-713-768-66298	Sequence 66298, A	781	98.5	4.5	9475	8	US-11-585-666-24	Sequence 24, Appl
C 709	99	4.5	1855	8	US-11-560-738A-27	Sequence 27, Appl	782	98.5	4.5	13290	8	US-11-585-666-23	Sequence 23, Appl
C 710	99	4.5	1861	8	US-11-713-768-17659	Sequence 17659, A	783	98.5	4.5	13302	8	US-11-257-477-160	Sequence 160, App
C 711	99	4.5	1868	8	US-11-649-663A-4319	Sequence 4319, Ap	C 784	98	4.4	550	8	US-11-196-018A-63	Sequence 63, Appl
C 712	99	4.5	1955	1	US-10-438-246-22511	Sequence 22511, A	C 785	98	4.4	721	8	US-11-713-768-96116	Sequence 96116, A
C 713	99	4.5	1982	8	US-11-514-704-15233	Sequence 15233, A	C 786	98	4.4	734	8	US-11-649-663A-247	Sequence 247, App
C 714	99	4.5	1984	8	US-11-514-704-13232	Sequence 13232, A	C 787	98	4.4	734	8	US-11-713-768-76466	Sequence 76466, A
C 715	99	4.5	2058	8	US-11-514-704-22438	Sequence 22438, A	C 788	98	4.4	735	8	US-11-713-768-1363	Sequence 1363, Ap
C 716	99	4.5	2117	8	US-11-514-704-4842	Sequence 4842, Ap	C 789	98	4.4	810	1	US-10-438-246-27133	Sequence 27133, A
C 717	99	4.5	2135	8	US-11-713-768-65492	Sequence 65492, A	790	98	4.4	859	8	US-11-514-704-5542	Sequence 5542, Ap
C 718	99	4.5	2408	8	US-11-514-704-6593	Sequence 6593, Ap	791	98	4.4	978	8	US-11-514-704-19934	Sequence 19934, A
C 719	99	4.5	2689	8	US-11-514-704-6643	Sequence 6643, Ap	792	98	4.4	1121	8	US-11-649-663A-3619	Sequence 3619, Ap
C 720	99	4.5	3041	8	US-11-514-704-5917	Sequence 5917, Ap	793	98	4.4	1152	8	US-11-728-567-431	Sequence 431, App
C 721	99	4.5	3093	8	US-11-514-704-3853	Sequence 3853, Ap	C 794	98	4.4	1282	8	US-11-514-704-4249	Sequence 4249, Ap
C 722	99	4.5	3093	8	US-11-514-704-22100	Sequence 22100, A	795	98	4.4	1306	8	US-11-713-768-16765	Sequence 16765, A
C 723	99	4.5	3101	8	US-11-514-704-5762	Sequence 5762, Ap	796	98	4.4	1316	8	US-11-713-768-10382	Sequence 10382, A
C 724	99	4.5	4189	8	US-11-514-704-14870	Sequence 14870, A	C 797	98	4.4	1316	8	US-11-713-768-60707	Sequence 60707, A
C 725	99	4.5	4777	8	US-11-713-768-101107	Sequence 101107,	C 798	98	4.4	1377	1	US-10-438-246-11476	Sequence 11476, A
C 726	99	4.5	5265	1	US-10-438-246-13848	Sequence 13848, A	C 799	98	4.4	1426	8	US-11-713-768-11115	Sequence 11115, A
C 727	99	4.5	5567	1	US-10-438-246-22996	Sequence 22996, A	800	98	4.4	1449	8	US-11-713-768-5574	Sequence 5574, Ap
C 728	99	4.5	5746	8	US-11-551-744-158	Sequence 158, App	801	98	4.4	1478	8	US-11-514-704-17827	Sequence 17827, A
C 729	99	4.5	6182	1	US-10-533-069-1283	Sequence 1283, Ap	802	98	4.4	1509	8	US-11-713-768-43466	Sequence 43466, A
C 730	99	4.5	6803	8	US-11-625-795-10	Sequence 10, Appl	803	98	4.4	1509	8	US-11-713-768-47031	Sequence 47031, A
C 731	99	4.5	7226	8	US-11-625-795-8	Sequence 8, Appli	804	98	4.4	1520	8	US-11-713-768-2243	Sequence 2243, Ap
C 732	98.5	4.5	803	1	US-10-438-246-380	Sequence 380, App	805	98	4.4	1640	8	US-11-514-704-5358	Sequence 5358, Ap
C 733	98.5	4.5	818	8	US-11-514-704-5500	Sequence 5500, Ap	806	98	4.4	1703	1	US-10-438-246-22340	Sequence 22340, A
C 734	98.5	4.5	1042	8	US-11-713-768-62185	Sequence 62185, A	807	98	4.4	1738	8	US-11-713-768-14192	Sequence 14192, A
C 735	98.5	4.5	1058	8	US-11-649-663A-5083	Sequence 5083, Ap	C 808	98	4.4	1854	1	US-10-547-956-731	Sequence 731, App
C 736	98.5	4.5	1080	8	US-11-514-704-20174	Sequence 20174, A	809	98	4.4	1987	8	US-11-514-704-24995	Sequence 24995, A
C 737	98.5	4.5	1108	8	US-11-713-768-6348	Sequence 6348, Ap	810	98	4.4	2108	8	US-11-347-780-15	Sequence 15, Appl
C 738	98.5	4.5	1164	1	US-10-438-246-11742	Sequence 11742, A	811	98	4.4	2259	8	US-11-514-704-17033	Sequence 17033, A
C 739	98.5	4.5	1174	8	US-11-649-663A-665	Sequence 665, App	812	98	4.4	2342	8	US-11-649-663A-4475	Sequence 4475, Ap
C 740	98.5	4.5	1174	8	US-11-713-768-9315	Sequence 9315, Ap	813	98	4.4	2518	8	US-11-514-704-19723	Sequence 19723, A

C 814	98	4.4	2522	8	US-11-514-704-15691	Sequence 15691, A	C 887	97.5	4.4	3237	8	US-11-514-704-13601	Sequence 13601, A
815	98	4.4	2691	8	US-11-713-768-73159	Sequence 73159, A	888	97.5	4.4	3261	8	US-11-514-704-17265	Sequence 17265, A
816	98	4.4	2749	8	US-11-514-704-13631	Sequence 13631, A	889	97.5	4.4	3303	8	US-11-514-704-11827	Sequence 11827, A
817	98	4.4	2875	8	US-11-514-704-11133	Sequence 11133, A	890	97.5	4.4	3481	8	US-11-514-704-1065	Sequence 1065, Ap
818	98	4.4	2931	1	US-10-438-246-29134	Sequence 29134, A	891	97.5	4.4	3955	8	US-11-514-704-6596	Sequence 6596, Ap
819	98	4.4	3172	8	US-11-514-704-15622	Sequence 15622, A	892	97.5	4.4	4589	8	US-11-514-704-10133	Sequence 10133, A
C 820	98	4.4	4144	8	US-11-514-704-10517	Sequence 10517, A	C 893	97.5	4.4	4764	8	US-11-514-704-4025	Sequence 4025, Ap
C 821	98	4.4	4179	8	US-11-514-704-19149	Sequence 19149, A	C 894	97.5	4.4	4886	8	US-11-514-704-3107	Sequence 3107, Ap
C 822	98	4.4	4314	8	US-11-514-704-22589	Sequence 22589, A	C 895	97.5	4.4	5004	8	US-11-514-704-19387	Sequence 19387, A
C 823	98	4.4	4603	8	US-11-514-704-21510	Sequence 21510, A	C 896	97.5	4.4	5349	8	US-11-514-704-2622	Sequence 2622, Ap
824	98	4.4	4637	8	US-11-514-704-6273	Sequence 6273, Ap	C 897	97.5	4.4	5632	8	US-11-514-704-7909	Sequence 7909, Ap
825	98	4.4	7741	8	US-11-514-704-20803	Sequence 20803, A	C 898	97.5	4.4	6282	1	US-10-438-246-5301	Sequence 5301, Ap
826	98	4.4	10057	1	US-10-533-069-212	Sequence 212, App	899	97.5	4.4	8212	8	US-11-407-888-24	Sequence 24, Appl
C 827	97.5	4.4	705	8	US-11-713-768-27777	Sequence 27777, A	900	97	4.4	673	1	US-10-438-246-13115	Sequence 13115, A
C 828	97.5	4.4	705	8	US-11-713-768-31367	Sequence 31367, A	C 901	97	4.4	715	8	US-11-713-768-38229	Sequence 38229, A
C 829	97.5	4.4	810	8	US-11-713-768-29374	Sequence 29374, A	902	97	4.4	866	1	US-10-438-246-28875	Sequence 28875, A
C 830	97.5	4.4	810	8	US-11-713-768-32964	Sequence 32964, A	903	97	4.4	936	1	US-10-438-246-11247	Sequence 11247, A
C 831	97.5	4.4	816	8	US-11-514-704-23143	Sequence 23143, A	C 904	97	4.4	996	8	US-11-713-768-62416	Sequence 62416, A
832	97.5	4.4	877	8	US-11-649-663A-3615	Sequence 3615, Ap	C 905	97	4.4	1026	8	US-11-514-704-6099	Sequence 6099, Ap
C 833	97.5	4.4	931	8	US-11-713-768-56066	Sequence 56066, A	C 906	97	4.4	1046	8	US-11-514-704-6062	Sequence 6062, Ap
C 834	97.5	4.4	939	8	US-11-713-768-80801	Sequence 80801, A	C 907	97	4.4	1147	8	US-11-713-768-7289	Sequence 7289, Ap
C 835	97.5	4.4	985	8	US-11-514-704-643	Sequence 643, App	908	97	4.4	1230	1	US-10-438-246-27294	Sequence 27294, A
836	97.5	4.4	994	1	US-10-438-246-11171	Sequence 11171, A	909	97	4.4	1273	8	US-11-514-704-11984	Sequence 11984, A
837	97.5	4.4	1002	1	US-10-438-246-12547	Sequence 12547, A	910	97	4.4	1388	8	US-11-713-768-54632	Sequence 54632, A
838	97.5	4.4	1002	1	US-10-438-246-21982	Sequence 21982, A	C 911	97	4.4	1399	8	US-11-649-663A-2893	Sequence 2893, Ap
839	97.5	4.4	1014	1	US-10-438-246-13165	Sequence 13165, A	C 912	97	4.4	1440	8	US-11-514-704-3918	Sequence 3918, Ap
840	97.5	4.4	1014	1	US-10-438-246-22454	Sequence 22454, A	C 913	97	4.4	1459	8	US-11-514-704-19150	Sequence 19150, A
841	97.5	4.4	1090	8	US-11-713-768-35686	Sequence 35686, A	C 914	97	4.4	1478	8	US-11-649-663A-3167	Sequence 3167, Ap
842	97.5	4.4	1090	8	US-11-713-768-50873	Sequence 50873, A	915	97	4.4	1488	1	US-10-554-789-6	Sequence 6, Appli
843	97.5	4.4	1128	8	US-11-514-704-13366	Sequence 13366, A	C 916	97	4.4	1490	8	US-11-713-768-65113	Sequence 65113, A
844	97.5	4.4	1157	8	US-11-713-768-65185	Sequence 65185, A	917	97	4.4	1501	8	US-11-713-768-9361	Sequence 9361, Ap
845	97.5	4.4	1189	8	US-11-514-704-9949	Sequence 9949, Ap	C 918	97	4.4	1599	8	US-11-649-663A-5079	Sequence 5079, Ap
846	97.5	4.4	1221	8	US-11-514-704-10375	Sequence 10375, A	919	97	4.4	1611	8	US-11-514-704-3506	Sequence 3506, Ap
847	97.5	4.4	1230	1	US-10-438-246-12456	Sequence 12456, A	C 920	97	4.4	1674	1	US-10-438-246-22399	Sequence 22399, A
848	97.5	4.4	1254	1	US-10-438-246-11187	Sequence 11187, A	921	97	4.4	1676	8	US-11-649-663A-627	Sequence 627, App
849	97.5	4.4	1277	8	US-11-713-768-3365	Sequence 3365, Ap	922	97	4.4	1676	8	US-11-713-768-7160	Sequence 7160, Ap
850	97.5	4.4	1336	8	US-11-713-768-2263	Sequence 2263, Ap	923	97	4.4	1810	8	US-11-649-663A-5201	Sequence 5201, Ap
851	97.5	4.4	1379	8	US-11-649-663A-645	Sequence 645, App	C 924	97	4.4	1810	8	US-11-514-704-11106	Sequence 11106, A
852	97.5	4.4	1379	8	US-11-713-768-2038	Sequence 2038, Ap	925	97	4.4	1922	8	US-11-514-704-15275	Sequence 15275, A
853	97.5	4.4	1411	1	US-10-438-246-21917	Sequence 21917, A	926	97	4.4	1922	1	US-10-438-246-3534	Sequence 3534, Ap
854	97.5	4.4	1415	1	US-10-438-246-29894	Sequence 29894, A	927	97	4.4	1953	8	US-11-514-704-18492	Sequence 18492, A
C 855	97.5	4.4	1461	8	US-11-713-768-11236	Sequence 11236, A	928	97	4.4	1957	8	US-11-649-663A-2191	Sequence 2191, Ap
856	97.5	4.4	1502	1	US-10-438-246-23476	Sequence 23476, A	929	97	4.4	1957	8	US-11-713-768-10679	Sequence 10679, A
857	97.5	4.4	1573	8	US-11-713-768-18605	Sequence 18605, A	C 930	97	4.4	1983	8	US-11-552-440-5	Sequence 5, Appli
858	97.5	4.4	1653	8	US-11-713-768-67411	Sequence 67411, A	C 931	97	4.4	2047	8	US-11-514-704-3910	Sequence 3910, Ap
859	97.5	4.4	1680	8	US-11-649-663A-711	Sequence 711, App	C 932	97	4.4	2050	8	US-11-514-704-13979	Sequence 13979, A
860	97.5	4.4	1680	8	US-11-713-768-16332	Sequence 16332, A	933	97	4.4	2111	8	US-11-713-768-66139	Sequence 66139, A
861	97.5	4.4	1709	8	US-11-713-768-16544	Sequence 16544, A	C 934	97	4.4	2223	8	US-11-514-704-13826	Sequence 13826, A
862	97.5	4.4	1716	8	US-11-514-704-21441	Sequence 21441, A	C 935	97	4.4	2268	8	US-11-514-704-1364	Sequence 1364, Ap
863	97.5	4.4	1745	8	US-11-649-663A-959	Sequence 959, App	936	97	4.4	2554	8	US-11-514-704-12477	Sequence 12477, A
864	97.5	4.4	1745	8	US-11-713-768-16127	Sequence 16127, A	937	97	4.4	2573	8	US-11-514-704-20954	Sequence 20954, A
865	97.5	4.4	1803	8	US-11-514-704-18484	Sequence 18484, A	C 938	97	4.4	3004	8	US-11-489-234-4	Sequence 4, Appli
C 866	97.5	4.4	1830	1	US-10-438-246-20923	Sequence 20923, A	C 939	97	4.4	3039	8	US-11-713-768-86311	Sequence 86311, A
867	97.5	4.4	1855	8	US-11-514-704-7910	Sequence 7910, Ap	C 940	97	4.4	3088	8	US-11-514-704-16346	Sequence 16346, A
868	97.5	4.4	1866	8	US-11-514-704-17035	Sequence 17035, A	941	97	4.4	3152	8	US-11-347-780-3	Sequence 3, Appli
869	97.5	4.4	1937	8	US-11-514-704-14872	Sequence 14872, A	C 942	97	4.4	3162	8	US-11-713-768-86282	Sequence 86282, A
870	97.5	4.4	1993	8	US-11-649-663A-3539	Sequence 3539, Ap	C 943	97	4.4	3459	1	US-10-438-246-12905	Sequence 12905, A
C 871	97.5	4.4	2008	8	US-11-713-768-35296	Sequence 35296, A	C 944	97	4.4	3578	8	US-11-514-704-22955	Sequence 22955, A
C 872	97.5	4.4	2024	8	US-11-514-704-2748	Sequence 2748, Ap	945	97	4.4	3594	1	US-10-438-246-22284	Sequence 22284, A
873	97.5	4.4	2119	8	US-11-514-704-11354	Sequence 11354, A	C 946	97	4.4	3796	8	US-11-514-704-22687	Sequence 22687, A
874	97.5	4.4	2161	8	US-11-514-704-17160	Sequence 17160, A	947	97	4.4	3836	8	US-11-514-704-20249	Sequence 20249, A
875	97.5	4.4	2230	8	US-11-514-704-23185	Sequence 23185, A	948	97	4.4	4098	8	US-11-514-704-18491	Sequence 18491, A
876	97.5	4.4	2254	8	US-11-514-704-1489	Sequence 1489, Ap	949	97	4.4	4503	8	US-11-514-704-1305	Sequence 1305, Ap
C 877	97.5	4.4	2355	1	US-10-438-246-13672	Sequence 13672, A	950	97	4.4	4517	8	US-11-514-704-8829	Sequence 8829, Ap
878	97.5	4.4	2594	8	US-11-514-704-17647	Sequence 17647, A	C 951	97	4.4	5336	8	US-11-514-704-24001	Sequence 24001, A
C 879	97.5	4.4	2627	8	US-11-514-704-20218	Sequence 20218, A	C 952	97	4.4	5718	8	US-11-514-704-20708	Sequence 20708, A
880	97.5	4.4	2724	8	US-11-713-768-90278	Sequence 90278, A	C 953	97	4.4	6519	8	US-11-796-730-2605	Sequence 2605, Ap
881	97.5	4.4	2724	8	US-11-713-768-94034	Sequence 94034, A	C 954	97	4.4	7419	8	US-11-514-704-21253	Sequence 21253, A
882	97.5	4.4	2912	8	US-11-514-704-5887	Sequence 5887, Ap	955	96.5	4.4	514	1	US-10-567-764-24	Sequence 24, Appl
883	97.5	4.4	2981	8	US-11-514-704-7251	Sequence 7251, Ap	C 956	96.5	4.4	770	8	US-11-713-768-3329	Sequence 3329, Ap
C 884	97.5	4.4	3073	8	US-11-514-704-21267	Sequence 21267, A	C 957	96.5	4.4	791	1	US-10-438-246-3273	Sequence 3273, Ap
C 885	97.5	4.4	3219	1	US-10-438-246-622	Sequence 622, App	958	96.5	4.4	861	8	US-11-514-704-17347	Sequence 17347, A
C 886	97.5	4.4	3234	8	US-11-514-704-6142	Sequence 6142, Ap	959	96.5	4.4	870	1	US-10-438-246-12057	Sequence 12057, A



C 960	96.5	4.4	924	8	US-11-514-704-21056	Sequence 21056, A	c1033	96	4.3	1508	8	US-11-713-768-56858	Sequence 56858, A
961	96.5	4.4	1062	8	US-11-713-768-61508	Sequence 61508, A	1034	96	4.3	1534	8	US-11-713-768-109087	Sequence 109087, A
962	96.5	4.4	1067	8	US-11-713-768-15998	Sequence 15998, A	c1035	96	4.3	1563	8	US-11-713-768-90350	Sequence 90350, A
963	96.5	4.4	1213	8	US-11-728-567-553	Sequence 553, App	c1036	96	4.3	1563	8	US-11-713-768-94106	Sequence 94106, A
C 964	96.5	4.4	1235	8	US-11-713-768-35705	Sequence 35705, A	1037	96	4.3	1668	1	US-10-533-069-1185	Sequence 1185, Ap
965	96.5	4.4	1241	8	US-11-514-704-15282	Sequence 15282, A	c1038	96	4.3	1725	8	US-11-713-768-66173	Sequence 66173, A
C 966	96.5	4.4	1327	8	US-11-713-768-104901	Sequence 104901, A	c1039	96	4.3	1772	8	US-11-514-704-18079	Sequence 18079, A
C 967	96.5	4.4	1344	8	US-11-713-768-70617	Sequence 70617, A	1040	96	4.3	1839	8	US-11-713-768-86035	Sequence 86035, A
C 968	96.5	4.4	1346	8	US-11-514-704-23101	Sequence 23101, A	c1041	96	4.3	1854	1	US-10-547-956-131	Sequence 131, App
C 969	96.5	4.4	1347	8	US-11-649-663A-843	Sequence 843, App	c1042	96	4.3	1860	8	US-11-514-704-20274	Sequence 20274, A
C 970	96.5	4.4	1347	8	US-11-713-768-33322	Sequence 29732, A	1043	96	4.3	1863	8	US-11-713-768-15756	Sequence 15756, A
C 971	96.5	4.4	1347	8	US-11-713-768-33322	Sequence 33322, A	1044	96	4.3	1885	8	US-11-713-768-69234	Sequence 69234, A
C 972	96.5	4.4	1365	8	US-11-544-679-2	Sequence 2, Appli	1045	96	4.3	1899	1	US-10-438-246-12635	Sequence 12635, A
973	96.5	4.4	1409	8	US-11-713-768-64374	Sequence 64374, A	1046	96	4.3	1902	8	US-11-514-704-4311	Sequence 4311, Ap
974	96.5	4.4	1425	8	US-11-713-768-62920	Sequence 62920, A	c1047	96	4.3	1960	8	US-11-514-704-3160	Sequence 3160, Ap
975	96.5	4.4	1428	8	US-11-713-768-64624	Sequence 64624, A	c1048	96	4.3	1965	1	US-10-438-246-21361	Sequence 21361, A
976	96.5	4.4	1478	8	US-11-713-768-16191	Sequence 16191, A	1049	96	4.3	2115	8	US-11-713-768-13273	Sequence 13273, A
977	96.5	4.4	1479	8	US-11-514-704-13364	Sequence 13364, A	1050	96	4.3	2127	8	US-11-514-704-3348	Sequence 3348, Ap
978	96.5	4.4	1482	8	US-11-713-768-67114	Sequence 67114, A	1051	96	4.3	2180	8	US-11-514-704-23625	Sequence 23625, A
979	96.5	4.4	1494	8	US-11-514-704-15247	Sequence 15247, A	1052	96	4.3	2206	8	US-11-713-768-58992	Sequence 58992, A
C 980	96.5	4.4	1513	8	US-11-713-768-50788	Sequence 50788, A	1053	96	4.3	2240	8	US-11-514-704-4572	Sequence 4572, Ap
C 981	96.5	4.4	1663	8	US-11-514-704-6143	Sequence 6143, Ap	c1054	96	4.3	2376	1	US-10-438-246-4407	Sequence 4407, Ap
982	96.5	4.4	1755	8	US-11-514-704-13423	Sequence 13423, A	c1055	96	4.3	2449	8	US-11-514-704-11104	Sequence 11104, A
983	96.5	4.4	1756	8	US-11-713-768-1568	Sequence 1568, Ap	c1056	96	4.3	2563	8	US-11-514-704-6617	Sequence 6617, Ap
C 984	96.5	4.4	1762	8	US-11-713-768-17027	Sequence 17027, A	c1057	96	4.3	2629	8	US-11-514-704-19791	Sequence 19791, A
985	96.5	4.4	1856	8	US-11-713-768-65029	Sequence 65029, A	1058	96	4.3	2658	8	US-11-514-704-3329	Sequence 3329, Ap
986	96.5	4.4	1872	8	US-11-514-704-24976	Sequence 24976, A	c1059	96	4.3	2764	8	US-11-514-704-20411	Sequence 20411, A
C 987	96.5	4.4	1909	8	US-11-649-663A-3777	Sequence 3777, Ap	c1060	96	4.3	2821	1	US-10-562-377-148	Sequence 148, App
988	96.5	4.4	1912	8	US-11-514-704-13395	Sequence 13395, A	c1061	96	4.3	2900	8	US-11-514-704-20426	Sequence 20426, A
C 989	96.5	4.4	1978	1	US-10-438-246-5391	Sequence 5391, Ap	c1062	96	4.3	3030	8	US-11-514-704-9448	Sequence 9448, Ap
C 990	96.5	4.4	2089	8	US-11-514-704-24996	Sequence 24996, A	c1063	96	4.3	3195	8	US-11-514-704-3591	Sequence 3591, Ap
991	96.5	4.4	2136	8	US-11-713-768-16390	Sequence 16390, A	c1064	96	4.3	3693	8	US-11-713-768-73920	Sequence 73920, A
992	96.5	4.4	2157	1	US-10-438-246-13677	Sequence 13677, A	c1065	96	4.3	3729	8	US-11-713-768-79047	Sequence 79047, A
993	96.5	4.4	2157	1	US-10-438-246-22796	Sequence 22796, A	1066	96	4.3	3829	8	US-11-728-567-201	Sequence 201, App
994	96.5	4.4	2247	1	US-10-438-246-14483	Sequence 14483, A	1067	96	4.3	3959	8	US-11-514-704-4962	Sequence 4962, Ap
995	96.5	4.4	2289	1	US-10-438-246-11250	Sequence 11250, A	c1068	96	4.3	4102	1	US-10-562-377-139	Sequence 139, App
996	96.5	4.4	2316	8	US-11-514-704-3034	Sequence 3034, Ap	1069	96	4.3	4168	8	US-11-514-704-12307	Sequence 12307, A
C 997	96.5	4.4	3005	8	US-11-514-704-22954	Sequence 22954, A	1070	96	4.3	4612	8	US-11-514-704-5691	Sequence 5691, Ap
998	96.5	4.4	3093	8	US-11-514-704-23986	Sequence 23986, A	c1071	96	4.3	4650	8	US-11-514-704-21769	Sequence 21769, A
999	96.5	4.4	3198	8	US-11-713-768-30942	Sequence 30942, A	c1072	96	4.3	5095	8	US-11-514-704-10099	Sequence 10099, A
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1001	96.5	4.4	3198	8	US-11-713-768-49018	Sequence 49018, A	1074	95.5	4.3	766	8	US-11-713-768-63590	Sequence 63590, A
c1002	96.5	4.4	3332	8	US-11-514-704-1369	Sequence 1369, Ap	1075	95.5	4.3	847	8	US-11-713-768-4298	Sequence 4298, Ap
c1003	96.5	4.4	3788	8	US-11-514-704-23621	Sequence 23621, A	1076	95.5	4.3	970	8	US-11-514-704-11144	Sequence 11144, A
c1004	96.5	4.4	4419	8	US-11-514-704-3106	Sequence 3106, Ap	1077	95.5	4.3	1005	8	US-11-713-768-104612	Sequence 104612, A
1005	96.5	4.4	4506	1	US-10-438-246-14504	Sequence 14504, A	1078	95.5	4.3	1031	1	US-10-438-246-26636	Sequence 26636, A
1006	96.5	4.4	4698	1	US-10-438-246-13852	Sequence 13852, A	1079	95.5	4.3	1048	8	US-11-514-704-5633	Sequence 5633, Ap
1007	96.5	4.4	4995	1	US-10-438-246-23006	Sequence 23006, A	1080	95.5	4.3	1113	8	US-11-796-730-2120	Sequence 2120, Ap
1008	96.5	4.4	6343	8	US-11-514-704-12309	Sequence 12309, A	1081	95.5	4.3	1119	1	US-10-438-246-12460	Sequence 12460, A
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1011	96	4.3	617	8	US-11-514-704-19532	Sequence 19532, A	1084	95.5	4.3	1179	8	US-11-514-704-24397	Sequence 24397, A
1012	96	4.3	831	1	US-10-438-246-11866	Sequence 11866, A	1085	95.5	4.3	1236	1	US-10-438-246-12803	Sequence 12803, A
c1013	96	4.3	958	8	US-11-713-768-4183	Sequence 4183, Ap	1086	95.5	4.3	1244	8	US-11-713-768-9407	Sequence 9407, Ap
c1014	96	4.3	958	8	US-11-713-768-12169	Sequence 12169, A	1087	95.5	4.3	1258	8	US-11-713-768-62287	Sequence 62287, A
c1015	96	4.3	958	8	US-11-713-768-19690	Sequence 19690, A	1088	95.5	4.3	1302	8	US-11-713-768-53093	Sequence 53093, A
1016	96	4.3	976	8	US-11-514-704-20333	Sequence 20333, A	1089	95.5	4.3	1321	8	US-11-713-768-67877	Sequence 67877, A
1017	96	4.3	1032	8	US-11-713-768-63897	Sequence 63897, A	1090	95.5	4.3	1329	8	US-11-713-768-91922	Sequence 91922, A
1018	96	4.3	1041	8	US-11-713-768-67076	Sequence 67076, A	1091	95.5	4.3	1329	8	US-11-713-768-95678	Sequence 95678, A
1019	96	4.3	1056	8	US-11-713-768-8147	Sequence 8147, Ap	c1092	95.5	4.3	1344	8	US-11-713-768-88600	Sequence 88600, A
1020	96	4.3	1098	1	US-10-438-246-21455	Sequence 21455, A	c1093	95.5	4.3	1344	8	US-11-713-768-92356	Sequence 92356, A
c1021	96	4.3	1106	8	US-11-514-704-20472	Sequence 20472, A	c1094	95.5	4.3	1354	8	US-11-514-704-4929	Sequence 4929, Ap
1022	96	4.3	1273	8	US-11-514-704-4042	Sequence 4042, Ap	1095	95.5	4.3	1365	1	US-10-438-246-22196	Sequence 22196, A
1023	96	4.3	1300	8	US-11-713-768-68979	Sequence 68979, A	1096	95.5	4.3	1368	8	US-11-713-768-16447	Sequence 16447, A
1024	96	4.3	1309	8	US-11-713-768-56553	Sequence 56553, A	c1097	95.5	4.3	1384	8	US-11-514-704-14150	Sequence 14150, A
c1025	96	4.3	1310	8	US-11-514-704-20471	Sequence 20471, A	1098	95.5	4.3	1442	1	US-10-438-246-26775	Sequence 26775, A
1026	96	4.3	1326	8	US-11-713-768-111357	Sequence 111357, A	1099	95.5	4.3	1468	8	US-11-514-704-23732	Sequence 23732, A
1027	96	4.3	1327	1	US-10-438-246-369	Sequence 369, App	1100	95.5	4.3	1497	1	US-10-438-246-2936	Sequence 2936, Ap
1028	96	4.3	1359	8	US-11-649-663A-275	Sequence 275, App	1101	95.5	4.3	1497	8	US-11-514-704-2167	Sequence 2167, Ap
1029	96	4.3	1478	8	US-11-713-768-59187	Sequence 59187, A	1102	95.5	4.3	1517	8	US-11-713-768-6442	Sequence 6442, Ap
1030	96	4.3	1496	8	US-11-514-704-23174	Sequence 23174, A	1103	95.5	4.3	1517	8	US-11-713-768-10550	Sequence 10550, A
1031	96	4.3	1498	8	US-11-713-768-65655	Sequence 65655, A	c1104	95.5	4.3	1535	8	US-11-514-704-22643	Sequence 22643, A
1032	96	4.3	1504	8	US-11-713-768-9376	Sequence 9376, Ap	1105	95.5	4.3	1562	8	US-11-713-768-60275	Sequence 60275, A



1106	95.5	4.3	1580	8	US-11-649-663A-3607	Sequence 3607, Ap	1179	95	4.3	1374	8	US-11-713-768-68134	Sequence 68134, A
1107	95.5	4.3	1582	8	US-11-713-768-17681	Sequence 17681, A	c1180	95	4.3	1391	8	US-11-713-768-7039	Sequence 7039, Ap
1108	95.5	4.3	1589	8	US-11-713-768-57022	Sequence 57022, A	1181	95	4.3	1422	8	US-11-582-540-54	Sequence 54, Appl
1109	95.5	4.3	1593	8	US-11-629-727-53	Sequence 53, Appl	1182	95	4.3	1463	8	US-11-514-704-5543	Sequence 5543, Ap
c1110	95.5	4.3	1599	8	US-11-514-704-23279	Sequence 23279, A	1183	95	4.3	1495	8	US-11-514-704-22080	Sequence 22080, A
c1111	95.5	4.3	1632	8	US-11-713-768-62601	Sequence 62601, A	1184	95	4.3	1529	8	US-11-713-768-68428	Sequence 68428, A
1112	95.5	4.3	1656	8	US-11-514-704-9725	Sequence 9725, Ap	1185	95	4.3	1543	8	US-11-514-704-23187	Sequence 23187, A
1113	95.5	4.3	1691	8	US-11-649-663A-5437	Sequence 5437, Ap	1186	95	4.3	1544	8	US-11-713-768-2719	Sequence 2719, Ap
1114	95.5	4.3	1758	8	US-11-514-704-6513	Sequence 6513, Ap	1187	95	4.3	1555	8	US-11-514-704-12359	Sequence 12359, A
1115	95.5	4.3	1788	1	US-10-547-956-351	Sequence 351, App	1188	95	4.3	1583	1	US-10-438-246-22615	Sequence 22615, A
1116	95.5	4.3	1828	8	US-11-713-768-63031	Sequence 63031, A	1189	95	4.3	1614	8	US-11-713-768-1798	Sequence 1798, Ap
1117	95.5	4.3	1894	8	US-11-514-704-24587	Sequence 24587, A	1190	95	4.3	1614	8	US-11-713-768-2664	Sequence 2664, Ap
c1118	95.5	4.3	1910	8	US-11-514-704-19872	Sequence 19872, A	1191	95	4.3	1614	8	US-11-713-768-8349	Sequence 8349, Ap
c1119	95.5	4.3	1913	8	US-11-713-768-17553	Sequence 17553, A	1192	95	4.3	1635	8	US-11-514-704-17860	Sequence 17860, A
1120	95.5	4.3	1971	8	US-11-713-768-89083	Sequence 89083, A	c1193	95	4.3	1714	8	US-11-713-768-11200	Sequence 11200, A
1121	95.5	4.3	1971	8	US-11-713-768-92839	Sequence 92839, A	c1194	95	4.3	1715	8	US-11-713-768-53798	Sequence 53798, A
1122	95.5	4.3	1990	8	US-11-713-768-100192	Sequence 100192, A	1195	95	4.3	1722	8	US-11-514-704-2044	Sequence 2044, Ap
1123	95.5	4.3	1991	8	US-11-713-768-35009	Sequence 35009, A	1196	95	4.3	1732	8	US-11-713-768-66557	Sequence 66557, A
1124	95.5	4.3	2025	8	US-11-713-768-69474	Sequence 69474, A	1197	95	4.3	1741	8	US-11-713-768-66088	Sequence 66088, A
1125	95.5	4.3	2103	8	US-11-629-727-52	Sequence 52, Appl	1198	95	4.3	1794	8	US-11-514-704-16159	Sequence 16159, A
1126	95.5	4.3	2152	8	US-11-514-704-271	Sequence 271, App	c1199	95	4.3	1797	1	US-10-438-246-2819	Sequence 2819, Ap
1127	95.5	4.3	2231	8	US-11-560-738A-19	Sequence 19, Appl	1200	95	4.3	1808	8	US-11-514-704-1539	Sequence 1539, Ap
1128	95.5	4.3	2286	8	US-11-713-768-17343	Sequence 17343, A	1201	95	4.3	1863	8	US-11-713-768-91379	Sequence 91379, A
1129	95.5	4.3	2314	8	US-11-514-704-23666	Sequence 23666, A	1202	95	4.3	1863	8	US-11-713-768-95135	Sequence 95135, A
1130	95.5	4.3	2324	8	US-11-514-704-8390	Sequence 8390, Ap	1203	95	4.3	1870	8	US-11-514-704-16348	Sequence 16348, A
1131	95.5	4.3	2333	8	US-11-514-704-14673	Sequence 14673, A	c1204	95	4.3	1881	1	US-10-438-246-10978	Sequence 10978, A
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1134	95.5	4.3	2704	8	US-11-713-768-46304	Sequence 46304, A	1207	95	4.3	1953	8	US-11-514-704-9098	Sequence 9098, Ap
1135	95.5	4.3	2729	8	US-11-514-704-18450	Sequence 18450, A	1208	95	4.3	1957	1	US-10-438-246-14255	Sequence 14255, A
1136	95.5	4.3	2957	8	US-11-514-704-12333	Sequence 12333, A	1209	95	4.3	1973	8	US-11-514-704-2472	Sequence 2472, Ap
c1137	95.5	4.3	3011	8	US-11-514-704-19103	Sequence 19103, A	1210	95	4.3	2058	8	US-11-514-704-15872	Sequence 15872, A
c1138	95.5	4.3	3214	8	US-11-514-704-6297	Sequence 6297, Ap	1211	95	4.3	2077	1	US-10-438-246-315	Sequence 315, App
1139	95.5	4.3	3248	8	US-11-514-704-9848	Sequence 9848, Ap	1212	95	4.3	2183	8	US-11-713-768-108593	Sequence 108593, A
c1140	95.5	4.3	3283	8	US-11-514-704-15803	Sequence 15803, A	1213	95	4.3	2230	8	US-11-713-768-47147	Sequence 47147, A
1141	95.5	4.3	3763	8	US-11-544-679-1	Sequence 1, Appli	1214	95	4.3	2242	8	US-11-514-704-11809	Sequence 11809, A
1142	95.5	4.3	3764	8	US-11-514-704-22440	Sequence 22440, A	1215	95	4.3	2264	8	US-11-713-768-77314	Sequence 77314, A
c1143	95.5	4.3	3901	8	US-11-514-704-14532	Sequence 14532, A	1216	95	4.3	2345	8	US-11-514-704-18720	Sequence 18720, A
c1144	95.5	4.3	3936	8	US-11-514-704-19592	Sequence 19592, A	1217	95	4.3	2361	8	US-11-713-768-69822	Sequence 69822, A
1145	95.5	4.3	4662	1	US-10-438-246-14649	Sequence 14649, A	1218	95	4.3	2481	8	US-11-713-768-75176	Sequence 75176, A
1146	95.5	4.3	4783	1	US-10-533-069-1020	Sequence 1020, Ap	1219	95	4.3	2666	8	US-11-643-077-3	Sequence 3, Appli
1147	95.5	4.3	5027	8	US-11-514-704-168	Sequence 168, App	1220	95	4.3	2856	8	US-11-713-768-96889	Sequence 96889, A
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1150	95.5	4.3	6579	1	US-10-438-246-11658	Sequence 11658, A	1223	95	4.3	3060	8	US-11-649-663A-1531	Sequence 1531, Ap
c1151	95.5	4.3	7001	1	US-10-438-246-21266	Sequence 21266, A	c1224	95	4.3	3152	8	US-11-514-704-5225	Sequence 5225, Ap
c1152	95.5	4.3	7371	8	US-11-514-704-23944	Sequence 23944, A	1225	95	4.3	3191	8	US-11-514-704-12080	Sequence 12080, A
1153	95.5	4.3	21725	8	US-11-700-462-1	Sequence 1, Appli	c1226	95	4.3	3199	8	US-11-514-704-1368	Sequence 1368, Ap
1154	95	4.3	421	1	US-10-567-764-20	Sequence 20, Appl	1227	95	4.3	3405	8	US-11-514-704-15027	Sequence 15027, A
1155	95	4.3	755	8	US-11-514-704-22876	Sequence 22876, A	1228	95	4.3	3933	1	US-10-533-069-130	Sequence 130, App
1156	95	4.3	855	8	US-11-713-768-38540	Sequence 38540, A	c1229	95	4.3	4038	1	US-10-438-246-12715	Sequence 12715, A
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1159	95	4.3	947	8	US-11-713-768-109717	Sequence 109717, A	c1232	95	4.3	5004	1	US-10-438-246-14367	Sequence 14367, A
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1163	95	4.3	1026	8	US-11-514-704-5483	Sequence 5483, Ap	1236	95	4.3	8612	8	US-11-514-704-12624	Sequence 12624, A
1164	95	4.3	1033	1	US-10-438-246-21052	Sequence 21052, A	1237	95	4.3	15059	1	US-10-533-069-1601	Sequence 1601, Ap
1165	95	4.3	1064	8	US-11-713-768-11647	Sequence 11647, A	1238	95	4.3	518360	8	US-11-257-477-125	Sequence 125, App
1166	95	4.3	1080	8	US-11-514-704-11985	Sequence 11985, A	1239	94.5	4.3	484	8	US-11-713-768-14959	Sequence 14959, A
1167	95	4.3	1108	8	US-11-514-704-9363	Sequence 9363, Ap	1240	94.5	4.3	603	1	US-10-438-246-12633	Sequence 12633, A
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c1170	95	4.3	1187	8	US-11-514-704-24030	Sequence 24030, A	1242	94.5	4.3	870	1	US-10-438-246-12058	Sequence 12058, A
1171	95	4.3	1244	8	US-11-713-768-5890	Sequence 5890, Ap	1243	94.5	4.3	870	1	US-10-438-246-21636	Sequence 21636, A
1172	95	4.3	1257	8	US-11-713-768-68476	Sequence 68476, A	1244	94.5	4.3	897	1	US-10-438-246-12461	Sequence 12461, A
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1176	95	4.3	1356	1	US-10-554-789-9	Sequence 9, Appli	1248	94.5	4.3	1099	8	US-11-514-704-8507	Sequence 8507, Ap
1177	95	4.3	1356	8	US-11-713-768-4714	Sequence 4714, Ap	c1249	94.5	4.3	1203	8	US-11-713-768-764	Sequence 764, App
c1178	95	4.3	1368	8	US-11-514-704-4251	Sequence 4251, Ap	1250	94.5	4.3	1275	8	US-11-713-768-46007	Sequence 46007, A
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1253	94.5	4.3	1353	8	US-11-713-768-65360	Sequence 65360, A	1326	94	4.3	1422	8	US-11-713-768-6340	Sequence 6340, Ap
1254	94.5	4.3	1466	8	US-11-514-704-11228	Sequence 11228, A	1327	94	4.3	1430	8	US-11-713-768-62773	Sequence 62773, A
c1255	94.5	4.3	1480	1	US-10-438-246-21874	Sequence 21874, A	c1328	94	4.3	1458	8	US-11-713-768-71829	Sequence 71829, A
1256	94.5	4.3	1532	8	US-11-649-663A-3149	Sequence 3149, Ap	1329	94	4.3	1529	8	US-11-713-768-59086	Sequence 59086, A
c1257	94.5	4.3	1543	8	US-11-514-704-5627	Sequence 5627, Ap	c1330	94	4.3	1534	8	US-11-713-768-9871	Sequence 9871, Ap
1258	94.5	4.3	1607	8	US-11-649-663A-4529	Sequence 4529, Ap	1331	94	4.3	1571	8	US-11-713-768-2621	Sequence 2621, Ap
1259	94.5	4.3	1625	8	US-11-713-768-112014	Sequence 112014, A	1332	94	4.3	1630	8	US-11-514-704-22029	Sequence 22029, A
1260	94.5	4.3	1734	8	US-11-713-768-45878	Sequence 45878, A	c1333	94	4.3	1635	8	US-11-713-768-100783	Sequence 100783,
1261	94.5	4.3	1746	8	US-11-713-768-8939	Sequence 8939, Ap	1334	94	4.3	1645	8	US-11-514-704-7929	Sequence 7929, Ap
1262	94.5	4.3	1761	8	US-11-552-061A-6	Sequence 6, Appli	1335	94	4.3	1722	8	US-11-514-704-16155	Sequence 16155, A
1263	94.5	4.3	1768	8	US-11-713-768-107895	Sequence 107895, A	1336	94	4.3	1728	8	US-11-514-704-4040	Sequence 4040, Ap
c1264	94.5	4.3	1774	8	US-11-514-704-19481	Sequence 19481, A	1337	94	4.3	1743	8	US-11-713-768-6967	Sequence 6967, Ap
1265	94.5	4.3	1776	8	US-11-514-704-15956	Sequence 15956, A	1338	94	4.3	1773	8	US-11-713-768-66589	Sequence 66589, A
c1266	94.5	4.3	1899	8	US-11-713-768-86765	Sequence 86765, A	c1339	94	4.3	1776	8	US-11-713-768-43830	Sequence 43830, A
1267	94.5	4.3	1916	8	US-11-713-768-66646	Sequence 66646, A	c1340	94	4.3	1776	8	US-11-713-768-46043	Sequence 46043, A
1268	94.5	4.3	1929	8	US-11-514-704-13450	Sequence 13450, A	c1341	94	4.3	1776	8	US-11-713-768-87583	Sequence 87583, A
1269	94.5	4.3	1929	8	US-11-514-704-19956	Sequence 19956, A	1342	94	4.3	1814	8	US-11-514-704-12318	Sequence 12318, A
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c1271	94.5	4.3	2044	8	US-11-713-768-83108	Sequence 83108, A	1344	94	4.3	1833	1	US-10-533-069-1167	Sequence 1167, Ap
1272	94.5	4.3	2050	8	US-11-713-768-97910	Sequence 97910, A	1345	94	4.3	1857	8	US-11-728-567-223	Sequence 223, App
1273	94.5	4.3	2117	8	US-11-713-768-100681	Sequence 100681, A	c1346	94	4.3	2106	8	US-11-514-704-6144	Sequence 6144, Ap
c1274	94.5	4.3	2182	8	US-11-514-704-12360	Sequence 12360, A	c1347	94	4.3	2140	8	US-11-713-768-63279	Sequence 63279, A
c1275	94.5	4.3	2195	8	US-11-514-704-10740	Sequence 10740, A	1348	94	4.3	2178	1	US-10-438-246-12412	Sequence 12412, A
1276	94.5	4.3	2203	8	US-11-514-704-8544	Sequence 8544, Ap	c1349	94	4.3	2181	8	US-11-342-364-1	Sequence 1, Appli
1277	94.5	4.3	2256	8	US-11-713-768-46280	Sequence 46280, A	c1350	94	4.3	2346	1	US-10-562-377-189	Sequence 189, App
1278	94.5	4.3	2292	8	US-11-544-679-10	Sequence 10, Appl	1351	94	4.3	2441	8	US-11-514-704-7870	Sequence 7870, Ap
1279	94.5	4.3	2382	8	US-11-514-704-6853	Sequence 6853, Ap	c1352	94	4.3	2451	8	US-11-342-364-8	Sequence 8, Appli
1280	94.5	4.3	2421	8	US-11-514-704-16888	Sequence 16888, A	c1353	94	4.3	2487	8	US-11-342-364-7	Sequence 7, Appli
c1281	94.5	4.3	2473	1	US-10-562-377-145	Sequence 145, App	1354	94	4.3	2527	8	US-11-514-704-2378	Sequence 2378, Ap
1282	94.5	4.3	2484	1	US-10-438-246-15791	Sequence 15791, A	1355	94	4.3	2580	1	US-10-594-266-37	Sequence 37, Appl
1283	94.5	4.3	2534	8	US-11-552-437-25	Sequence 25, Appl	c1356	94	4.3	2637	8	US-11-342-364-6	Sequence 6, Appli
1284	94.5	4.3	2665	8	US-11-677-509-1	Sequence 1, Appli	1357	94	4.3	2781	8	US-11-514-704-7675	Sequence 7675, Ap
1285	94.5	4.3	2830	8	US-11-514-704-8941	Sequence 8941, Ap	c1358	94	4.3	2808	8	US-11-342-364-5	Sequence 5, Appli
c1286	94.5	4.3	2860	8	US-11-514-704-2211	Sequence 2211, Ap	1359	94	4.3	2832	1	US-10-438-246-12330	Sequence 12330, A
1287	94.5	4.3	3025	8	US-11-514-704-2803	Sequence 2803, Ap	c1360	94	4.3	2850	8	US-11-514-704-18858	Sequence 18858, A
1288	94.5	4.3	3162	1	US-10-533-069-2073	Sequence 2073, Ap	c1361	94	4.3	2971	8	US-11-514-704-13671	Sequence 13671, A
c1289	94.5	4.3	3280	8	US-11-514-704-626	Sequence 626, App	c1362	94	4.3	3030	8	US-11-342-364-3	Sequence 3, Appli
c1290	94.5	4.3	3472	8	US-11-514-704-18777	Sequence 18777, A	c1363	94	4.3	3060	8	US-11-342-364-11	Sequence 11, Appl
c1291	94.5	4.3	3558	8	US-11-514-704-737	Sequence 737, App	1364	94	4.3	3091	8	US-11-514-704-6763	Sequence 6763, Ap
1292	94.5	4.3	3639	1	US-10-438-246-13781	Sequence 13781, A	1365	94	4.3	3237	8	US-11-514-704-7092	Sequence 7092, Ap
1293	94.5	4.3	4121	1	US-10-533-069-1010	Sequence 1010, Ap	1366	94	4.3	3349	1	US-10-533-069-1778	Sequence 1778, Ap
1294	94.5	4.3	4692	1	US-10-438-246-12656	Sequence 12656, A	c1367	94	4.3	3467	8	US-11-514-704-17702	Sequence 17702, A
c1295	94.5	4.3	4849	8	US-11-514-704-2116	Sequence 2116, Ap	c1368	94	4.3	3474	8	US-11-342-364-9	Sequence 9, Appli
c1296	94.5	4.3	4957	1	US-10-438-246-22084	Sequence 22084, A	1369	94	4.3	3821	8	US-11-514-704-3507	Sequence 3507, Ap
c1297	94.5	4.3	5033	8	US-11-646-784-1	Sequence 1, Appli	1370	94	4.3	4129	8	US-11-514-704-11096	Sequence 11096, A
c1298	94.5	4.3	5033	8	US-11-646-945-1	Sequence 1, Appli	1371	94	4.3	4586	8	US-11-514-704-5449	Sequence 5449, Ap
c1299	94.5	4.3	5055	8	US-11-514-704-21476	Sequence 21476, A	1372	94	4.3	4755	8	US-11-514-704-17666	Sequence 17666, A
1300	94.5	4.3	5101	8	US-11-514-704-5287	Sequence 5287, Ap	1373	94	4.3	4974	1	US-10-438-246-15454	Sequence 15454, A
c1301	94.5	4.3	7398	8	US-11-514-704-24782	Sequence 24782, A	1374	94	4.3	4990	8	US-11-514-704-11110	Sequence 11110, A
1302	94.5	4.3	7893	1	US-10-438-246-11666	Sequence 11666, A	1375	94	4.3	5638	1	US-10-438-246-22902	Sequence 22902, A
c1303	94.5	4.3	8425	1	US-10-438-246-21268	Sequence 21268, A	1376	94	4.3	6484	8	US-11-514-704-13921	Sequence 13921, A
1304	94.5	4.3	9731	1	US-10-438-246-23019	Sequence 23019, A	c1377	94	4.3	7705	8	US-11-514-704-21078	Sequence 21078, A
1305	94.5	4.3	10237	8	US-11-514-704-5086	Sequence 5086, Ap	1378	94	4.3	8831	8	US-11-739-906-74	Sequence 74, Appl
1306	94.5	4.3	14248	1	US-10-533-069-1584	Sequence 1584, Ap	1379	94	4.3	8831	8	US-11-739-872-74	Sequence 74, Appl
1307	94.5	4.3	33476	8	US-11-578-096-6	Sequence 6, Appli	c1380	94	4.3	25782	8	US-11-551-744-159	Sequence 159, App
1308	94.5	4.3	33583	8	US-11-578-096-5	Sequence 5, Appli	c1381	94	4.3	186854	8	US-11-796-028-34	Sequence 34, Appl
1309	94.5	4.3	33589	8	US-11-578-096-7	Sequence 7, Appli	c1382	94	4.3	186854	8	US-11-796-027-34	Sequence 34, Appl
1310	94.5	4.3	34986	8	US-11-365-203-2	Sequence 2, Appli	1383	93.5	4.2	730	1	US-10-438-246-22485	Sequence 22485, A
1311	94.5	4.3	36066	8	US-11-578-096-4	Sequence 4, Appli	1384	93.5	4.2	757	8	US-11-653-567-15	Sequence 15, Appl
1312	94	4.3	789	8	US-11-713-768-63959	Sequence 63959, A	1385	93.5	4.2	866	1	US-10-438-246-3790	Sequence 3790, Ap
1313	94	4.3	837	1	US-10-438-246-12431	Sequence 12431, A	1386	93.5	4.2	872	1	US-10-438-246-3156	Sequence 3156, Ap
1314	94	4.3	891	8	US-11-514-704-24912	Sequence 24912, A	1387	93.5	4.2	891	8	US-11-514-704-24939	Sequence 24939, A
1315	94	4.3	894	8	US-11-713-768-59357	Sequence 59357, A	c1388	93.5	4.2	904	8	US-11-514-704-12863	Sequence 12863, A
1316	94	4.3	909	1	US-10-438-246-21900	Sequence 21900, A	1389	93.5	4.2	912	1	US-10-438-246-12418	Sequence 12418, A
1317	94	4.3	1005	1	US-10-438-246-11231	Sequence 11231, A	1390	93.5	4.2	924	8	US-11-713-768-63527	Sequence 63527, A
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1319	94	4.3	1071	8	US-11-514-704-7996	Sequence 7996, Ap	1392	93.5	4.2	976	8	US-11-514-704-13521	Sequence 13521, A
1320	94	4.3	1215	1	US-10-438-246-2544	Sequence 2544, Ap	1393	93.5	4.2	1019	8	US-11-514-704-12090	Sequence 12090, A
1321	94	4.3	1244	8	US-11-713-768-11108	Sequence 11108, A	1394	93.5	4.2	1061	8	US-11-514-704-4416	Sequence 4416, Ap
1322	94	4.3	1371	8	US-11-649-663A-4219	Sequence 4219, Ap	c1395	93.5	4.2	1072	8	US-11-713-768-30291	Sequence 30291, A
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1324	94	4.3	1382	8	US-11-560-738A-154	Sequence 154, App	1397	93.5	4.2	1149	8	US-11-514-704-18607	Sequence 18607, A

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1399 93.5 4.2 1168 8 US-11-713-768-110431 Sequence 110431,  
1400 93.5 4.2 1192 8 US-11-514-704-2677 Sequence 2677, Ap  
1401 93.5 4.2 1193 8 US-11-649-663A-4525 Sequence 4525, Ap  
1402 93.5 4.2 1241 8 US-11-713-768-63375 Sequence 63375, A  
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106	2072	93.7	2015	74	US-11-395-249-39	Sequence 39, Appl
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117	2022	91.5	2221	48	US-10-529-348-2290	Sequence 2290, Ap
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127	1851	83.7	1423	23	US-09-488-725B-9363	Sequence 9363, Ap
128	1851	83.7	1423	26	US-09-552-317-9363	Sequence 9363, Ap
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130	1851	83.7	1423	45	US-10-302-689A-78457	Sequence 78457, A
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136	1822	82.4	1314	40	US-10-235-926-4381	Sequence 4381, Ap
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143	1430	64.7	1036	33	US-09-898-888A-12786	Sequence 12786, A
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163	791	35.8	855	59	US-10-917-503C-2041	Sequence 2041, Ap
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174	730	33.0	472	32	US-09-838-601-599	Sequence 599, App
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c 179	709	32.1	3114	57	US-10-750-185-32681	Sequence 32681, A
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c 187	650	29.4	400	35	US-09-943-143-1814	Sequence 1814, Ap
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196	584	26.4	556	28	US-09-649-163-2570	Sequence 2570, Ap
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203	551	24.9	311	46	US-10-349-781-46627	Sequence 46627, A
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c1151	156	7.1	48626	85	US-60-164-769-26058	Sequence 26058, A
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c1157	156	7.1	745443	22	US-09-335-032A-12213	Sequence 12213, A
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1163	154.5	7.0	272	25	US-09-540-229-176422	Sequence 176422, Ap
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1171	154.5	7.0	13715	1	PCT-US01-27760A-365	Sequence 365, App
1172	154.5	7.0	13715	28	US-09-687-527-399	Sequence 399, App
1173	154.5	7.0	13715	46	US-10-399-103-365	Sequence 365, App
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1180	154	7.0	127943	46	US-10-330-773-628	Sequence 628, App
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1183	154	7.0	127943	75	US-11-403-116-628	Sequence 113, App
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1189	153.5	6.9	4755	85	US-60-175-871-133	Sequence 133, App
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1233	151.5	6.9	1005	73	US-11-360-355-47092	Sequence 47092, A	1306	149	6.7	2154	92	US-60-655-875-76914	Sequence 76914, A
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c1235	151.5	6.9	1396	73	US-11-360-355-76736	Sequence 76736, A	1308	149	6.7	3480	92	US-60-655-875-13116	Sequence 13116, A
c1236	151.5	6.9	1396	92	US-60-655-875-76736	Sequence 76736, A	1309	149	6.7	4830	46	US-10-369-493-25222	Sequence 25222, A
1237	151.5	6.9	2751	39	US-10-179-131-997	Sequence 997, App	1310	149	6.7	4830	88	US-60-360-039-25222	Sequence 25222, A
1238	151.5	6.9	3922	85	US-60-167-217-17393	Sequence 17393, A	1311	149	6.7	4830	94	US-60-851-434-25	Sequence 25, Appl
1239	151.5	6.9	4829	27	US-09-614-150-17339	Sequence 17339, A	1312	149	6.7	4911	59	US-10-932-182A-75783	Sequence 75783, A
1240	151.5	6.9	4829	27	US-09-614-150A-17339	Sequence 17339, A	1313	149	6.7	4911	69	US-11-217-529-75783	Sequence 75783, A
1241	151.5	6.9	4829	65	US-11-097-143-17339	Sequence 17339, A	1314	149	6.7	315341	19	US-09-012-031-304	Sequence 304, App
1242	151.5	6.9	4829	85	US-60-171-625-362	Sequence 362, App	1315	149	6.7	315341	19	US-09-012-031B-304	Sequence 304, App
1243	151.5	6.9	4829	85	US-60-173-464-14245	Sequence 14245, A	1316	149	6.7	315341	19	US-09-012-031C-304	Sequence 304, App
1244	151.5	6.9	4829	85	US-60-191-637-17389	Sequence 17389, A	1317	149	6.7	315341	22	US-09-335-032-12206	Sequence 12206, A
1245	151.5	6.9	4829	85	US-60-191-681-13753	Sequence 13753, A	1318	149	6.7	315341	22	US-09-335-032A-12206	Sequence 12206, A
1246	151.5	6.9	4912	73	US-11-360-355-12974	Sequence 12974, A	1319	149	6.7	315341	59	US-10-915-727-12206	Sequence 12206, A
1247	151.5	6.9	4912	92	US-60-655-875-12974	Sequence 12974, A	1320	148.5	6.7	1515	76	US-10-915-727-12206	Sequence 12206, A
1248	151.5	6.9	8479	39	US-10-144-771-16337	Sequence 16337, A	1321	148.5	6.7	3044	86	US-11-443-428A-587458	Sequence 587458, A
1249	151.5	6.9	8479	88	US-60-360-207-16337	Sequence 16337, A	1322	148	6.7	996	76	US-11-443-428A-71851	Sequence 71851, A
1250	151.5	6.9	57082	2	PCT-US03-37041-1	Sequence 1, Appli	1323	148	6.7	1044	48	US-10-508-263-109	Sequence 109, App
1251	151.5	6.9	57082	47	US-10-475-117-311	Sequence 311, App	1324	148	6.7	1178	73	US-11-360-355-56580	Sequence 56580, A
1252	151.5	6.9	57082	56	US-10-715-066A-1	Sequence 1, Appli	1325	148	6.7	1178	92	US-60-655-875-56580	Sequence 56580, A
1253	151.5	6.9	57082	89	US-60-427-045-311	Sequence 311, App	1326	148	6.7	1514	73	US-11-360-355-25816	Sequence 25816, A
c1254	151	6.8	1571	69	US-11-266-748A-15633	Sequence 15633, A	1327	148	6.7	1514	92	US-60-655-875-25816	Sequence 25816, A
c1255	151	6.8	1571	69	US-11-266-748A-21283	Sequence 21283, A	c1328	148	6.7	1751	47	US-10-437-963-9763	Sequence 9763, Ap
c1256	151	6.8	1571	69	US-11-266-748A-65013	Sequence 65013, A	1329	148	6.7	2220	76	US-11-443-428A-71848	Sequence 71848, A
c1257	151	6.8	1571	69	US-11-266-748A-67869	Sequence 67869, A	c1330	148	6.7	2570	1	PCT-US02-14342-73	Sequence 73, Appl
c1258	151	6.8	1797	39	US-10-144-771-37909	Sequence 37909, A	c1331	148	6.7	2570	39	US-10-138-588-73	Sequence 73, Appl
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1260	151	6.8	4626	85	US-60-173-464-4930	Sequence 4930, Ap	c1333	148	6.7	2859	76	US-11-443-428A-477722	Sequence 477722, A
1261	151	6.8	5089	76	US-11-443-428A-73518	Sequence 73518, A	c1334	148	6.7	3418	85	US-60-191-637-21867	Sequence 21867, A
1262	151	6.8	5929	27	US-09-614-150-6038	Sequence 6038, Ap	c1335	148	6.7	3418	85	US-60-191-681-17253	Sequence 17253, A
1263	151	6.8	5929	27	US-09-614-150A-6038	Sequence 6038, Ap	c1336	148	6.7	6000	94	US-60-873-737-1276	Sequence 1276, Ap
1264	151	6.8	5929	65	US-11-097-143-6038	Sequence 6038, Ap	c1337	148	6.7	7417	27	US-09-614-150-21793	Sequence 21793, A
1265	151	6.8	5929	85	US-60-191-637-6056	Sequence 6056, Ap	c1338	148	6.7	7417	27	US-09-614-150A-21793	Sequence 21793, A
1266	151	6.8	5929	85	US-60-191-681-4742	Sequence 4742, Ap	c1339	148	6.7	7417	65	US-11-097-143-21793	Sequence 21793, A
c1267	151	6.8	10054	85	US-60-173-464-4929	Sequence 4929, Ap	c1340	148	6.7	8734	85	US-60-167-217-17392	Sequence 17392, A
c1268	151	6.8	11963	27	US-09-614-150-6037	Sequence 6037, Ap	1341	148	6.7	31497	1	PCT-US02-11734-309	Sequence 309, App
c1269	151	6.8	11963	27	US-09-614-150A-6037	Sequence 6037, Ap	1342	148	6.7	31497	47	US-10-475-117-309	Sequence 309, App
c1270	151	6.8	11963	65	US-11-097-143-6037	Sequence 6037, Ap	1343	148	6.7	31497	89	US-60-427-045-309	Sequence 309, App
c1271	151	6.8	11963	85	US-60-191-637-6055	Sequence 6055, Ap	c1344	148	6.7	39746	27	US-09-614-150-17338	Sequence 17338, A
c1272	151	6.8	11963	85	US-60-191-681-4741	Sequence 4741, Ap	c1345	148	6.7	39746	27	US-09-614-150A-17338	Sequence 17338, A
c1273	151	6.8	48836	85	US-60-164-769-25728	Sequence 25728, A	c1346	148	6.7	39746	65	US-11-097-143-17338	Sequence 17338, A
1274	151	6.8	48981	24	US-09-528-237A-1455	Sequence 1455, Ap	c1347	148	6.7	39746	85	US-60-171-625-361	Sequence 361, App
1275	150.5	6.8	978	73	US-11-360-355-35549	Sequence 35549, A	c1348	148	6.7	39746	85	US-60-173-464-14244	Sequence 14244, A
1276	150.5	6.8	978	92	US-60-655-875-35549	Sequence 35549, A	c1349	148	6.7	39746	85	US-60-191-637-17388	Sequence 17388, A
1277	150.5	6.8	2583	3	PCT-US05-43512-2	Sequence 2, Appli	c1350	148	6.7	39746	85	US-60-191-681-13752	Sequence 13752, A
1278	150.5	6.8	2583	70	US-11-292-431-2	Sequence 2, Appli	1351	148	6.7	42248	85	US-60-164-769-26271	Sequence 26271, A
1279	150.5	6.8	3090	3	PCT-US05-43512-1	Sequence 1, Appli	1352	148	6.7	43816	3	PCT-US07-01959-171	Sequence 171, App
1280	150.5	6.8	3090	70	US-11-292-431-1	Sequence 1, Appli	1353	148	6.7	43816	80	US-11-657-719-171	Sequence 171, App
1281	150.5	6.8	21601	39	US-10-170-235-13952	Sequence 13952, A	1354	148	6.7	43816	80	US-11-699-229-58	Sequence 58, Appl
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1283	150.5	6.8	150223	78	US-11-550-934-1	Sequence 1, Appli	1356	148	6.7	43816	94	US-60-859-546-975	Sequence 975, App
1284	150.5	6.8	150223	78	US-11-550-934A-1	Sequence 1, Appli	1357	148	6.7	52158	85	US-60-161-932-408	Sequence 408, App
1285	150.5	6.8	8885655	35	US-09-947-916-97	Sequence 97, Appl	1358	148	6.7	52158	85	US-60-164-769-25854	Sequence 25854, A
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1287	150	6.8	359	22	US-09-362-510A-2132	Sequence 2132, Ap	1360	148	6.7	66765	47	US-10-475-117-314	Sequence 314, App
1288	150	6.8	359	34	US-09-904-013-2132	Sequence 2132, Ap	1361	148	6.7	66765	48	US-10-544-944-2	Sequence 2, Appli
1289	150	6.8	513	1	PCT-US01-43704-821	Sequence 821, App	1362	148	6.7	66765	56	US-10-715-066A-4	Sequence 4, Appli
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1291	150	6.8	513	37	US-09-998-598-821	Sequence 821, App	1364	148	6.7	66765	89	US-60-427-045-314	Sequence 314, App
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1293	150	6.8	897	32	US-09-824-518-9666	Sequence 9666, Ap	1366	147.5	6.7	1236	73	US-11-363-869-3	Sequence 3, Appli
1294	150	6.8	13014	62	US-11-066-316A-9888	Sequence 9888, Ap	1367	147.5	6.7	1236	73	US-11-363-870-3	Sequence 3, Appli
1295	150	6.8	38546	62	US-11-066-316A-380	Sequence 380, App	1368	147.5	6.7	1236	87	US-60-269-157-3	Sequence 3, Appli
1296	150	6.8	38665	62	US-11-066-316A-379	Sequence 379, App	1369	147.5	6.7	3736	27	US-09-614-150-40697	Sequence 40697, A
1297	150	6.8	39790	62	US-11-066-316A-382	Sequence 382, App	1370	147.5	6.7	3736	27	US-09-614-150A-40697	Sequence 40697, A
1298	150	6.8	41958	62	US-11-066-316A-383	Sequence 383, App	1371	147.5	6.7	3736	65	US-11-097-143-40697	Sequence 40697, A
1299	150	6.8	43342	62	US-11-066-316A-384	Sequence 384, App	1372	147.5	6.7	3736	85	US-60-184-775-284	Sequence 284, App
1300	150	6.8	158834	62	US-11-066-316A-9976	Sequence 9976, Ap	1373	147.5	6.7	3736	85	US-60-191-637-40322	Sequence 40322, A
1301	149	6.7	471	31	US-09-785-276A-18087	Sequence 18087, A	1374	147.5	6.7	3736	85	US-60-191-700-308	Sequence 308, App
1302	149	6.7	471	46	US-10-357-930-18087	Sequence 18087, A	1375	147.5	6.7	3753	85	US-60-173-386-274	Sequence 274, App
1303	149	6.7	515	31	US-09-785-276A-47904	Sequence 47904, A	1376	147.5	6.7	3753	85	US-60-175-871-319	Sequence 319, App
1304	149	6.7	515	46	US-10-357-930-47904	Sequence 47904, A	1377	147.5	6.7	3999	85	US-60-167-324-292	Sequence 292, App
1305	149	6.7	2154	73	US-11-360-355-76914	Sequence 76914, A	1378	147	6.6	1669	75	US-11-433-832-47155	Sequence 47155, A

1379	147	6.6	1669	75	US-11-433-832A-47155	Sequence 47155, A	1452	145	6.6	2291	27	US-09-614-150-40484	Sequence 40484, A
1380	147	6.6	1669	92	US-60-680-473-47155	Sequence 47155, A	1453	145	6.6	2291	27	US-09-614-150A-40484	Sequence 40484, A
1381	147	6.6	1669	92	US-60-680-544-47155	Sequence 47155, A	1454	145	6.6	2291	65	US-11-097-143-40484	Sequence 40484, A
1382	147	6.6	3069	76	US-11-443-428A-380845	Sequence 380845, A	1455	145	6.6	2291	85	US-60-173-386-116	Sequence 116, App
1383	147	6.6	4767	87	US-60-278-258-10763	Sequence 10763, A	1456	145	6.6	2291	85	US-60-175-871-134	Sequence 134, App
1384	147	6.6	6180	94	US-60-836-986-27646	Sequence 27646, A	1457	145	6.6	2291	85	US-60-184-775-125	Sequence 125, App
1385	146.5	6.6	1794	3	PCT-US04-21492-121	Sequence 121, App	1458	145	6.6	2291	85	US-60-191-637-40110	Sequence 40110, A
1386	146.5	6.6	1794	3	PCT-US04-21492A-121	Sequence 121, App	1459	145	6.6	2291	85	US-60-191-700-134	Sequence 134, App
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1388	146.5	6.6	1794	48	US-10-560-957-121	Sequence 121, App	1461	145	6.6	2732	88	US-60-360-207-14773	Sequence 14773, A
1389	146.5	6.6	1794	93	US-60-772-786-155	Sequence 155, App	1462	145	6.6	2732	88	US-60-360-207-14773	Sequence 14773, A
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1395	146	6.6	2709	65	US-11-097-143-8609	Sequence 8609, App	1468	145	6.6	9636	12	US-08-323-170-1	Sequence 1, Appli
1396	146	6.6	2709	85	US-60-191-637-8635	Sequence 8635, App	1469	145	6.6	10654	85	US-60-167-217-1031	Sequence 1031, Ap
1397	146	6.6	2709	85	US-60-191-681-6712	Sequence 6712, App	1470	145	6.6	13170	85	US-60-173-464-826	Sequence 826, App
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1399	146	6.6	230196	19	US-09-012-031B-302	Sequence 302, App	1472	145	6.6	13403	85	US-60-191-681-22616	Sequence 22616, A
1400	146	6.6	230196	19	US-09-012-031C-302	Sequence 302, App	1473	145	6.6	13631	27	US-09-614-150-27772	Sequence 27772, A
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1402	146	6.6	230196	22	US-09-335-032A-12204	Sequence 12204, A	1475	145	6.6	13631	65	US-11-097-143-27772	Sequence 27772, A
1403	146	6.6	230196	59	US-10-915-727-12204	Sequence 12204, A	1476	145	6.6	14116	87	US-60-242-679-726	Sequence 726, App
1404	146	6.6	767677	59	US-10-940-774-12147	Sequence 12147, A	1477	145	6.6	183926	24	US-09-528-237A-1195	Sequence 1195, Ap
1405	146	6.6	767677	59	US-10-940-774-17361	Sequence 17361, A	1478	145	6.6	961710	61	US-10-990-328-94469	Sequence 94469, A
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1408	146	6.6	1048668	62	US-11-033-056A-36314	Sequence 36314, A	1481	144.5	6.5	1226	93	US-60-711-444-1040	Sequence 1040, Ap
1409	145.5	6.6	843	39	US-10-100-683-12710	Sequence 12710, A	1482	144.5	6.5	2156	67	US-11-158-863-167	Sequence 167, App
1410	145.5	6.6	843	62	US-11-001-793-12710	Sequence 12710, A	1483	144.5	6.5	2628	3	PCT-US05-22501-4589	Sequence 4589, Ap
1411	145.5	6.6	843	80	US-11-689-173-12710	Sequence 12710, A	1484	144.5	6.5	2630	75	US-11-433-832-44540	Sequence 44540, A
1412	145.5	6.6	1587	73	US-11-360-355-22925	Sequence 22925, A	1485	144.5	6.5	2630	75	US-11-433-832A-44540	Sequence 44540, A
1413	145.5	6.6	1587	73	US-11-360-355-53625	Sequence 53625, A	1486	144.5	6.5	2630	92	US-60-680-473-44540	Sequence 44540, A
1414	145.5	6.6	1587	92	US-60-655-875-22925	Sequence 22925, A	1487	144.5	6.5	2630	92	US-60-680-544-44540	Sequence 44540, A
1415	145.5	6.6	1587	92	US-60-655-875-53625	Sequence 53625, A	1488	144.5	6.5	3423	57	US-10-793-639-91	Sequence 91, Appl
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1417	145.5	6.6	2114	21	US-09-219-245-158	Sequence 158, App	1490	144.5	6.5	4115	1	PCT-US02-29964-697	Sequence 5429, Ap
1418	145.5	6.6	2114	21	US-09-285-323-158	Sequence 158, App	1491	144.5	6.5	4115	23	US-09-496-914A-5429	Sequence 5429, Ap
1419	145.5	6.6	2114	23	US-09-476-235-158	Sequence 158, App	1492	144.5	6.5	4115	26	US-09-560-875A-5429	Sequence 5429, Ap
1420	145.5	6.6	2114	25	US-09-538-037-158	Sequence 158, App	1493	144.5	6.5	4115	45	US-10-302-689A-88608	Sequence 88608, A
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1430	145.5	6.6	7593	46	US-10-363-345A-4842	Sequence 4842, Ap							
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1432	145.5	6.6	7593	46	US-10-363-345B-4842	Sequence 4842, Ap							
1433	145.5	6.6	7593	46	US-10-363-483A-4841	Sequence 4841, Ap							
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1437	145	6.6	571	39	US-10-100-683-12709	Sequence 12709, A							
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1439	145	6.6	571	80	US-11-689-173-12709	Sequence 12709, A							
1440	145	6.6	2226	39	US-10-144-771-2460	Sequence 2460, Ap							
1441	145	6.6	2226	38	US-60-360-207-2460	Sequence 2460, Ap							
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1443	145	6.6	2239	85	US-60-173-464-839	Sequence 839, App							
1444	145	6.6	2244	3	PCT-US04-21492-133	Sequence 133, App							
1445	145	6.6	2244	3	PCT-US04-21492A-133	Sequence 133, App							
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Job time : 12589 secs



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	148	6.7	43816	8	US-60-970-396-1
3	122.5	5.5	1904	7	US-11-833-133-55
4	121.5	5.5	2000	7	US-11-623-607A-13
5	121.5	5.5	2000	7	US-11-623-689-44
6	121.5	5.5	2000	7	US-11-852-274-44
7	120.5	5.5	2444	7	US-11-781-665-1089
8	120.5	5.5	2444	7	US-11-781-665-2385
9	120.5	5.5	2445	7	US-11-235-701A-354
10	120.5	5.5	2445	7	US-11-235-701A-366
11	120.5	5.5	2445	7	US-11-490-374A-1850
Sequence 1838, Ap					
Sequence 1, Appli					
Sequence 55, Appl					
Sequence 13, Appl					
Sequence 44, Appl					
Sequence 44, Appl					
Sequence 1089, Ap					
Sequence 2385, Ap					
Sequence 354, App					
Sequence 366, App					
Sequence 1850, Ap					

12	120.5	5.5	2445	7	US-11-490-374A-1862	Sequence 1862, Ap
13	119.5	5.4	3132	5	US-09-889-075B-1	Sequence 1, Appli
14	119	5.4	1008	8	US-60-970-876-81	Sequence 81, Appl
15	119	5.4	1203	7	US-11-781-151-11	Sequence 11, Appl
16	119	5.4	1497	7	US-11-844-953-29	Sequence 29, Appl
17	119	5.4	1497	7	US-11-844-956-29	Sequence 29, Appl
18	119	5.4	1497	7	US-11-844-963-29	Sequence 29, Appl
19	119	5.4	1497	7	US-11-844-967-29	Sequence 29, Appl
20	119	5.4	1497	7	US-11-844-970-29	Sequence 29, Appl
21	119	5.4	1497	7	US-11-844-973-29	Sequence 29, Appl
22	119	5.4	4509	7	US-11-844-953-5	Sequence 5, Appli
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26	119	5.4	4509	7	US-11-844-973-5	Sequence 5, Appli
27	119	5.4	30729	7	US-11-884-086-2	Sequence 2, Appli
28	119	5.4	35149	7	US-11-884-086-1	Sequence 1, Appli
29	119	5.4	1316	7	US-11-781-665-2798	Sequence 2798, Ap
30	118	5.3	2444	7	US-11-781-665-2384	Sequence 2384, Ap
31	118	5.3	4858	7	US-11-847-733-3	Sequence 3, Appli
32	118	5.3	1715	7	US-11-374-300-103	Sequence 103, App
33	117.5	5.3	2204	8	US-60-970-876-184	Sequence 184, App
34	117.5	5.3	4313	7	US-11-659-690-3	Sequence 3, Appli
35	117.5	5.3	7201	6	US-10-872-859A-20	Sequence 20, Appl
36	117	5.3	876	7	US-11-884-496-446	Sequence 446, App
37	116.5	5.3	2904	7	US-11-795-915-110	Sequence 110, App
38	116.5	5.3	2967	7	US-11-795-915-171	Sequence 171, App
39	116.5	5.3	1623	7	US-11-509-924-1	Sequence 1, Appli
40	116	5.2	2067	7	US-11-397-222A-1	Sequence 1, Appli
41	115.5	5.2	1608	7	US-11-836-317-20	Sequence 20, Appl
42	115	5.2	1608	7	US-11-836-317-22	Sequence 22, Appl
43	115	5.2	1665	7	US-11-836-317-17	Sequence 17, Appl
44	115	5.2	1665	7	US-11-836-317-19	Sequence 19, Appl
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46	115	5.2	1752	7	US-11-836-317-16	Sequence 16, Appl
47	115	5.2	1992	1	PCT-US07-75398-63	Sequence 63, Appl
48	115	5.2	1992	7	US-11-835-328-63	Sequence 63, Appl
49	115	5.2	1970	7	US-11-235-701A-359	Sequence 359, App
50	114	5.2	1970	7	US-11-235-701A-365	Sequence 365, App
51	114	5.2	1970	7	US-11-490-374A-1855	Sequence 1855, Ap
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54	114	5.2	864	7	US-11-715-276-274	Sequence 274, App
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66	113	5.1	1465	7	US-11-883-235-1	Sequence 1, Appli
67	112.5	5.1	2367	7	US-11-235-701A-356	Sequence 356, App
68	112.5	5.1	2367	7	US-11-490-374A-1852	Sequence 1852, Ap
69	112.5	5.1	8194	7	US-11-830-023-128	Sequence 128, App
70	112.5	5.1	1048	1	PCT-US07-17776B-4496	Sequence 4496, Ap
71	112	5.1	1644	6	US-10-583-089-3	Sequence 3, Appli
72	112	5.1	1660	8	US-60-970-876-43	Sequence 43, Appl
73	112	5.1	4479	7	US-11-844-953-75	Sequence 75, Appl
74	112	5.1	4479	7	US-11-844-956-75	Sequence 75, Appl
75	112	5.1	4479	7	US-11-844-963-75	Sequence 75, Appl
76	112	5.1	4479	7	US-11-844-967-75	Sequence 75, Appl
77	112	5.1	4479	7	US-11-844-970-75	Sequence 75, Appl
78	112	5.1	4479	7	US-11-844-973-75	Sequence 75, Appl
79	112	5.1	1536	8	US-60-970-876-186	Sequence 186, App
80	111.5	5.0	3420	7	US-11-884-496-335	Sequence 335, App
81	111.5	5.0	8394	7	US-11-844-953-70	Sequence 70, Appl
82	111.5	5.0	8394	7	US-11-844-956-70	Sequence 70, Appl
83	111.5	5.0	8394	7	US-11-844-963-70	Sequence 70, Appl
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85	111.5	5.0	8394	7	US-11-844-967-70	Sequence 70, Appl	158	105	4.7	8733	7	US-11-844-973-1	Sequence 1, Appli
86	111.5	5.0	8394	7	US-11-844-970-70	Sequence 70, Appl	159	104.5	4.7	1101	8	US-60-970-876-112	Sequence 112, App
87	111.5	5.0	8394	7	US-11-844-973-70	Sequence 70, Appl	160	104.5	4.7	1537	7	US-11-833-133-67	Sequence 67, Appl
88	111.5	5.0	12495	7	US-11-844-953-71	Sequence 71, Appl	161	104.5	4.7	1664	7	US-11-833-133-34	Sequence 34, Appl
89	111.5	5.0	12495	7	US-11-844-956-71	Sequence 71, Appl	162	104.5	4.7	1794	7	US-11-834-037-12	Sequence 12, Appl
90	111.5	5.0	12495	7	US-11-844-963-71	Sequence 71, Appl	163	104.5	4.7	1797	7	US-11-834-037-20	Sequence 20, Appl
91	111.5	5.0	12495	7	US-11-844-967-71	Sequence 71, Appl	164	104.5	4.7	1803	7	US-11-834-037-3	Sequence 3, Appli
92	111.5	5.0	12495	7	US-11-844-970-71	Sequence 71, Appl	165	104.5	4.7	1807	7	US-11-834-037-8	Sequence 8, Appli
93	111.5	5.0	12495	7	US-11-844-973-71	Sequence 71, Appl	166	104.5	4.7	1816	7	US-11-834-037-14	Sequence 14, Appl
94	111	5.0	1836	7	US-11-833-133-1	Sequence 1, Appli	167	104.5	4.7	1818	7	US-11-834-037-10	Sequence 10, Appl
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97	110.5	5.0	3754	7	US-11-816-601-737	Sequence 737, App	170	104.5	4.7	7208	7	US-11-834-037-5	Sequence 5, Appli
98	110.5	5.0	3754	7	US-11-816-601-813	Sequence 813, App	c 171	104.5	4.7	12021	7	US-11-884-496-428	Sequence 428, App
c 99	110.5	5.0	12649	7	US-11-749-889-24	Sequence 24, Appl	172	104	4.7	906	7	US-11-833-133-69	Sequence 69, Appl
c 100	110.5	5.0	12649	7	US-11-830-023-110	Sequence 110, App	173	104	4.7	1026	8	US-60-970-876-45	Sequence 45, Appl
101	110	5.0	8588	7	US-11-846-177-13	Sequence 13, Appl	174	104	4.7	1471	7	US-11-781-665-2303	Sequence 2303, Ap
102	110	5.0	9021	7	US-11-884-496-303	Sequence 303, App	175	104	4.7	2428	7	US-11-572-719-19	Sequence 19, Appl
c 103	110	5.0	9979	7	US-11-804-164A-2	Sequence 2, Appli	176	104	4.7	6200	6	US-10-910-811B-378	Sequence 378, App
c 104	110	5.0	10690	7	US-11-804-164A-1	Sequence 1, Appli	177	104	4.7	6200	6	US-10-945-565B-378	Sequence 378, App
c 105	109.5	5.0	1803	7	US-11-804-164A-3	Sequence 3, Appli	178	104	4.7	9909	7	US-11-884-496-299	Sequence 299, App
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c 110	108.5	4.9	4641	7	US-11-838-500-63	Sequence 63, Appl	183	103.5	4.7	1610	7	US-11-884-496-605	Sequence 605, App
c 111	108.5	4.9	4641	7	US-11-838-500-77	Sequence 77, Appl	184	103.5	4.7	3085	7	US-11-884-496-155	Sequence 155, App
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114	108	4.9	1467	8	US-60-970-876-154	Sequence 154, App	187	103	4.7	3068	5	US-09-889-075B-11	Sequence 11, Appl
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116	107.5	4.9	1683	7	US-11-833-133-25	Sequence 25, Appl	c 189	103	4.7	3744	1	PCT-US07-13803-346	Sequence 346, App
117	107.5	4.9	2859	7	US-11-490-374A-2008	Sequence 2008, Ap	c 190	103	4.7	8936	6	US-10-741-191B-26	Sequence 26, Appl
118	106.5	4.8	1311	1	PCT-US07-17776B-2866	Sequence 2866, Ap	191	102.5	4.6	981	8	US-60-970-876-114	Sequence 114, App
119	106.5	4.8	4507	1	PCT-US07-13803-403	Sequence 403, App	192	102.5	4.6	1923	7	US-11-795-915-160	Sequence 160, App
120	106.5	4.8	35937	7	US-11-249-873A-28	Sequence 28, Appl	193	102.5	4.6	2070	1	PCT-US07-75398-82	Sequence 82, Appl
121	106	4.8	1155	7	US-11-883-235-2	Sequence 2, Appli	194	102.5	4.6	2070	7	US-11-835-328-82	Sequence 82, Appl
c 122	106	4.8	2829	1	PCT-US07-18368A-152	Sequence 152, App	195	102.5	4.6	2133	7	US-11-844-956-17	Sequence 17, Appl
c 123	106	4.8	3057	1	PCT-US07-18368A-277	Sequence 277, App	196	102.5	4.6	2133	7	US-11-844-953-17	Sequence 17, Appl
124	106	4.8	3516	7	US-11-816-601-301	Sequence 301, App	197	102.5	4.6	2133	7	US-11-844-963-17	Sequence 17, Appl
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128	105.5	4.8	1344	7	US-11-832-579-5	Sequence 5, Appli	c 201	102.5	4.6	2864	7	US-11-490-374A-2009	Sequence 2009, Ap
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130	105.5	4.8	1344	7	US-11-832-579-112	Sequence 112, App	203	102.5	4.6	7941	7	US-11-733-861-32	Sequence 32, Appl
131	105	4.7	978	8	US-60-970-876-78	Sequence 78, Appl	204	102	4.6	1239	7	US-11-833-133-33	Sequence 33, Appl
132	105	4.7	1429	7	US-11-374-300-191	Sequence 191, App	c 205	102	4.6	1251	6	US-10-276-032-56	Sequence 56, Appl
133	105	4.7	1500	7	US-11-844-953-7	Sequence 7, Appli	c 206	102	4.6	1278	7	US-11-833-133-57	Sequence 57, Appl
134	105	4.7	1500	7	US-11-844-956-7	Sequence 7, Appli	c 207	102	4.6	1496	6	US-10-870-198B-87	Sequence 87, Appl
135	105	4.7	1500	7	US-11-844-963-7	Sequence 7, Appli	208	102	4.6	1598	7	US-11-833-133-31	Sequence 31, Appl
136	105	4.7	1500	7	US-11-844-967-7	Sequence 7, Appli	209	102	4.6	2301	7	US-11-781-665-386	Sequence 386, App
137	105	4.7	1500	7	US-11-844-970-7	Sequence 7, Appli	210	102	4.6	2951	7	US-11-490-374A-1393	Sequence 1393, Ap
138	105	4.7	1500	7	US-11-844-973-7	Sequence 7, Appli	211	102	4.6	3264	7	US-11-884-496-529	Sequence 529, App
139	105	4.7	1578	7	US-11-833-133-3	Sequence 3, Appli	212	102	4.6	3461	7	US-11-814-954-1	Sequence 1, Appli
140	105	4.7	1801	7	US-11-834-037-6	Sequence 6, Appli	213	102	4.6	3537	7	US-11-816-601-132	Sequence 132, App
141	105	4.7	1813	7	US-11-834-037-16	Sequence 16, Appl	214	102	4.6	3537	7	US-11-816-601-284	Sequence 284, App
142	105	4.7	3476	7	US-11-733-861-11	Sequence 11, Appl	215	102	4.6	3537	7	US-11-816-601-788	Sequence 788, App
143	105	4.7	6000	1	PCT-US07-13803-145	Sequence 145, App	216	102	4.6	4874	7	US-11-235-701A-494	Sequence 494, App
144	105	4.7	8730	7	US-11-781-861-13	Sequence 13, Appl	217	102	4.6	4874	7	US-11-235-701A-502	Sequence 502, App
145	105	4.7	8730	7	US-11-781-867-13	Sequence 13, Appl	218	102	4.6	5001	7	US-11-235-701A-503	Sequence 503, App
146	105	4.7	8730	7	US-11-781-870-13	Sequence 13, Appl	219	102	4.6	82725	1	PCT-US07-63080-128	Sequence 128, App
147	105	4.7	8730	7	US-11-781-871-13	Sequence 13, Appl	220	101.5	4.6	814	1	PCT-US07-17776B-6205	Sequence 3, Appli
148	105	4.7	8730	7	US-11-781-874-13	Sequence 13, Appl	221	101.5	4.6	1106	7	US-11-883-235-3	Sequence 533, App
149	105	4.7	8730	7	US-11-781-875-13	Sequence 13, Appl	222	101.5	4.6	1410	7	US-11-884-496-533	Sequence 12, Appl
150	105	4.7	8730	7	US-11-781-877-13	Sequence 13, Appl	223	101.5	4.6	1668	6	US-10-552-571-12	Sequence 18, Appl
151	105	4.7	8730	7	US-11-781-880-13	Sequence 13, Appl	224	101.5	4.6	1668	6	US-10-552-571-18	Sequence 54, Appl
152	105	4.7	8730	7	US-11-781-882-13	Sequence 13, Appl	225	101.5	4.6	2325	7	US-11-781-665-54	Sequence 351, App
153	105	4.7	8733	7	US-11-844-953-1	Sequence 1, Appli	226	101.5	4.6	2704	7	US-11-374-300-351	Sequence 11, Appl
154	105	4.7	8733	7	US-11-844-956-1	Sequence 1, Appli	227	101.5	4.6	2829	7	US-11-649-155-11	Sequence 1, Appl
155	105	4.7	8733	7	US-11-844-963-1	Sequence 1, Appli	228	101.5	4.6	3633	7	US-11-649-155-1	Sequence 1, Appli
156	105	4.7	8733	7	US-11-844-967-1	Sequence 1, Appli	229	101.5	4.6	3633	7	US-11-815-985-1	Sequence 12, Appl
157	105	4.7	8733	7	US-11-844-970-1	Sequence 1, Appli	230	101.5	4.6	4321	5	US-09-889-075B-12	

231 101.5 4.6 7684 8 US-60-956-437-8 Sequence 8, Appli  
c 232 101.5 4.6 13313 6 US-10-552-571-16 Sequence 16, Appli  
c 233 101 4.6 1113 1 PCT-US07-17776B-7262 Sequence 7262, Ap  
c 234 101 4.6 2829 1 PCT-US07-18368A-151 Sequence. 151, App  
235 101 4.6 3047 1 PCT-US07-13803-316 Sequence 316, App  
c 236 101 4.6 3575 7 US-11-816-601-144 Sequence 144, App  
237 101 4.6 3635 7 US-11-490-374A-1390 Sequence 1390, Ap  
238 101 4.6 3720 7 US-11-490-374A-1392 Sequence 1392, Ap  
239 101 4.6 3730 7 US-11-490-374A-1389 Sequence 1389, Ap  
240 101 4.6 4059 7 US-11-908-114-15 Sequence 15, Appl  
241 101 4.6 4059 8 US-60-911-843A-21 Sequence 21, Appl  
c 242 101 4.6 5819 7 US-11-490-374A-2020 Sequence 2020, Ap  
243 100.5 4.5 1509 8 US-60-970-876-183 Sequence 183, App  
c 244 100.5 4.5 1589 7 US-11-749-032B-3 Sequence 3, Appli  
245 100.5 4.5 4479 7 US-11-844-953-73 Sequence 73, Appl  
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c 250 100.5 4.5 4853 7 US-11-838-500-71 Sequence 71, Appl  
c 251 100.5 4.5 5502 7 US-11-838-500-72 Sequence 72, Appl  
c 252 100.5 4.5 2613 7 US-11-833-133-45 Sequence 45, Appl  
253 100 4.5 2740 7 US-11-833-133-43 Sequence 43, Appl  
c 254 100 4.5 5142 6 US-10-910-811B-376 Sequence 376, App  
c 255 100 4.5 5142 6 US-10-945-565B-376 Sequence 376, App  
c 256 100 4.5 7912 7 US-11-490-374A-1473 Sequence 1473, Ap  
257 100 4.5 7935 7 US-11-490-374A-1491 Sequence 1491, Ap  
258 100 4.5 8155 7 US-11-490-374A-1488 Sequence 1488, Ap  
259 100 4.5 8272 7 US-11-490-374A-1489 Sequence 1489, Ap  
260 100 4.5 767 1 PCT-US07-17776B-2001 Sequence 2001, Ap  
261 99.5 4.5 790 1 PCT-US07-17776B-6281 Sequence 6281, Ap  
262 99.5 4.5 1031 7 US-11-374-300-634 Sequence 634, App  
263 99.5 4.5 1062 7 US-11-883-996-64 Sequence 64, Appl  
264 99.5 4.5 1980 7 US-11-623-607A-15 Sequence 15, Appl  
c 265 99.5 4.5 1980 7 US-11-623-689-46 Sequence 46, Appl  
266 99.5 4.5 1980 7 US-11-852-274-46 Sequence 46, Appl  
267 99.5 4.5 3935 7 US-11-597-986A-10 Sequence 10, Appl  
268 99.5 4.5 7450 6 US-10-582-007-5 Sequence 5, Appli  
c 269 99.5 4.5 20290 7 US-11-828-155-1 Sequence 1, Appli  
270 99 4.5 957 7 US-11-840-356-3 Sequence 3, Appli  
271 99 4.5 1270 7 US-11-374-300-574 Sequence 574, App  
272 99 4.5 1365 8 US-60-914-361-60 Sequence 60, Appl  
273 99 4.5 1431 8 US-60-914-361-86 Sequence 86, Appl  
274 99 4.5 1480 7 US-11-781-151-19 Sequence 19, Appl  
275 99 4.5 1500 7 US-11-825-627-303 Sequence 303, App  
276 99 4.5 1867 7 US-11-831-404-33 Sequence 33, Appl  
277 99 4.5 2035 7 US-11-781-665-425 Sequence 425, App  
278 99 4.5 2438 7 US-11-884-496-238 Sequence 238, App  
279 99 4.5 3302 7 US-11-816-601-74 Sequence 74, Appl  
280 99 4.5 7497 7 US-11-782-310-67 Sequence 67, Appl  
281 99 4.5 954 1 PCT-US07-17776B-4368 Sequence 4368, Ap  
282 98.5 4.5 1228 7 US-11-597-986A-9 Sequence 9, Appli  
283 98.5 4.5 1776 7 US-11-374-300-353 Sequence 353, App  
284 98.5 4.5 2906 7 US-11-834-069-3 Sequence 3, Appli  
c 285 98.5 4.5 3186 7 US-11-834-069-4 Sequence 4, Appli  
c 286 98.5 4.5 3770 7 US-11-597-986A-8 Sequence 8, Appli  
287 98.5 4.5 11893 7 US-11-781-865-8 Sequence 8, Appli  
288 98.5 4.5 710 7 US-11-582-527A-3 Sequence 3, Appli  
289 98 4.4 817 1 PCT-US07-17776B-7412 Sequence 7412, Ap  
290 98 4.4 1185 7 US-11-833-133-9 Sequence 9, Appli  
291 98 4.4 2226 7 US-11-781-665-2442 Sequence 2442, Ap  
c 292 98 4.4 6953 7 US-11-844-953-73 Sequence 73, Appl  
293 98 4.4 1278 7 US-11-844-956-9 Sequence 9, Appli  
294 97.5 4.4 1278 7 US-11-844-963-9 Sequence 9, Appli  
295 97.5 4.4 1278 7 US-11-844-967-9 Sequence 9, Appli  
296 97.5 4.4 1278 7 US-11-844-970-9 Sequence 9, Appli  
297 97.5 4.4 1278 7 US-11-844-973-9 Sequence 9, Appli  
298 97.5 4.4 2887 7 US-11-884-496-249 Sequence 249, App  
299 97.5 4.4 3646 1 PCT-US07-13803-274 Sequence 274, App  
300 97.5 4.4 3646 1 PCT-US07-13803-498 Sequence 498, App  
301 97.5 4.4 5817 7 US-11-884-496-352 Sequence 352, App

304 97.5 4.4 6232 6 US-10-741-191B-16 Sequence 16, Appl  
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c 306 97.5 4.4 8257 7 US-11-884-496-304 Sequence 304, App  
307 97.5 4.4 13040 7 US-11-569-756-8 Sequence 8, Appli  
308 97.5 4.4 39669 7 US-11-781-861-1 Sequence 1, Appli  
309 97.5 4.4 39669 7 US-11-781-867-1 Sequence 1, Appli  
310 97.5 4.4 39669 7 US-11-781-870-1 Sequence 1, Appli  
311 97.5 4.4 39669 7 US-11-781-871-1 Sequence 1, Appli  
312 97.5 4.4 39669 7 US-11-781-874-1 Sequence 1, Appli  
313 97.5 4.4 39669 7 US-11-781-875-1 Sequence 1, Appli  
314 97.5 4.4 39669 7 US-11-781-877-1 Sequence 1, Appli  
315 97.5 4.4 39669 7 US-11-781-880-1 Sequence 1, Appli  
316 97.5 4.4 39669 7 US-11-781-882-1 Sequence 1, Appli  
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318 97 4.4 799 1 PCT-US07-17776B-1456 Sequence 1456, Ap  
319 97 4.4 1152 7 US-11-833-133-27 Sequence 27, Appl  
320 97 4.4 1337 8 US-60-970-876-79 Sequence 79, Appl  
321 97 4.4 1350 7 US-11-833-133-6 Sequence 6, Appli  
322 97 4.4 1458 1 PCT-US07-17776B-7691 Sequence 7691, Ap  
323 97 4.4 1497 6 US-10-498-694-1 Sequence 1, Appli  
324 97 4.4 3576 7 US-11-649-155-26 Sequence 26, Appl  
325 97 4.4 4751 7 US-11-847-733-2 Sequence 2, Appli  
c 326 97 4.4 5249 7 US-11-816-601-99 Sequence 99, Appl  
327 97 4.4 6519 7 US-11-801-963A-2605 Sequence 2605, Ap  
328 97 4.4 8647 7 US-11-844-953-72 Sequence 72, Appl  
329 97 4.4 8647 7 US-11-844-956-72 Sequence 72, Appl  
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331 97 4.4 8647 7 US-11-844-967-72 Sequence 72, Appl  
332 97 4.4 8647 7 US-11-844-970-72 Sequence 72, Appl  
333 97 4.4 8647 7 US-11-844-973-72 Sequence 72, Appl  
c 334 96.5 4.4 864 7 US-11-715-276-272 Sequence 272, App  
c 335 96.5 4.4 864 7 US-11-715-300-272 Sequence 272, App  
336 96.5 4.4 1053 7 US-11-883-996-74 Sequence 74, Appl  
337 96.5 4.4 1559 6 US-10-419-296A-3 Sequence 3, Appli  
338 96.5 4.4 1992 1 PCT-US02-29565-19 Sequence 19, Appl  
339 96.5 4.4 2858 7 US-11-908-114-6 Sequence 6, Appli  
c 340 96.5 4.4 3168 7 US-11-781-665-1541 Sequence 1541, Ap  
c 341 96.5 4.4 4853 7 US-11-838-500-76 Sequence 76, Appl  
c 342 96.5 4.4 5502 7 US-11-838-500-1 Sequence 1, Appli  
c 343 96.5 4.4 5502 7 US-11-838-500-75 Sequence 75, Appl  
c 344 96 4.3 774 1 PCT-US07-17776B-718 Sequence 718, App  
345 96 4.3 1125 7 US-11-833-133-36 Sequence 36, Appl  
346 96 4.3 1392 8 US-60-970-876-135 Sequence 135, App  
347 96 4.3 1422 8 US-60-970-876-204 Sequence 204, App  
348 96 4.3 1446 7 US-11-833-133-12 Sequence 12, Appl  
349 96 4.3 1527 8 US-60-970-876-202 Sequence 202, App  
350 96 4.3 1708 8 US-60-970-876-133 Sequence 133, App  
351 96 4.3 2046 8 US-60-970-876-181 Sequence 181, App  
352 96 4.3 2151 6 US-10-554-521-44 Sequence 44, Appl  
353 96 4.3 2494 7 US-11-825-627-301 Sequence 301, App  
354 96 4.3 2666 7 US-11-847-733-4 Sequence 4, Appli  
355 96 4.3 2961 1 PCT-US07-16605-3 Sequence 3, Appli  
356 96 4.3 2961 7 US-11-490-374A-2010 Sequence 2010, Ap  
357 96 4.3 3173 7 US-11-354-210-108 Sequence 108, App  
358 96 4.3 3753 7 US-11-354-210-118 Sequence 118, App  
359 96 4.3 4026 7 US-11-354-210-126 Sequence 126, App  
360 96 4.3 4536 7 US-11-354-210-112 Sequence 112, App  
361 96 4.3 4710 7 US-11-354-210-114 Sequence 114, App  
362 96 4.3 4884 7 US-11-354-210-104 Sequence 104, App  
363 96 4.3 5198 7 US-11-816-601-725 Sequence 725, App  
364 96 4.3 5198 7 US-11-816-601-798 Sequence 798, App  
365 96 4.3 5776 7 US-11-354-210-128 Sequence 128, App  
366 96 4.3 10550 7 US-11-235-701A-368 Sequence 368, App  
367 96 4.3 13018 7 US-11-235-701A-369 Sequence 369, App  
368 96 4.3 30729 7 US-11-884-086-2 Sequence 2, Appli  
369 95.5 4.3 1044 7 US-11-880-377-2451 Sequence 2451, Ap  
370 95.5 4.3 1113 7 US-11-801-963A-2120 Sequence 2120, Ap  
371 95.5 4.3 1194 7 US-11-833-133-40 Sequence 40, Appl  
372 95.5 4.3 1269 8 US-60-970-876-55 Sequence 55, Appl  
373 95.5 4.3 1893 1 PCT-US07-75398-81 Sequence 81, Appl  
374 95.5 4.3 1893 7 US-11-835-328-81 Sequence 81, Appl  
375 95.5 4.3 2800 7 US-11-781-151-29 Sequence 29, Appl  
c 376 95.5 4.3 2833 7 US-11-884-496-326 Sequence 326, App

377	95.5	4.3	3585	6	US-10-050-000C-2	Sequence 2, Appli	450	94	4.3	3574	7	US-11-815-559-5	Sequence 5, Appli
378	95.5	4.3	3633	7	US-11-649-155-13	Sequence 13, Appl	451	94	4.3	3585	1	PCT-US07-17013-29	Sequence 29, Appl
c 379	95.5	4.3	4790	7	US-11-838-500-70	Sequence 70, Appl	452	94	4.3	3965	7	US-11-795-824-28	Sequence 28, Appl
c 380	95.5	4.3	8679	8	US-60-914-361-115	Sequence 115, App	453	94	4.3	4000	7	US-11-235-701A-508	Sequence 508, App
c 381	95.5	4.3	14760	7	US-11-490-374A-1331	Sequence 1331, Ap	454	94	4.3	5184	7	US-11-235-701A-509	Sequence 509, App
c 382	95.5	4.3	14760	7	US-11-490-374A-1332	Sequence 1332, Ap	455	94	4.3	8548	7	US-11-884-496-256	Sequence 256, App
c 383	95.5	4.3	14760	7	US-11-490-374A-1333	Sequence 1333, Ap	456	94	4.3	9944	7	US-11-490-374A-2183	Sequence 2183, Ap
384	95	4.3	834	8	US-60-970-876-156	Sequence 156, App	457	94	4.3	9959	7	US-11-490-374A-2181	Sequence 2181, Ap
385	95	4.3	891	1	PCT-US07-17776B-2703	Sequence 2703, Ap	458	94	4.3	9962	7	US-11-490-374A-2180	Sequence 2180, Ap
386	95	4.3	1932	7	US-11-649-155-15	Sequence 15, Appl	459	94	4.3	10061	7	US-11-490-374A-2184	Sequence 2184, Ap
387	95	4.3	1968	7	US-11-649-155-17	Sequence 17, Appl	460	94	4.3	10562	7	US-11-490-374A-2182	Sequence 2182, Ap
388	95	4.3	2791	7	US-11-781-665-1300	Sequence 1300, Ap	c 461	93.5	4.2	633	1	PCT-US07-17776B-211	Sequence 211, App
389	95	4.3	2791	7	US-11-781-665-1301	Sequence 1301, Ap	c 462	93.5	4.2	774	1	PCT-US07-17776B-1020	Sequence 1020, Ap
390	95	4.3	2961	1	PCT-US07-16605-5	Sequence 5, Appli	463	93.5	4.2	1012	1	PCT-US07-17776B-3410	Sequence 3410, Ap
391	95	4.3	3494	7	US-11-795-824-31	Sequence 31, Appl	464	93.5	4.2	1728	7	US-11-781-665-91	Sequence 91, Appl
392	95	4.3	3750	1	PCT-US07-18368A-136	Sequence 136, App	465	93.5	4.2	1884	7	US-11-833-133-51	Sequence 51, Appl
393	95	4.3	3812	8	US-60-956-093-74	Sequence 74, Appl	c 466	93.5	4.2	2004	7	US-11-817-499-7	Sequence 7, Appli
394	95	4.3	3812	8	US-60-956-094-74	Sequence 74, Appl	467	93.5	4.2	2029	7	US-11-833-133-4	Sequence 4, Appli
395	95	4.3	3938	7	US-11-847-733-1	Sequence 1, Appli	c 468	93.5	4.2	2076	7	US-11-817-499-1	Sequence 1, Appli
396	95	4.3	3958	8	US-60-956-093-73	Sequence 73, Appl	469	93.5	4.2	3034	7	US-11-708-858-44	Sequence 44, Appl
397	95	4.3	3958	8	US-60-956-094-73	Sequence 73, Appl	c 470	93.5	4.2	3720	7	US-11-835-336-38	Sequence 38, Appl
c 398	95	4.3	4270	7	US-11-884-496-228	Sequence 228, App	471	93.5	4.2	3971	7	US-11-816-601-155	Sequence 155, App
399	95	4.3	7407	1	PCT-US02-29565-3	Sequence 3, Appli	472	93.5	4.2	3971	7	US-11-816-601-295	Sequence 295, App
400	95	4.3	7848	7	US-11-490-374A-1485	Sequence 1485, Ap	473	93.5	4.2	4125	7	US-11-490-374A-2159	Sequence 2159, Ap
401	95	4.3	7959	7	US-11-490-374A-1475	Sequence 1475, Ap	474	93.5	4.2	4240	7	US-11-490-374A-2158	Sequence 2158, Ap
402	95	4.3	8013	7	US-11-490-374A-1483	Sequence 1483, Ap	475	93.5	4.2	4286	7	US-11-137-671A-14	Sequence 14, Appl
403	95	4.3	8226	7	US-11-490-374A-1492	Sequence 1492, Ap	476	93.5	4.2	4749	7	US-11-884-496-194	Sequence 194, App
404	95	4.3	8278	7	US-11-490-374A-1482	Sequence 1482, Ap	477	93.5	4.2	4749	7	US-11-884-496-362	Sequence 362, App
405	95	4.3	8278	7	US-11-490-374A-1484	Sequence 1484, Ap	478	93.5	4.2	5903	1	PCT-US07-15888-0	Sequence 0, Appli
406	95	4.3	8278	7	US-11-490-374A-1493	Sequence 1493, Ap	479	93	4.2	921	8	US-60-914-361-93	Sequence 93, Appl
407	95	4.3	8371	7	US-11-490-374A-1476	Sequence 1476, Ap	480	93	4.2	1310	7	US-11-833-133-76	Sequence 76, Appl
408	95	4.3	8374	7	US-11-490-374A-1478	Sequence 1478, Ap	481	93	4.2	1341	7	US-11-832-579-8	Sequence 8, Appli
409	95	4.3	8449	7	US-11-490-374A-1490	Sequence 1490, Ap	482	93	4.2	1341	7	US-11-832-579-18	Sequence 18, Appl
410	94.5	4.3	706	1	PCT-US07-17776B-363	Sequence 363, App	483	93	4.2	1341	7	US-11-832-579-25	Sequence 25, Appl
411	94.5	4.3	909	8	US-60-970-876-30	Sequence 30, Appl	484	93	4.2	1341	7	US-11-832-579-31	Sequence 31, Appl
412	94.5	4.3	1127	1	PCT-US07-17776B-3015	Sequence 3015, Ap	485	93	4.2	1341	7	US-11-832-579-90	Sequence 90, Appl
413	94.5	4.3	1368	7	US-11-833-133-15	Sequence 15, Appl	c 486	93	4.2	1350	8	US-60-914-361-95	Sequence 95, Appl
414	94.5	4.3	1410	6	US-10-343-663B-40	Sequence 40, Appl	487	93	4.2	1987	7	US-11-374-300-706	Sequence 706, App
415	94.5	4.3	1512	7	US-11-844-953-31	Sequence 31, Appl	488	93	4.2	2028	6	US-10-375-932A-202	Sequence 202, App
416	94.5	4.3	1512	7	US-11-844-956-31	Sequence 31, Appl	489	93	4.2	2157	7	US-11-832-579-91	Sequence 91, Appl
417	94.5	4.3	1512	7	US-11-844-963-31	Sequence 31, Appl	490	93	4.2	2441	7	US-11-832-579-1	Sequence 1, Appli
418	94.5	4.3	1512	7	US-11-844-967-31	Sequence 31, Appl	491	93	4.2	2641	7	US-11-374-300-63	Sequence 63, Appl
419	94.5	4.3	1512	7	US-11-844-970-31	Sequence 31, Appl	492	93	4.2	3072	8	US-60-914-361-121	Sequence 121, App
420	94.5	4.3	1512	7	US-11-844-973-31	Sequence 31, Appl	493	93	4.2	3318	8	US-60-970-876-117	Sequence 117, App
421	94.5	4.3	1746	7	US-11-665-276-4	Sequence 4, Appli	494	93	4.2	4189	8	US-60-970-876-115	Sequence 115, App
422	94.5	4.3	3158	1	PCT-US07-13803-430	Sequence 430, App	495	93	4.2	5880	7	US-11-802-321A-68	Sequence 68, Appl
423	94.5	4.3	3683	8	US-60-970-876-124	Sequence 124, App	496	93	4.2	5880	7	US-11-802-321A-69	Sequence 69, Appl
424	94.5	4.3	4045	7	US-11-794-690-11	Sequence 11, Appl	497	93	4.2	5880	7	US-11-802-321A-71	Sequence 71, Appl
425	94.5	4.3	4653	7	US-11-569-756-10	Sequence 10, Appl	498	93	4.2	5880	7	US-11-490-374A-1937	Sequence 1937, Ap
426	94.5	4.3	5304	7	US-11-569-756-2	Sequence 2, Appli	499	93	4.2	5903	7	US-11-802-321A-81	Sequence 81, Appl
427	94.5	4.3	5487	7	US-11-884-546-90	Sequence 90, Appl	500	93	4.2	5903	7	US-11-490-374A-1941	Sequence 1941, Ap
428	94.5	4.3	9200	7	US-11-235-701A-367	Sequence 367, App	501	93	4.2	9189	6	US-10-741-191B-1	Sequence 1, Appli
429	94.5	4.3	12050	7	US-11-884-496-41	Sequence 41, Appl	c 502	93	4.2	9765	7	US-11-825-627-494	Sequence 494, App
430	94.5	4.3	14123	7	US-11-569-756-6	Sequence 6, Appli	503	92.5	4.2	495	8	US-60-969-195-7500	Sequence 7500, Ap
431	94.5	4.3	14177	7	US-11-569-756-4	Sequence 4, Appli	504	92.5	4.2	821	1	PCT-US07-17776B-7307	Sequence 7307, Ap
432	94.5	4.3	33592	7	US-11-249-873A-1	Sequence 1, Appli	505	92.5	4.2	2115	7	US-11-833-133-10	Sequence 10, Appl
433	94.5	4.3	33699	7	US-11-249-873A-3	Sequence 3, Appli	506	92.5	4.2	2189	7	US-11-816-601-716	Sequence 716, Appl
434	94.5	4.3	33988	7	US-11-249-873A-14	Sequence 14, Appl	507	92.5	4.2	2377	7	US-11-829-058-3	Sequence 3, Appli
435	94.5	4.3	34341	7	US-11-249-873A-2	Sequence 2, Appli	508	92.5	4.2	2558	7	US-11-733-861-12	Sequence 12, Appl
436	94.5	4.3	34448	7	US-11-249-873A-4	Sequence 4, Appli	509	92.5	4.2	2757	8	US-60-970-876-120	Sequence 120, App
437	94.5	4.3	34555	6	US-10-559-596-5	Sequence 5, Appli	510	92.5	4.2	2830	7	US-11-884-496-575	Sequence 575, App
438	94.5	4.3	34737	7	US-11-249-873A-15	Sequence 15, Appl	511	92.5	4.2	3939	7	US-11-884-496-35	Sequence 35, Appl
439	94.5	4.3	35149	7	US-11-884-086-1	Sequence 1, Appli	512	92.5	4.2	5370	7	US-11-908-114-1	Sequence 1, Appli
440	94.5	4.3	35724	7	US-11-249-873A-13	Sequence 13, Appl	513	92.5	4.2	6000	1	PCT-US07-13803-154	Sequence 154, App
441	94.5	4.3	36114	7	US-11-249-873A-16	Sequence 16, Appl	514	92.5	4.2	7823	7	US-11-490-374A-1480	Sequence 1480, Ap
442	94.5	4.3	39301	7	US-11-712-794-17	Sequence 17, Appl	515	92.5	4.2	7823	7	US-11-490-374A-1487	Sequence 1487, Ap
443	94.5	4.3	50475	7	US-11-712-794-16	Sequence 16, Appl	516	92.5	4.2	8647	7	US-11-490-374A-1474	Sequence 1474, Ap
444	94	4.3	774	8	US-60-911-925A-40	Sequence 40, Appl	517	92.5	4.2	8815	7	US-11-490-374A-1481	Sequence 1481, Ap
445	94	4.3	1290	1	PCT-US07-17776B-3321	Sequence 3321, Ap	518	92.5	4.2	12021	7	US-11-884-496-428	Sequence 428, App
446	94	4.3	1499	7	US-11-781-665-1891	Sequence 1891, Ap	519	92	4.2	669	8	US-60-970-876-150	Sequence 150, App
447	94	4.3	2119	7	US-11-830-023-1	Sequence 1, Appli	520	92	4.2	757	1	PCT-US07-17776B-5272	Sequence 5272, Ap
448	94	4.3	2583	7	US-11-235-701A-510	Sequence 510, App	521	92	4.2	830	7	US-11-582-527A-1	Sequence 1, Appli
449	94	4.3	3497	8	US-60-911-925A-41	Sequence 41, Appl	522	92	4.2	850	7	US-11-582-527A-5	Sequence 5, Appli



523	92	4.2	1125	7	US-11-833-133-54	Sequence 54, Appl	596	91.5	4.1	1974	7	US-11-649-155-3	Sequence 3, Appli
524	92	4.2	1341	7	US-11-832-579-15	Sequence 15, Appl	c 597	91.5	4.1	1995	7	US-11-817-499-9	Sequence 9, Appli
525	92	4.2	1341	7	US-11-832-579-21	Sequence 21, Appl	c 598	91.5	4.1	2067	7	US-11-817-499-3	Sequence 3, Appli
526	92	4.2	1341	7	US-11-832-579-29	Sequence 29, Appl	599	91.5	4.1	2118	7	US-11-649-155-5	Sequence 5, Appli
527	92	4.2	1434	7	US-11-830-023-117	Sequence 117, App	c 600	91.5	4.1	2274	7	US-11-817-499-13	Sequence 13, Appl
528	92	4.2	1616	7	US-11-832-579-11	Sequence 11, Appl	c 601	91.5	4.1	2274	7	US-11-884-496-531	Sequence 531, App
529	92	4.2	1637	7	US-11-833-133-52	Sequence 52, Appl	602	91.5	4.1	2709	7	US-11-884-496-165	Sequence 165, App
530	92	4.2	1725	1	PCT-US07-06371-3	Sequence 3, Appli	603	91.5	4.1	2766	6	US-10-276-032-42	Sequence 42, Appl
c 531	92	4.2	1797	7	US-11-781-665-2915	Sequence 2915, Ap	604	91.5	4.1	3057	7	US-11-781-665-751	Sequence 751, App
532	92	4.2	2443	6	US-10-815-495A-17	Sequence 17, Appl	605	91.5	4.1	3434	1	PCT-US07-13803-515	Sequence 515, App
533	92	4.2	2443	7	US-11-837-279-17	Sequence 17, Appl	606	91.5	4.1	3474	8	US-60-970-876-118	Sequence 118, App
534	92	4.2	2520	6	US-10-815-495A-21	Sequence 21, Appl	607	91.5	4.1	5674	8	US-60-970-876-52	Sequence 52, Appl
535	92	4.2	2520	7	US-11-837-279-21	Sequence 21, Appl	c 608	91.5	4.1	6000	1	PCT-US07-13803-102	Sequence 102, App
c 536	92	4.2	2607	1	PCT-US07-18368A-177	Sequence 177, App	609	91	4.1	923	7	US-11-781-151-1	Sequence 1, Appli
c 537	92	4.2	2620	1	PCT-US07-18368A-178	Sequence 178, App	c 610	91	4.1	1122	8	US-60-914-361-11	Sequence 11, Appl
538	92	4.2	2784	1	PCT-US07-13803-391	Sequence 391, App	c 611	91	4.1	1415	7	US-11-884-496-67	Sequence 67, Appl
c 539	92	4.2	3107	7	US-11-835-336-81	Sequence 81, Appl	612	91	4.1	2022	6	US-10-554-521-53	Sequence 53, Appl
540	92	4.2	3542	7	US-11-884-496-307	Sequence 307, App	613	91	4.1	2469	7	US-11-817-478-3	Sequence 3, Appli
541	92	4.2	3693	1	PCT-US07-06371-5	Sequence 5, Appli	614	91	4.1	2728	6	US-10-587-995-1	Sequence 1, Appli
542	92	4.2	4457	1	PCT-US07-06371-6	Sequence 6, Appli	615	91	4.1	2771	7	US-11-733-861-59	Sequence 59, Appl
543	92	4.2	6177	7	US-11-781-861-15	Sequence 15, Appl	616	91	4.1	3263	7	US-11-847-733-69	Sequence 69, Appl
544	92	4.2	6177	7	US-11-781-867-15	Sequence 15, Appl	617	91	4.1	3387	7	US-11-884-496-496	Sequence 496, App
545	92	4.2	6177	7	US-11-781-870-15	Sequence 15, Appl	618	91	4.1	3387	7	US-11-884-496-535	Sequence 535, App
546	92	4.2	6177	7	US-11-781-871-15	Sequence 15, Appl	c 619	91	4.1	8085	7	US-11-835-336-72	Sequence 72, Appl
547	92	4.2	6177	7	US-11-781-874-15	Sequence 15, Appl	620	91	4.1	11185	1	PCT-US07-13803-307	Sequence 307, App
548	92	4.2	6177	7	US-11-781-875-15	Sequence 15, Appl	621	91	4.1	11466	6	US-10-466-960B-4	Sequence 4, Appli
549	92	4.2	6177	7	US-11-781-877-15	Sequence 15, Appl	c 622	91	4.1	155470	6	US-10-910-811B-373	Sequence 373, App
550	92	4.2	6177	7	US-11-781-880-15	Sequence 15, Appl	c 623	91	4.1	155470	6	US-10-945-565B-373	Sequence 373, App
551	92	4.2	6177	7	US-11-781-882-15	Sequence 15, Appl	624	90.5	4.1	594	1	PCT-US07-1776B-8962	Sequence 8962, Ap
552	92	4.2	6180	7	US-11-844-953-3	Sequence 3, Appli	625	90.5	4.1	711	8	US-60-970-876-42	Sequence 42, Appl
c 553	92	4.2	6180	7	US-11-844-953-36	Sequence 36, Appl	626	90.5	4.1	827	1	PCT-US07-1776B-5707	Sequence 5707, Ap
554	92	4.2	6180	7	US-11-844-953-37	Sequence 37, Appl	c 627	90.5	4.1	1002	7	US-11-781-665-306	Sequence 306, App
555	92	4.2	6180	7	US-11-844-953-69	Sequence 69, Appl	628	90.5	4.1	1038	8	US-60-970-876-57	Sequence 57, Appl
556	92	4.2	6180	7	US-11-844-956-3	Sequence 3, Appli	629	90.5	4.1	1434	1	PCT-US07-18368A-218	Sequence 218, App
c 557	92	4.2	6180	7	US-11-844-956-36	Sequence 36, Appl	630	90.5	4.1	2212	7	US-11-708-858-41	Sequence 41, Appl
558	92	4.2	6180	7	US-11-844-956-37	Sequence 37, Appl	631	90.5	4.1	2545	7	US-11-880-377-2455	Sequence 2455, Ap
559	92	4.2	6180	7	US-11-844-956-69	Sequence 69, Appl	632	90.5	4.1	2749	7	US-11-880-377-2461	Sequence 2461, Ap
560	92	4.2	6180	7	US-11-844-963-3	Sequence 3, Appli	633	90.5	4.1	3207	7	US-11-884-496-125	Sequence 125, App
c 561	92	4.2	6180	7	US-11-844-963-36	Sequence 36, Appl	634	90.5	4.1	3211	7	US-11-884-496-132	Sequence 132, App
562	92	4.2	6180	7	US-11-844-963-37	Sequence 37, Appl	635	90.5	4.1	5452	7	US-11-235-701A-495	Sequence 495, App
563	92	4.2	6180	7	US-11-844-963-69	Sequence 69, Appl	c 636	90	4.1	964	1	PCT-US07-1776B-5428	Sequence 5428, Ap
564	92	4.2	6180	7	US-11-844-967-3	Sequence 3, Appli	637	90	4.1	1026	8	US-60-970-876-168	Sequence 168, App
c 565	92	4.2	6180	7	US-11-844-967-36	Sequence 36, Appl	638	90	4.1	1149	8	US-60-914-361-132	Sequence 132, App
566	92	4.2	6180	7	US-11-844-967-37	Sequence 37, Appl	639	90	4.1	1350	7	US-11-844-953-27	Sequence 27, Appl
567	92	4.2	6180	7	US-11-844-967-69	Sequence 69, Appl	640	90	4.1	1350	7	US-11-844-956-27	Sequence 27, Appl
568	92	4.2	6180	7	US-11-844-970-3	Sequence 3, Appli	641	90	4.1	1350	7	US-11-844-963-27	Sequence 27, Appl
c 569	92	4.2	6180	7	US-11-844-970-36	Sequence 36, Appl	642	90	4.1	1350	7	US-11-844-967-27	Sequence 27, Appl
570	92	4.2	6180	7	US-11-844-970-37	Sequence 37, Appl	643	90	4.1	1350	7	US-11-844-970-27	Sequence 27, Appl
571	92	4.2	6180	7	US-11-844-973-3	Sequence 3, Appli	644	90	4.1	1350	7	US-11-844-973-27	Sequence 27, Appl
c 572	92	4.2	6180	7	US-11-844-973-36	Sequence 36, Appl	645	90	4.1	1380	7	US-11-781-151-21	Sequence 21, Appl
573	92	4.2	6180	7	US-11-844-973-37	Sequence 37, Appl	c 646	90	4.1	1392	7	US-11-769-327A-13	Sequence 13, Appl
574	92	4.2	6180	7	US-11-844-973-37	Sequence 37, Appl	647	90	4.1	1407	7	US-11-557-761-4	Sequence 4, Appli
575	92	4.2	6180	7	US-11-844-973-69	Sequence 69, Appl	648	90	4.1	1407	7	US-11-557-783-4	Sequence 4, Appli
c 576	92	4.2	17534	1	PCT-US07-06371-7	Sequence 7, Appli	c 649	90	4.1	1407	7	US-11-769-327A-10	Sequence 10, Appl
c 577	92	4.2	21001	1	PCT-US07-75297-3	Sequence 3, Appli	650	90	4.1	2344	7	US-11-833-133-49	Sequence 49, Appl
578	92	4.2	30756	1	PCT-US07-06371-16	Sequence 16, Appl	651	90	4.1	2766	8	US-60-970-876-126	Sequence 126, App
579	91.5	4.1	752	1	PCT-US07-17776B-6870	Sequence 6870, Ap	652	90	4.1	2855	7	US-11-884-496-563	Sequence 563, App
c 580	91.5	4.1	784	1	PCT-US07-17776B-1624	Sequence 1624, Ap	653	90	4.1	3217	7	US-11-207-739B-7	Sequence 7, Appli
581	91.5	4.1	794	1	PCT-US07-17776B-5692	Sequence 5692, Ap	654	90	4.1	3325	1	PCT-US07-13803-518	Sequence 518, App
c 582	91.5	4.1	1061	1	PCT-US07-17776B-8342	Sequence 8342, Ap	c 655	90	4.1	3332	7	US-11-733-861-21	Sequence 21, Appl
583	91.5	4.1	1189	7	US-11-374-300-54	Sequence 54, Appl	656	90	4.1	3807	7	US-11-557-761-2	Sequence 2, Appli
584	91.5	4.1	1218	7	US-11-649-155-9	Sequence 9, Appli	657	90	4.1	3807	7	US-11-557-783-2	Sequence 2, Appli
585	91.5	4.1	1530	7	US-11-844-953-25	Sequence 25, Appl	658	90	4.1	4131	1	PCT-US07-13803-343	Sequence 343, App
586	91.5	4.1	1530	7	US-11-844-956-25	Sequence 25, Appl	c 659	90	4.1	4673	7	US-11-816-601-779	Sequence 779, App
587	91.5	4.1	1530	7	US-11-844-963-25	Sequence 25, Appl	660	90	4.1	5898	7	US-11-557-761-1	Sequence 1, Appli
588	91.5	4.1	1530	7	US-11-844-967-25	Sequence 25, Appl	661	90	4.1	5898	7	US-11-557-783-1	Sequence 1, Appli
589	91.5	4.1	1530	7	US-11-844-970-25	Sequence 25, Appl	c 662	90	4.1	6000	1	PCT-US07-13803-76	Sequence 76, Appl
590	91.5	4.1	1530	7	US-11-844-973-25	Sequence 25, Appl	c 663	90	4.1	34555	6	US-10-559-596-5	Sequence 5, Appli
591	91.5	4.1	1595	7	US-11-816-601-713	Sequence 713, App	c 664	89.5	4.0	811	1	PCT-US07-17776B-6415	Sequence 6415, Ap
592	91.5	4.1	1786	7	US-11-374-300-709	Sequence 709, App	665	89.5	4.0	811	1	PCT-US07-17776B-7081	Sequence 7081, Ap
593	91.5	4.1	1854	1	PCT-US07-75398-64	Sequence 64, Appl	666	89.5	4.0	829	1	PCT-US07-17776B-7896	Sequence 7896, Ap
594	91.5	4.1	1854	7	US-11-835-328-64	Sequence 64, Appl	667	89.5	4.0	840	8	US-60-970-876-141	Sequence 141, App
595	91.5	4.1	1887	7	US-11-649-155-7	Sequence 7, Appli	c 668	89.5	4.0	842	1	PCT-US07-17776B-9643	Sequence 9643, Ap



669	89.5	4.0	934	7	US-11-374-300-581	Sequence 581, App	742	88.5	4.0	3774	8	US-60-951-363-182	Sequence 182, App
c 670	89.5	4.0	1260	8	US-60-970-876-171	Sequence 171, App	743	88.5	4.0	3774	8	US-60-951-363-184	Sequence 184, App
671	89.5	4.0	1449	8	US-60-914-361-58	Sequence 58, Appl	744	88.5	4.0	4147	1	PCT-US07-13803-404	Sequence 404, App
c 672	89.5	4.0	1500	7	US-11-844-953-63	Sequence 63, Appl	c 745	88.5	4.0	5477	7	US-11-835-336-108	Sequence 108, App
c 673	89.5	4.0	1500	7	US-11-844-956-63	Sequence 63, Appl	746	88.5	4.0	6470	7	US-11-884-496-258	Sequence 258, App
c 674	89.5	4.0	1500	7	US-11-844-963-63	Sequence 63, Appl	747	88.5	4.0	8115	7	US-11-825-627-322	Sequence 322, App
c 675	89.5	4.0	1500	7	US-11-844-967-63	Sequence 63, Appl	c 748	88.5	4.0	9155	7	US-11-884-496-412	Sequence 412, App
c 676	89.5	4.0	1500	7	US-11-844-970-63	Sequence 63, Appl	749	88	4.0	768	1	PCT-US07-17776B-1951	Sequence 1951, Ap
c 677	89.5	4.0	1500	7	US-11-844-973-63	Sequence 63, Appl	750	88	4.0	885	1	PCT-US07-17776B-5636	Sequence 5636, Ap
c 678	89.5	4.0	1569	8	US-60-970-876-169	Sequence 169, App	c 751	88	4.0	921	1	PCT-US07-17776B-9587	Sequence 9587, Ap
679	89.5	4.0	1782	1	PCT-US07-17013-77	Sequence 77, Appl	c 752	88	4.0	966	7	US-11-883-506-4	Sequence 4, Appli
680	89.5	4.0	1965	1	PCT-US07-75398-87	Sequence 87, Appl	c 753	88	4.0	966	7	US-11-883-499-4	Sequence 4, Appli
681	89.5	4.0	1965	7	US-11-835-328-87	Sequence 87, Appl	754	88	4.0	1006	1	PCT-US07-17776B-9498	Sequence 9498, Ap
682	89.5	4.0	2004	1	PCT-US07-75398-80	Sequence 80, Appl	755	88	4.0	1013	6	US-10-870-198B-27	Sequence 27, Appl
683	89.5	4.0	2004	7	US-11-835-328-80	Sequence 80, Appl	756	88	4.0	1022	1	PCT-US07-17776B-4418	Sequence 4418, Ap
684	89.5	4.0	2043	6	US-10-375-932A-216	Sequence 216, App	c 757	88	4.0	1040	1	PCT-US07-17776B-3442	Sequence 3442, Ap
685	89.5	4.0	2243	7	US-11-847-733-54	Sequence 54, Appl	c 758	88	4.0	1106	1	PCT-US07-17776B-8283	Sequence 8283, Ap
686	89.5	4.0	2858	7	US-11-781-665-741	Sequence 741, App	759	88	4.0	1592	7	US-11-833-133-7	Sequence 7, Appli
c 687	89.5	4.0	4410	7	US-11-781-861-23	Sequence 23, Appl	c 760	88	4.0	1844	7	US-11-781-665-1615	Sequence 1615, Ap
c 688	89.5	4.0	4410	7	US-11-781-867-23	Sequence 23, Appl	761	88	4.0	2136	7	US-11-832-009-20	Sequence 20, Appl
c 689	89.5	4.0	4410	7	US-11-781-870-23	Sequence 23, Appl	762	88	4.0	4374	7	US-11-884-496-217	Sequence 217, App
c 690	89.5	4.0	4410	7	US-11-781-871-23	Sequence 23, Appl	763	88	4.0	4702	7	US-11-490-374A-1567	Sequence 1567, Ap
c 691	89.5	4.0	4410	7	US-11-781-874-23	Sequence 23, Appl	764	88	4.0	5862	7	US-11-816-601-20	Sequence 20, Appl
c 692	89.5	4.0	4410	7	US-11-781-875-23	Sequence 23, Appl	c 765	88	4.0	6000	1	PCT-US07-13803-248	Sequence 248, App
c 693	89.5	4.0	4410	7	US-11-781-877-23	Sequence 23, Appl	766	88	4.0	6127	1	PCT-US07-13803-424	Sequence 424, App
c 694	89.5	4.0	4410	7	US-11-781-880-23	Sequence 23, Appl	767	88	4.0	6233	7	US-11-793-909-82	Sequence 82, Appl
c 695	89.5	4.0	4410	7	US-11-781-882-23	Sequence 23, Appl	768	88	4.0	9778	7	US-11-884-496-164	Sequence 164, App
c 696	89.5	4.0	4410	7	US-11-844-953-61	Sequence 61, Appl	c 769	87.5	4.0	546	1	PCT-US07-17776B-4719	Sequence 4719, Ap
c 697	89.5	4.0	4410	7	US-11-844-956-61	Sequence 61, Appl	770	87.5	4.0	711	1	PCT-US07-17321A-61	Sequence 61, Appl
c 698	89.5	4.0	4410	7	US-11-844-963-61	Sequence 61, Appl	771	87.5	4.0	750	1	PCT-US07-17321A-156	Sequence 156, App
c 699	89.5	4.0	4410	7	US-11-844-967-61	Sequence 61, Appl	772	87.5	4.0	930	7	US-11-374-300-332	Sequence 332, App
c 700	89.5	4.0	4410	7	US-11-844-970-61	Sequence 61, Appl	773	87.5	4.0	1068	7	US-11-852-274-61	Sequence 61, Appl
c 701	89.5	4.0	4410	7	US-11-844-973-61	Sequence 61, Appl	774	87.5	4.0	1188	7	US-11-781-151-3	Sequence 3, Appli
c 702	89.5	4.0	5119	7	US-11-884-496-255	Sequence 255, App	c 775	87.5	4.0	1309	1	PCT-US07-17776B-3528	Sequence 3528, Ap
c 703	89.5	4.0	6187	7	US-11-793-909-75	Sequence 75, Appl	776	87.5	4.0	1401	7	US-11-833-133-85	Sequence 85, Appl
704	89.5	4.0	8312	7	US-11-884-496-221	Sequence 221, App	777	87.5	4.0	1431	7	US-11-374-300-80	Sequence 80, Appl
705	89.5	4.0	11883	7	US-11-796-131-4	Sequence 4, Appli	778	87.5	4.0	1573	7	US-11-781-665-1819	Sequence 1819, Ap
706	89.5	4.0	11916	7	US-11-796-131-1	Sequence 1, Appli	779	87.5	4.0	1804	1	PCT-US07-75398-11	Sequence 11, Appl
707	89	4.0	681	8	US-60-970-876-63	Sequence 63, Appl	780	87.5	4.0	1804	7	US-11-835-328-11	Sequence 11, Appl
708	89	4.0	684	7	US-11-833-133-42	Sequence 42, Appl	781	87.5	4.0	1821	7	US-11-538-319-29	Sequence 29, Appl
709	89	4.0	1388	7	US-11-825-627-182	Sequence 182, App	782	87.5	4.0	2022	7	US-11-573-744-9	Sequence 9, Appli
710	89	4.0	1718	8	US-60-970-876-76	Sequence 76, Appl	783	87.5	4.0	2103	6	US-10-815-495A-5	Sequence 5, Appli
711	89	4.0	1741	7	US-11-374-300-664	Sequence 664, App	784	87.5	4.0	2103	7	US-11-837-279-5	Sequence 5, Appli
c 712	89	4.0	2047	7	US-11-781-665-863	Sequence 863, App	785	87.5	4.0	2361	7	US-11-650-345-8	Sequence 8, Appli
c 713	89	4.0	2378	7	US-11-884-496-283	Sequence 283, App	c 786	87.5	4.0	2692	1	PCT-US07-15762-2	Sequence 2, Appli
c 714	89	4.0	2509	7	US-11-781-665-2430	Sequence 2430, Ap	c 787	87.5	4.0	3728	7	US-11-711-146-12	Sequence 12, Appl
715	89	4.0	4403	7	US-11-825-627-330	Sequence 330, App	c 788	87.5	4.0	3728	7	US-11-711-146-13	Sequence 13, Appl
716	89	4.0	4683	7	US-11-490-374A-1647	Sequence 1647, Ap	c 789	87.5	4.0	5144	7	US-11-490-374A-1684	Sequence 1684, Ap
717	89	4.0	4683	7	US-11-490-374A-1648	Sequence 1648, Ap	c 790	87.5	4.0	5228	7	US-11-708-858-34	Sequence 34, Appl
718	89	4.0	4838	7	US-11-490-374A-1650	Sequence 1650, Ap	c 791	87	3.9	698	1	PCT-US07-17776B-3319	Sequence 3319, Ap
719	89	4.0	6000	1	PCT-US07-13803-247	Sequence 247, App	c 792	87	3.9	698	1	PCT-US07-17776B-4098	Sequence 4098, Ap
c 720	89	4.0	7108	7	US-11-847-733-21	Sequence 21, Appl	c 793	87	3.9	832	1	PCT-US07-17776B-8015	Sequence 8015, Ap
c 721	89	4.0	8515	7	US-11-884-496-15	Sequence 15, Appl	794	87	3.9	919	1	PCT-US07-17776B-3280	Sequence 3280, Ap
722	89	4.0	9263	7	US-11-884-496-191	Sequence 191, App	795	87	3.9	963	7	US-11-833-133-78	Sequence 78, Appl
723	88.5	4.0	689	1	PCT-US07-17776B-9803	Sequence 9803, Ap	796	87	3.9	978	8	US-60-970-876-144	Sequence 144, App
c 724	88.5	4.0	972	1	PCT-US07-17776B-4620	Sequence 4620, Ap	c 797	87	3.9	1034	1	PCT-US07-17776B-4552	Sequence 4552, Ap
725	88.5	4.0	1056	7	US-11-800-955-17	Sequence 17, Appl	c 798	87	3.9	1052	1	PCT-US07-17776B-9473	Sequence 9473, Ap
726	88.5	4.0	1215	1	PCT-US07-18368A-148	Sequence 148, App	799	87	3.9	1077	7	US-11-830-023-125	Sequence 125, App
727	88.5	4.0	1215	1	PCT-US07-18368A-149	Sequence 149, App	800	87	3.9	1170	1	PCT-US07-18368A-54	Sequence 54, Appl
728	88.5	4.0	1215	1	PCT-US07-18368A-150	Sequence 150, App	801	87	3.9	1214	1	PCT-US07-17776B-8200	Sequence 8200, Ap
729	88.5	4.0	1460	8	US-60-970-876-85	Sequence 85, Appl	802	87	3.9	1314	6	PCT-US07-17776B-8200	Sequence 1, Appli
c 730	88.5	4.0	1501	7	US-11-781-151-13	Sequence 13, Appl	803	87	3.9	1366	1	PCT-US07-13803-273	Sequence 273, App
731	88.5	4.0	1839	7	US-11-847-733-32	Sequence 32, Appl	804	87	3.9	1388	7	US-11-781-665-970	Sequence 970, App
732	88.5	4.0	1897	7	US-11-836-667-34	Sequence 34, Appl	c 805	87	3.9	1398	7	US-11-804-222-55	Sequence 55, Appl
733	88.5	4.0	2136	7	US-11-374-300-163	Sequence 163, App	806	87	3.9	1695	1	PCT-US07-18368A-167	Sequence 167, App
734	88.5	4.0	2637	7	US-11-781-199-3	Sequence 3, Appli	c 807	87	3.9	1885	7	US-11-781-665-181	Sequence 181, App
735	88.5	4.0	2637	7	US-11-781-203-3	Sequence 3, Appli	c 808	87	3.9	1959	7	US-11-801-963A-1756	Sequence 1756, Ap
736	88.5	4.0	2912	1	PCT-US07-13803-399	Sequence 399, App	809	87	3.9	2049	8	US-60-914-361-52	Sequence 52, Appl
737	88.5	4.0	3299	7	US-11-781-665-2818	Sequence 2818, Ap	810	87	3.9	2403	7	US-11-816-294-7	Sequence 7, Appli
738	88.5	4.0	3747	8	US-60-951-363-186	Sequence 186, App	811	87	3.9	2476	7	US-11-374-300-320	Sequence 320, App
739	88.5	4.0	3762	8	US-60-951-363-178	Sequence 178, App	c 812	87	3.9	2814	7	US-11-783-064-4	Sequence 4, Appli
740	88.5	4.0	3762	8	US-60-951-363-180	Sequence 180, App	813	87	3.9	2855	7	US-11-374-300-7	Sequence 7, Appli
741	88.5	4.0	3774	8	US-60-951-363-179	Sequence 179, App	c 814	87	3.9	2931	7	US-11-783-064-10	Sequence 10, Appl

C 815	87	3.9	3144	7	US-11-783-064-9	Sequence 9, Appli	888	86	3.9	4562	7	US-11-847-733-59	Sequence 59, Appl
C 816	87	3.9	3174	7	US-11-783-064-7	Sequence 7, Appli	889	86	3.9	5469	7	US-11-490-374A-1608	Sequence 1608, Ap
C 817	87	3.9	3809	7	US-11-783-064-6	Sequence 6, Appli	890	86	3.9	5648	7	US-11-490-374A-1605	Sequence 1605, Ap
C 818	87	3.9	3865	7	US-11-783-064-3	Sequence 3, Appli	891	86	3.9	5648	7	US-11-490-374A-1609	Sequence 1609, Ap
819	87	3.9	5096	7	US-11-881-406-40	Sequence 40, Appl	892	86	3.9	5695	7	US-11-490-374A-1597	Sequence 1597, Ap
820	87	3.9	5432	7	US-11-838-500-29	Sequence 29, Appl	893	86	3.9	5715	7	US-11-490-374A-1598	Sequence 1598, Ap
821	87	3.9	5432	7	US-11-838-500-57	Sequence 57, Appl	894	86	3.9	5715	7	US-11-490-374A-1598	Sequence 1598, Ap
822	87	3.9	6000	1	PCT-US07-13803-249	Sequence 249, App	895	86	3.9	5829	7	US-11-490-374A-1604	Sequence 1604, Ap
823	87	3.9	6096	1	PCT-US07-78059-10	Sequence 10, Appl	896	86	3.9	5829	7	US-11-490-374A-1607	Sequence 1607, Ap
824	87	3.9	6519	7	US-11-801-963A-2605	Sequence 2605, Ap	897	86	3.9	5866	7	US-11-490-374A-1600	Sequence 1600, Ap
825	87	3.9	6753	7	US-11-816-601-75	Sequence 75, Appl	898	86	3.9	5920	7	US-11-490-374A-1599	Sequence 1599, Ap
826	87	3.9	7028	7	US-11-881-406-39	Sequence 39, Appl	899	86	3.9	5925	7	US-11-815-198-28	Sequence 28, Appl
827	87	3.9	7822	7	US-11-830-023-144	Sequence 144, App	900	86	3.9	5925	7	US-11-490-374A-1601	Sequence 1601, Ap
828	87	3.9	8165	7	US-11-749-889-22	Sequence 22, Appl	901	86	3.9	5988	7	US-11-490-374A-1602	Sequence 1602, Ap
829	87	3.9	8165	7	US-11-830-023-164	Sequence 164, App	902	86	3.9	5988	7	US-11-490-374A-1606	Sequence 1606, Ap
830	87	3.9	8841	7	US-11-884-496-131	Sequence 131, App	903	86	3.9	6000	1	PCT-US07-13803-69	Sequence 69, Appl
831	87	3.9	12690	7	US-11-830-023-124	Sequence 124, App	C 904	86	3.9	6000	1	PCT-US07-13803-148	Sequence 148, App
C 832	87	3.9	12690	7	US-11-830-023-124	Sequence 124, App	905	86	3.9	8230	7	US-11-490-374A-1253	Sequence 1253, Ap
833	87	3.9	13313	6	US-10-552-571-16	Sequence 16, Appl	906	86	3.9	8481	7	US-11-490-374A-1254	Sequence 1254, Ap
834	87	3.9	13711	7	US-11-490-374A-1308	Sequence 1308, Ap	907	86	3.9	8481	7	US-11-847-733-36	Sequence 36, Appl
835	87	3.9	13711	7	US-11-490-374A-1310	Sequence 1310, Ap	908	86	3.9	8679	8	US-60-914-361-115	Sequence 115, App
836	87	3.9	13711	7	US-11-490-374A-1311	Sequence 1311, Ap	909	85.5	3.9	582	1	PCT-US07-17776B-5023	Sequence 5023, Ap
837	87	3.9	14194	7	US-11-490-374A-1309	Sequence 1309, Ap	910	85.5	3.9	819	7	US-11-749-889-25	Sequence 25, Appl
C 838	87	3.9	35937	7	US-11-249-873A-28	Sequence 28, Appl	911	85.5	3.9	819	7	US-11-830-023-119	Sequence 119, App
839	86.5	3.9	741	7	US-11-833-133-18	Sequence 18, Appl	C 912	85.5	3.9	933	7	US-11-834-069-2	Sequence 2, Appli
840	86.5	3.9	765	8	US-60-970-876-39	Sequence 39, Appl	913	85.5	3.9	1040	1	PCT-US07-17776B-4386	Sequence 4386, Ap
841	86.5	3.9	787	1	PCT-US07-17776B-5805	Sequence 59, Appl	914	85.5	3.9	1307	8	US-60-970-876-40	Sequence 40, Appl
842	86.5	3.9	867	1	PCT-US07-17776B-7887	Sequence 7887, Ap	915	85.5	3.9	1368	7	US-11-631-698-23	Sequence 23, Appl
843	86.5	3.9	908	7	US-11-374-300-293	Sequence 293, App	916	85.5	3.9	1477	6	US-10-860-724B-63	Sequence 63, Appl
844	86.5	3.9	939	7	US-11-833-133-63	Sequence 63, Appl	C 917	85.5	3.9	1962	7	US-11-817-499-11	Sequence 11, Appl
845	86.5	3.9	958	1	PCT-US07-17776B-6868	Sequence 6868, Ap	C 918	85.5	3.9	2710	7	US-11-884-496-166	Sequence 166, App
846	86.5	3.9	1055	7	US-11-825-627-158	Sequence 158, App	C 919	85.5	3.9	3720	7	US-11-835-336-37	Sequence 37, Appl
C 847	86.5	3.9	1057	1	PCT-US07-17776B-3304	Sequence 3304, Ap	920	85.5	3.9	3980	6	US-10-488-672A-17	Sequence 17, Appl
C 848	86.5	3.9	1083	7	US-11-883-996-59	Sequence 59, Appl	921	85.5	3.9	5535	7	US-11-908-114-2	Sequence 2, Appli
849	86.5	3.9	1265	7	US-11-795-824-11	Sequence 11, Appl	922	85.5	3.9	5868	1	PCT-US07-13803-288	Sequence 288, App
850	86.5	3.9	1265	7	US-11-795-824-12	Sequence 12, Appl	923	85.5	3.9	5868	1	PCT-US07-13803-526	Sequence 526, App
851	86.5	3.9	1265	7	US-11-795-824-13	Sequence 13, Appl	924	85.5	3.9	6453	7	US-11-816-601-136	Sequence 136, App
852	86.5	3.9	1265	7	US-11-795-824-14	Sequence 14, Appl	C 925	85.5	3.9	6621	7	US-11-835-336-15	Sequence 15, Appl
853	86.5	3.9	1265	7	US-11-795-824-35	Sequence 35, Appl	926	85	3.8	513	1	PCT-US07-17776B-5040	Sequence 5040, Ap
C 854	86.5	3.9	1492	7	US-11-374-300-197	Sequence 197, App	927	85	3.8	521	1	PCT-US07-17776B-10024	Sequence 10024, A
855	86.5	3.9	1493	7	US-11-884-496-453	Sequence 453, App	928	85	3.8	654	1	PCT-US07-17776B-7776	Sequence 7776, Ap
C 856	86.5	3.9	1845	7	US-11-374-300-341	Sequence 341, App	929	85	3.8	705	6	US-10-532-681-17	Sequence 17, Appl
857	86.5	3.9	1936	7	US-11-830-023-130	Sequence 130, App	C 930	85	3.8	782	1	PCT-US07-17776B-7901	Sequence 7901, Ap
858	86.5	3.9	2087	7	US-11-490-374A-1449	Sequence 1449, Ap	C 931	85	3.8	933	8	US-60-970-876-84	Sequence 84, Appl
859	86.5	3.9	2180	7	US-11-708-858-51	Sequence 51, Appl	C 932	85	3.8	1030	1	PCT-US07-17776B-3173	Sequence 3173, Ap
860	86.5	3.9	2287	7	US-11-781-665-2270	Sequence 2270, Ap	933	85	3.8	1042	7	US-11-374-300-467	Sequence 467, App
861	86.5	3.9	2615	7	US-11-884-496-444	Sequence 444, App	934	85	3.8	1047	7	US-11-654-358-18	Sequence 18, Appl
862	86.5	3.9	2988	7	US-11-354-210-90	Sequence 90, Appl	935	85	3.8	1134	8	US-60-970-876-7	Sequence 7, Appli
C 863	86.5	3.9	3034	7	US-11-708-858-44	Sequence 44, Appl	936	85	3.8	1335	8	US-60-970-876-102	Sequence 102, App
C 864	86.5	3.9	3077	7	US-11-708-858-45	Sequence 45, Appl	937	85	3.8	1371	7	US-11-623-607A-3	Sequence 3, Appli
865	86.5	3.9	3145	7	US-11-884-496-409	Sequence 409, App	938	85	3.8	1371	7	US-11-623-689-36	Sequence 36, Appl
866	86.5	3.9	3393	7	US-11-354-210-92	Sequence 92, Appl	939	85	3.8	1371	7	US-11-852-274-36	Sequence 36, Appl
867	86.5	3.9	3726	8	US-60-914-361-128	Sequence 128, App	940	85	3.8	1380	7	US-11-631-698-2	Sequence 2, Appli
868	86.5	3.9	5045	7	US-11-884-496-530	Sequence 530, App	941	85	3.8	1491	7	US-11-374-300-87	Sequence 87, Appl
C 869	86.5	3.9	5372	7	US-11-908-114-13	Sequence 13, Appl	942	85	3.8	1515	1	PCT-US07-77281-15	Sequence 15, Appl
870	86.5	3.9	5468	7	US-11-235-701A-489	Sequence 489, App	943	85	3.8	1515	7	US-11-490-374A-1839	Sequence 1839, Ap
871	86.5	3.9	6000	1	PCT-US07-13803-81	Sequence 81, Appl	944	85	3.8	1515	7	US-11-490-374A-1968	Sequence 1968, Ap
C 872	86.5	3.9	6000	1	PCT-US07-13803-188	Sequence 188, App	945	85	3.8	1515	7	US-11-490-374A-2136	Sequence 2136, Ap
C 873	86.5	3.9	6705	7	US-11-781-665-3045	Sequence 3045, Ap	946	85	3.8	1520	7	US-11-374-300-185	Sequence 185, App
874	86	3.9	813	1	PCT-US07-17776B-8024	Sequence 8024, Ap	C 947	85	3.8	1630	7	US-11-374-300-559	Sequence 559, App
875	86	3.9	1080	8	US-60-914-361-131	Sequence 131, App	948	85	3.8	1751	7	US-11-884-496-226	Sequence 226, App
876	86	3.9	1269	8	US-60-970-876-165	Sequence 165, App	949	85	3.8	2025	6	US-10-375-932A-204	Sequence 204, App
877	86	3.9	1326	7	US-11-883-197-12	Sequence 12, Appl	950	85	3.8	2193	7	US-11-781-665-3063	Sequence 3063, Ap
878	86	3.9	1497	7	US-11-795-824-29	Sequence 29, Appl	951	85	3.8	2238	8	US-60-970-876-100	Sequence 100, App
879	86	3.9	1603	6	US-10-583-089-9	Sequence 9, Appli	952	85	3.8	2583	7	US-11-785-365B-1	Sequence 1, Appli
880	86	3.9	1651	7	US-11-781-665-845	Sequence 845, App	C 953	85	3.8	2714	7	US-11-816-601-805	Sequence 805, App
881	86	3.9	1671	8	US-60-970-876-28	Sequence 28, Appl	C 954	85	3.8	2811	7	US-11-781-818-51	Sequence 51, Appl
882	86	3.9	1746	8	US-60-970-876-139	Sequence 139, App	C 955	85	3.8	2811	7	US-11-781-818-52	Sequence 52, Appl
C 883	86	3.9	1751	7	US-11-884-496-226	Sequence 226, App	956	85	3.8	3212	7	US-11-785-365B-13	Sequence 13, Appl
884	86	3.9	2329	7	US-11-884-496-271	Sequence 271, App	957	85	3.8	3288	7	US-11-785-365B-18	Sequence 18, Appl
885	86	3.9	2636	7	US-11-781-665-862	Sequence 862, App	958	85	3.8	3329	7	US-11-785-365B-15	Sequence 15, Appl
886	86	3.9	3192	7	US-11-884-496-29	Sequence 29, Appl	959	85	3.8	3740	7	US-11-733-861-18	Sequence 18, Appl
887	86	3.9	3494	7	US-11-795-824-33	Sequence 33, Appl	960	85	3.8	3872	7	US-11-884-496-524	Sequence 524, App

C 961	85	3.8	4501	7	US-11-835-336-63	Sequence 63, Appl	1034	84	3.8	2220	6	US-10-554-521-58	Sequence 58, Appl
	962	85	4853	7	US-11-884-496-600	Sequence 600, App	1035	84	3.8	2694	7	US-11-490-374A-1446	Sequence 1446, Ap
	963	85	5053	7	US-11-235-701A-500	Sequence 500, App	1036	84	3.8	2694	7	US-11-490-374A-1447	Sequence 1447, Ap
	964	85	30612	7	US-11-665-940-64	Sequence 64, Appl	1037	84	3.8	2694	7	US-11-490-374A-1448	Sequence 1448, Ap
	965	84.5	633	8	US-60-914-361-101	Sequence 101, App	c1038	84	3.8	2940	7	US-11-802-321A-18	Sequence 18, Appl
C 966	84.5	3.8	690	8	US-60-970-876-159	Sequence 159, App	c1039	84	3.8	2940	7	US-11-802-321A-20	Sequence 20, Appl
	967	84.5	699	1	PCT-US07-17776B-9251	Sequence 9251, Ap	c1040	84	3.8	2940	7	US-11-802-321A-21	Sequence 21, Appl
	968	84.5	814	7	US-11-374-300-56	Sequence 56, Appl	c1041	84	3.8	2940	7	US-11-802-321A-22	Sequence 22, Appl
	969	84.5	844	1	PCT-US07-17776B-2765	Sequence 2765, Ap	c1042	84	3.8	3000	7	US-11-623-607A-9	Sequence 9, Appli
	970	84.5	993	1	PCT-US07-18368A-190	Sequence 190, App	c1043	84	3.8	3000	7	US-11-623-689-42	Sequence 42, Appl
C 971	84.5	3.8	1052	1	PCT-US07-18368A-52	Sequence 52, Appl	c1044	84	3.8	3000	7	US-11-852-274-42	Sequence 42, Appl
	972	84.5	1059	8	PCT-US07-17776B-4547	Sequence 4547, Ap	1045	84	3.8	3018	1	PCT-US07-13803-349	Sequence 349, App
	973	84.5	1099	1	US-60-970-876-157	Sequence 157, App	1046	84	3.8	3120	7	US-11-802-321A-53	Sequence 53, Appl
	C 974	84.5	1176	6	US-10-552-571-15	Sequence 15, Appl	1047	84	3.8	3149	7	US-11-825-627-252	Sequence 252, App
	C 975	84.5	1257	1	PCT-US07-17776B-3260	Sequence 3260, Ap	1048	84	3.8	3305	7	US-11-802-321A-54	Sequence 54, Appl
C 976	84.5	3.8	1308	8	US-60-970-876-145	Sequence 145, App	1049	84	3.8	3305	7	US-11-802-321A-55	Sequence 55, Appl
	977	84.5	1432	7	US-11-374-300-390	Sequence 390, App	1050	84	3.8	3319	7	US-11-802-321A-80	Sequence 80, Appl
	978	84.5	1462	7	US-11-374-300-207	Sequence 207, App	1051	84	3.8	3387	7	US-11-490-374A-1243	Sequence 1243, Ap
	979	84.5	1489	7	US-11-591-361B-1	Sequence 1, Appli	c1052	84	3.8	4060	7	US-11-733-861-60	Sequence 60, Appl
	980	84.5	1492	7	US-11-374-300-197	Sequence 197, App	1053	84	3.8	4143	7	US-11-490-374A-1450	Sequence 1450, Ap
C 981	84.5	3.8	1900	7	US-11-374-300-356	Sequence 356, App	c1054	84	3.8	4502	7	US-11-490-374A-2152	Sequence 2152, Ap
	982	84.5	2050	7	US-11-884-546-68	Sequence 68, Appl	c1055	84	3.8	4502	7	US-11-490-374A-2154	Sequence 2154, Ap
	983	84.5	2619	7	US-11-490-374A-1989	Sequence 1989, Ap	1056	84	3.8	4504	7	US-11-884-496-435	Sequence 435, App
	984	84.5	2659	1	PCT-US07-13803-293	Sequence 293, App	c1057	84	3.8	5119	7	US-11-884-496-255	Sequence 255, App
	985	84.5	3128	7	US-11-490-374A-1990	Sequence 1990, Ap	c1058	84	3.8	5143	7	US-11-781-665-31	Sequence 31, Appl
C 986	84.5	3.8	3216	6	US-10-419-296A-32	Sequence 32, Appl	c1059	84	3.8	5898	7	US-11-557-761-1	Sequence 1, Appli
	987	84.5	3263	7	US-11-137-671A-15	Sequence 15, Appl	c1060	84	3.8	5898	7	US-11-557-783-1	Sequence 1, Appli
	988	84.5	3444	1	PCT-US07-17013-27	Sequence 27, Appl	1061	84	3.8	6444	7	US-11-831-404-85	Sequence 85, Appl
	989	84.5	3729	7	US-11-795-915-155	Sequence 155, App	1062	84	3.8	36909	8	US-60-956-153-7	Sequence 7, Appli
	990	84.5	3729	7	US-11-881-406-161	Sequence 161, App	1063	84	3.8	36909	8	US-60-968-754-7	Sequence 7, Appli
C 991	84.5	3.8	3922	7	US-11-881-406-161	Sequence 493, App	1064	84	3.8	36909	8	US-60-970-269-7	Sequence 7, Appli
	992	84.5	5619	7	US-11-235-701A-493	Sequence 493, App	1065	84	3.8	36909	8	US-60-970-281-7	Sequence 7, Appli
	993	84.5	5674	7	US-11-235-701A-488	Sequence 488, App	1066	84	3.8	49107	8	US-60-970-281-42	Sequence 42, Appl
	994	84.5	5674	7	US-11-235-701A-490	Sequence 490, App	1067	84	3.8	49765	8	US-60-956-153-13	Sequence 13, Appl
	995	84.5	5674	7	US-11-235-701A-501	Sequence 501, App	1068	84	3.8	49765	8	US-60-968-754-13	Sequence 13, Appl
C 996	84.5	3.8	5748	7	US-11-235-701A-491	Sequence 491, App	1069	84	3.8	49911	8	US-60-956-153-6	Sequence 6, Appli
	997	84.5	6000	1	PCT-US07-13803-136	Sequence 136, App	1070	84	3.8	49911	8	US-60-968-754-6	Sequence 6, Appli
	998	84.5	8206	7	US-11-490-374A-1902	Sequence 1902, Ap	1071	84	3.8	49911	8	US-60-970-269-6	Sequence 6, Appli
	999	84.5	8206	7	US-11-490-374A-2123	Sequence 2123, Ap	1072	84	3.8	49911	8	US-60-970-281-6	Sequence 6, Appli
	1000	84.5	8411	7	US-11-490-374A-1900	Sequence 1900, Ap	1073	84	3.8	52701	8	US-60-970-281-41	Sequence 41, Appl
C 1001	84.5	3.8	8435	7	US-11-490-374A-1903	Sequence 1903, Ap	1074	83.5	3.8	795	1	PCT-US07-17776B-1679	Sequence 1679, Ap
	1002	84.5	8850	7	US-11-490-374A-1901	Sequence 1901, Ap	1075	83.5	3.8	831	1	PCT-US07-17776B-7083	Sequence 7083, Ap
	1003	84.5	8850	7	US-11-490-374A-2120	Sequence 2120, Ap	c1076	83.5	3.8	852	1	PCT-US07-17776B-9542	Sequence 9542, Ap
	c1004	84.5	8976	7	US-11-490-374A-2121	Sequence 2121, Ap	1077	83.5	3.8	867	1	PCT-US07-17776B-7919	Sequence 7919, Ap
	c1005	84.5	8976	7	US-11-490-374A-2122	Sequence 2122, Ap	1078	83.5	3.8	1078	7	US-11-781-665-1288	Sequence 1288, Ap
C 1006	84.5	3.8	8976	7	US-11-490-374A-2124	Sequence 2124, Ap	1079	83.5	3.8	1178	8	US-60-970-876-64	Sequence 64, Appl
	1007	84.5	9448	7	US-11-490-374A-2125	Sequence 2125, Ap	1080	83.5	3.8	1227	1	PCT-US07-17776B-3300	Sequence 3300, Ap
	1008	84.5	10448	7	US-11-830-023-129	Sequence 129, App	1081	83.5	3.8	1630	7	US-11-374-300-559	Sequence 559, App
	c1009	84.5	12563	7	US-11-816-601-789	Sequence 789, App	1082	83.5	3.8	1736	7	US-11-374-300-717	Sequence 717, App
	c1010	84.5	18099	7	US-11-884-496-169	Sequence 169, App	c1083	83.5	3.8	1795	7	US-11-490-374A-1307	Sequence 1307, Ap
C 1011	84	3.8	690	1	PCT-US07-17776B-4072	Sequence 4072, Ap	1084	83.5	3.8	2213	1	PCT-US07-18368A-117	Sequence 117, App
	1012	84	705	8	US-60-970-876-66	Sequence 66, Appl	1085	83.5	3.8	2393	7	US-11-825-627-97	Sequence 97, Appl
	c1013	84	746	1	PCT-US07-17776B-1175	Sequence 1175, Ap	1086	83.5	3.8	2793	7	US-11-816-601-98	Sequence 98, Appl
	1014	84	762	1	PCT-US07-17776B-1438	Sequence 1438, Ap	1087	83.5	3.8	2831	7	US-11-829-656-24	Sequence 24, Appl
	1015	84	768	7	US-11-374-300-180	Sequence 180, App	1088	83.5	3.8	2831	7	US-11-782-545-24	Sequence 24, Appl
C 1016	84	3.8	795	7	US-11-677-866A-4	Sequence 4, Appli	1089	83.5	3.8	2831	7	US-11-829-011-24	Sequence 24, Appl
	c1017	84	841	1	PCT-US07-17776B-9383	Sequence 9383, Ap	1090	83.5	3.8	3033	7	US-11-781-665-2408	Sequence 2408, Ap
	1018	84	885	1	PCT-US07-18368A-5	Sequence 5, Appli	1091	83.5	3.8	3221	6	US-10-910-811B-379	Sequence 379, App
	1019	84	1103	7	US-11-374-300-525	Sequence 525, App	1092	83.5	3.8	3221	6	US-10-945-565B-379	Sequence 379, App
	c1020	84	1108	1	PCT-US07-17776B-3067	Sequence 3067, Ap	1093	83.5	3.8	3822	1	PCT-US07-77281-24	Sequence 24, Appl
C 1021	84	3.8	1284	7	US-11-801-963A-968	Sequence 968, App	1094	83.5	3.8	4279	7	US-11-060-659A-41	Sequence 41, Appl
	c1022	84	1300	7	US-11-374-300-505	Sequence 505, App	1095	83.5	3.8	4279	7	US-11-060-659A-43	Sequence 43, Appl
	1023	84	1305	7	US-11-833-133-16	Sequence 16, Appl	1096	83.5	3.8	4311	6	US-10-494-333A-5	Sequence 5, Appli
	1024	84	1310	7	US-11-137-671A-13	Sequence 13, Appl	c1097	83.5	3.8	4451	7	US-11-847-733-47	Sequence 47, Appl
	1025	84	1368	7	US-11-631-698-25	Sequence 25, Appl	1098	83.5	3.8	5451	7	US-11-815-198-1	Sequence 1, Appli
C 1026	84	3.8	1462	7	US-11-374-300-630	Sequence 630, App	1099	83.5	3.8	5774	8	US-60-956-437-3	Sequence 3, Appli
	1027	84	1628	7	US-11-374-300-130	Sequence 130, App	1100	83.5	3.8	6000	1	PCT-US07-13803-202	Sequence 202, App
	c1028	84	1759	7	US-11-781-665-792	Sequence 792, App	1101	83.5	3.8	6112	7	US-11-835-336-65	Sequence 65, Appl
	1029	84	1834	7	US-11-374-300-644	Sequence 644, App	1102	83.5	3.8	6156	7	US-11-816-601-739	Sequence 739, App
	1030	84	1855	7	US-11-831-468-97	Sequence 97, Appl	1103	83.5	3.8	6349	7	US-11-793-909-16	Sequence 16, Appl
C 1031	84	3.8	2001	7	US-11-881-406-3178	Sequence 3178, Ap	1104	83.5	3.8	6372	7	US-11-793-909-31	Sequence 31, Appl
	1032	84	2025	6	US-10-375-932A-256	Sequence 256, App	1105	83.5	3.8	6386	7	US-11-793-909-21	Sequence 21, Appl
	1033	84	2048	1	PCT-US07-13803-460	Sequence 460, App	c1106	83.5	3.8	6389	7	US-11-793-909-36	Sequence 36, Appl



1107	83.5	3.8	6394	7	US-11-793-909-26	Sequence 26, Appl	c1180	83	3.8	9944	7	US-11-490-374A-2183	Sequence 2183, Ap
1108	83.5	3.8	6450	7	US-11-793-909-58	Sequence 58, Appl	c1181	83	3.8	9959	7	US-11-490-374A-2181	Sequence 2181, Ap
1109	83.5	3.8	6464	7	US-11-793-909-42	Sequence 42, Appl	c1182	83	3.8	9962	7	US-11-490-374A-2180	Sequence 2180, Ap
1110	83.5	3.8	6573	7	US-11-490-374A-1572	Sequence 1572, Ap	c1183	83	3.8	10562	7	US-11-490-374A-2182	Sequence 2182, Ap
1111	83.5	3.8	6583	7	US-11-793-909-55	Sequence 55, Appl	c1184	83	3.8	33592	7	US-11-249-873A-1	Sequence 1, Appli
1112	83.5	3.8	6604	7	US-11-793-909-45	Sequence 45, Appl	c1185	83	3.8	33699	7	US-11-249-873A-3	Sequence 3, Appli
1113	83.5	3.8	6609	7	US-11-793-909-52	Sequence 52, Appl	c1186	83	3.8	33988	7	US-11-249-873A-14	Sequence 14, Appl
1114	83.5	3.8	6759	7	US-11-793-909-59	Sequence 59, Appl	c1187	83	3.8	34341	7	US-11-249-873A-2	Sequence 2, Appli
1115	83.5	3.8	6780	7	US-11-793-909-60	Sequence 60, Appl	c1188	83	3.8	34448	7	US-11-249-873A-4	Sequence 4, Appli
1116	83.5	3.8	8666	7	US-11-835-336-95	Sequence 95, Appl	c1189	83	3.8	34737	7	US-11-249-873A-15	Sequence 15, Appl
1117	83.5	3.8	11025	7	US-11-712-794-1	Sequence 1, Appli	c1190	83	3.8	35724	7	US-11-249-873A-13	Sequence 13, Appl
1118	83.5	3.8	11933	7	US-11-712-794-2	Sequence 2, Appli	c1191	83	3.8	36114	7	US-11-249-873A-16	Sequence 16, Appl
1119	83	3.8	654	7	US-11-538-319-5	Sequence 5, Appli	c1192	83	3.8	39301	7	US-11-712-794-17	Sequence 17, Appl
1120	83	3.8	657	7	US-11-538-319-31	Sequence 31, Appl	c1193	83	3.8	50475	7	US-11-712-794-16	Sequence 16, Appl
1121	83	3.8	705	6	US-10-532-681-9	Sequence 9, Appli	1194	82.5	3.7	751	8	US-60-970-876-87	Sequence 87, Appl
1122	83	3.8	705	7	US-11-374-300-458	Sequence 458, App	c1195	82.5	3.7	751	1	PCT-US07-1776B-9238	Sequence 9238, Ap
1123	83	3.8	775	1	PCT-US07-1776B-655	Sequence 655, App	1196	82.5	3.7	758	7	US-11-816-601-785	Sequence 785, App
1124	83	3.8	831	1	PCT-US07-1776B-4104	Sequence 4104, Ap	1197	82.5	3.7	826	1	PCT-US07-1776B-3965	Sequence 3965, Ap
1125	83	3.8	884	1	PCT-US07-1776B-9354	Sequence 9354, Ap	c1198	82.5	3.7	1196	7	US-11-374-300-241	Sequence 241, App
1126	83	3.8	1098	7	PCT-US07-1776B-3453	Sequence 3453, Ap	c1199	82.5	3.7	1232	1	PCT-US07-1776B-3554	Sequence 3554, Ap
1127	83	3.8	1143	7	US-11-833-133-24	Sequence 24, Appl	1200	82.5	3.7	1275	7	US-11-833-133-61	Sequence 61, Appl
1128	83	3.8	1198	1	PCT-US07-1776B-3330	Sequence 3330, Ap	c1201	82.5	3.7	1284	7	US-11-801-963A-1279	Sequence 1279, Ap
1129	83	3.8	1269	1	PCT-US07-18368A-356	Sequence 356, App	1202	82.5	3.7	1455	8	US-60-970-876-82	Sequence 82, Appl
1130	83	3.8	1416	1	PCT-US02-29565-15	Sequence 15, Appl	1203	82.5	3.7	1658	7	US-11-833-133-22	Sequence 22, Appl
1131	83	3.8	1500	7	US-11-844-953-23	Sequence 23, Appl	c1204	82.5	3.7	1731	1	PCT-US07-77297-13	Sequence 13, Appl
1132	83	3.8	1500	7	US-11-844-956-23	Sequence 23, Appl	c1205	82.5	3.7	1887	1	PCT-US07-77297-7	Sequence 7, Appli
1133	83	3.8	1500	7	US-11-844-963-23	Sequence 23, Appl	1206	82.5	3.7	2059	7	US-11-884-496-430	Sequence 430, App
1134	83	3.8	1500	7	US-11-844-967-23	Sequence 23, Appl	1207	82.5	3.7	2432	7	US-11-832-579-17	Sequence 17, Appl
1135	83	3.8	1500	7	US-11-844-970-23	Sequence 23, Appl	1208	82.5	3.7	2461	7	US-11-832-579-7	Sequence 7, Appli
1136	83	3.8	1500	7	US-11-844-973-23	Sequence 23, Appl	1209	82.5	3.7	3003	6	US-10-836-063B-69	Sequence 69, Appl
1137	83	3.8	1603	6	US-10-583-089-1	Sequence 1, Appli	1210	82.5	3.7	3060	6	US-10-836-063B-95	Sequence 95, Appl
1138	83	3.8	1613	7	US-11-374-300-734	Sequence 734, App	1211	82.5	3.7	3060	7	US-11-781-151-27	Sequence 27, Appl
1139	83	3.8	1614	7	US-11-538-319-1	Sequence 1, Appli	c1212	82.5	3.7	3515	7	US-11-490-374A-2111	Sequence 2111, Ap
1140	83	3.8	1652	7	US-11-781-665-490	Sequence 490, App	c1213	82.5	3.7	3529	7	US-11-490-374A-2112	Sequence 2112, Ap
1141	83	3.8	1701	7	US-11-538-319-15	Sequence 15, Appl	c1214	82.5	3.7	3530	7	US-11-490-374A-2114	Sequence 2114, Ap
1142	83	3.8	1728	8	US-60-970-876-109	Sequence 109, App	c1215	82.5	3.7	3585	1	PCT-US07-17013-3	Sequence 3, Appli
1143	83	3.8	2034	7	US-11-817-499-5	Sequence 5, Appli	c1216	82.5	3.7	5083	7	US-11-781-665-2337	Sequence 2337, Ap
1144	83	3.8	2053	7	US-11-781-665-1399	Sequence 1399, Ap	c1217	82.5	3.7	6000	1	PCT-US07-13803-48	Sequence 48, Appl
1145	83	3.8	2056	7	US-11-884-496-554	Sequence 554, App	c1218	82.5	3.7	6050	7	US-11-835-336-20	Sequence 20, Appl
1146	83	3.8	2121	7	US-11-816-601-87	Sequence 87, Appl	c1219	82.5	3.7	6644	7	US-11-847-733-88	Sequence 88, Appl
1147	83	3.8	2195	6	US-10-276-032-40	Sequence 40, Appl	1220	82.5	3.7	7085	7	US-11-749-889-82	Sequence 82, Appl
1148	83	3.8	2395	7	US-11-831-404-17	Sequence 17, Appl	1221	82.5	3.7	7085	8	US-60-911-925A-29	Sequence 29, Appl
1149	83	3.8	2589	6	US-10-836-063B-71	Sequence 71, Appl	c1222	82.5	3.7	7872	8	US-60-911-925A-30	Sequence 30, Appl
1150	83	3.8	2632	7	US-11-847-733-14	Sequence 14, Appl	1223	82.5	3.7	8671	7	US-11-749-889-93	Sequence 93, Appl
1151	83	3.8	3145	7	US-11-781-665-1360	Sequence 1360, Ap	c1224	82.5	3.7	11706	8	US-60-911-925A-39	Sequence 39, Appl
1152	83	3.8	3145	7	US-11-781-665-1361	Sequence 1361, Ap	c1225	82.5	3.7	74424	7	US-11-829-279-153	Sequence 153, App
1153	83	3.8	3195	7	US-11-781-665-1362	Sequence 1362, Ap	c1226	82	3.7	495	7	US-11-801-963A-1467	Sequence 1467, Ap
1154	83	3.8	3195	7	US-11-781-665-1363	Sequence 1363, Ap	1227	82	3.7	564	7	US-11-838-500-43	Sequence 43, Appl
1155	83	3.8	3294	7	US-11-781-151-73	Sequence 73, Appl	1228	82	3.7	725	1	PCT-US07-1776B-971	Sequence 971, App
1156	83	3.8	3294	7	US-11-781-151-75	Sequence 75, Appl	c1229	82	3.7	731	1	PCT-US07-1776B-9221	Sequence 9221, Ap
1157	83	3.8	3387	8	US-60-951-363-185	Sequence 185, App	1230	82	3.7	732	1	PCT-US07-14648-3	Sequence 3, Appli
1158	83	3.8	3480	8	US-60-951-363-172	Sequence 172, App	1231	82	3.7	752	1	PCT-US07-14648-60	Sequence 60, Appl
1159	83	3.8	3522	8	US-60-951-363-183	Sequence 183, App	c1232	82	3.7	756	1	PCT-US07-1776B-1614	Sequence 1614, Ap
1160	83	3.8	3621	8	US-60-951-363-177	Sequence 177, App	1233	82	3.7	799	7	US-11-374-300-506	Sequence 506, App
1161	83	3.8	3663	8	US-60-951-363-170	Sequence 170, App	1234	82	3.7	851	1	PCT-US07-1776B-4519	Sequence 4519, Ap
1162	83	3.8	3663	8	US-60-951-363-181	Sequence 181, App	c1235	82	3.7	870	8	US-60-914-361-137	Sequence 137, App
1163	83	3.8	4744	7	US-11-884-496-632	Sequence 632, App	c1236	82	3.7	994	1	PCT-US07-1776B-3465	Sequence 3465, Ap
1164	83	3.8	4840	7	US-11-838-500-58	Sequence 58, Appl	1237	82	3.7	1017	1	PCT-US07-1776B-4539	Sequence 4539, Ap
1165	83	3.8	5432	7	US-11-838-500-29	Sequence 29, Appl	1238	82	3.7	1124	7	US-11-374-300-249	Sequence 249, App
1166	83	3.8	5432	7	US-11-838-500-57	Sequence 57, Appl	1239	82	3.7	1266	1	PCT-US07-1776B-4015	Sequence 4015, Ap
1167	83	3.8	6000	1	PCT-US07-13803-164	Sequence 164, App	c1240	82	3.7	1278	1	PCT-US02-29565-5	Sequence 5, Appli
1168	83	3.8	6249	7	US-11-787-237-4	Sequence 4, Appli	1241	82	3.7	1319	1	PCT-US07-1776B-5934	Sequence 5934, Ap
1169	83	3.8	6592	7	US-11-847-733-80	Sequence 80, Appl	c1242	82	3.7	1368	7	US-11-631-698-6	Sequence 6, Appli
1170	83	3.8	7303	1	PCT-US07-67567-17	Sequence 17, Appl	1243	82	3.7	1368	8	US-60-970-876-138	Sequence 138, App
1171	83	3.8	7382	7	US-11-884-496-451	Sequence 451, App	1244	82	3.7	1380	7	US-11-830-023-3	Sequence 3, Appli
1172	83	3.8	8733	7	US-11-844-953-35	Sequence 35, Appl	1245	82	3.7	1591	7	US-11-781-665-441	Sequence 441, App
1173	83	3.8	8733	7	US-11-844-956-35	Sequence 35, Appl	1246	82	3.7	1599	7	US-11-781-665-3108	Sequence 3108, Ap
1174	83	3.8	8733	7	US-11-844-963-35	Sequence 35, Appl	1247	82	3.7	1608	6	US-10-583-089-5	Sequence 5, Appli
1175	83	3.8	8733	7	US-11-844-967-35	Sequence 35, Appl	1248	82	3.7	1716	8	US-60-970-876-13	Sequence 13, Appl
1176	83	3.8	8733	7	US-11-844-970-35	Sequence 35, Appl	c1249	82	3.7	1721	1	PCT-US07-1776B-5003	Sequence 5003, Ap
1177	83	3.8	8733	7	US-11-844-973-35	Sequence 35, Appl	1250	82	3.7	1905	7	US-11-573-744-4	Sequence 4, Appli
1178	83	3.8	8964	7	US-11-706-376-132	Sequence 132, App	1251	82	3.7	2070	7	US-11-490-374A-1451	Sequence 1451, Ap
1179	83	3.8	9189	6	US-10-741-191B-1	Sequence 1, Appli	1252	82	3.7	2130	7	US-11-354-210-94	Sequence 94, Appl



1253	82	3.7	2377	7	US-11-829-659-15	Sequence 15, Appl	81	1326	81	3.7	825	7	US-11-781-818-60	Sequence 60, Appl
1254	82	3.7	2377	7	US-11-829-667-15	Sequence 15, Appl	81	1327	81	3.7	825	7	US-11-781-818-61	Sequence 61, Appl
1255	82	3.7	2535	7	US-11-354-210-96	Sequence 96, Appl	81	1328	81	3.7	990	1	PCT-US07-17776B-3524	Sequence 3524, Ap
1256	82	3.7	2851	7	US-11-884-496-442	Sequence 442, App	81	cl1329	81	3.7	1000	1	PCT-US07-17776B-4513	Sequence 4513, Ap
1257	82	3.7	3300	7	US-11-490-374A-1570	Sequence 1570, Ap	81	cl1330	81	3.7	1003	1	PCT-US07-17776B-2991	Sequence 2991, Ap
1258	82	3.7	3300	7	US-11-490-374A-1571	Sequence 1571, Ap	81	1331	81	3.7	1037	1	PCT-US07-17776B-2945	Sequence 2945, Ap
1259	82	3.7	3300	7	US-11-490-374A-1573	Sequence 1573, Ap	81	cl1332	81	3.7	1072	7	US-11-374-300-495	Sequence 495, App
cl1260	82	3.7	3715	7	US-11-835-336-100	Sequence 100, App	81	cl1333	81	3.7	1098	1	PCT-US07-17776B-8263	Sequence 8263, App
cl1261	82	3.7	4698	1	PCT-US07-13803-440	Sequence 440, App	81	cl1334	81	3.7	1197	8	US-60-915-455-132	Sequence 132, App
cl1262	82	3.7	4889	7	US-11-816-601-86	Sequence 86, Appl	81	1335	81	3.7	1454	7	US-11-235-701A-416	Sequence 416, App
cl1263	82	3.7	4889	7	US-11-816-601-289	Sequence 289, App	81	1336	81	3.7	1497	7	US-11-815-095-33	Sequence 33, Appl
cl1264	82	3.7	4889	7	US-11-816-601-810	Sequence 810, App	81	cl1337	81	3.7	1704	7	US-11-801-963A-1175	Sequence 1175, Ap
cl1265	82	3.7	4915	7	US-11-884-496-682	Sequence 682, App	81	cl1338	81	3.7	1925	7	US-11-374-300-342	Sequence 342, App
1266	82	3.7	5175	7	US-11-573-744-15	Sequence 15, Appl	81	1339	81	3.7	1943	1	PCT-US07-17776B-10013	Sequence 10013, A
1267	82	3.7	5668	7	US-11-733-861-17	Sequence 17, Appl	81	cl1340	81	3.7	2000	1	PCT-US07-63132-1	Sequence 1, Appli
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cl1269	82	3.7	6000	1	PCT-US07-13803-209	Sequence 209, App	81	1342	81	3.7	2002	7	US-11-374-300-420	Sequence 420, App
1270	82	3.7	6072	6	US-10-741-191B-21	Sequence 21, Appl	81	cl1343	81	3.7	2092	7	US-11-781-665-1038	Sequence 1038, Ap
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cl1272	82	3.7	7523	7	US-11-884-496-215	Sequence 215, App	81	cl1345	81	3.7	2397	7	US-11-781-665-1893	Sequence 1893, Ap
cl1273	82	3.7	218241	7	US-11-765-730A-1	Sequence 1, Appli	81	1346	81	3.7	2526	7	US-11-884-496-616	Sequence 616, App
1274	81.5	3.7	642	1	PCT-US07-17776B-4311	Sequence 4311, Ap	81	1347	81	3.7	2707	7	US-11-781-665-1600	Sequence 1600, Ap
1275	81.5	3.7	726	8	US-60-970-876-36	Sequence 36, Appl	81	cl1348	81	3.7	3419	7	US-11-490-374A-2113	Sequence 2113, Ap
cl1276	81.5	3.7	982	1	PCT-US07-17776B-8791	Sequence 8791, Ap	81	1349	81	3.7	4015	7	US-11-851-267-8	Sequence 8, Appli
1277	81.5	3.7	992	6	US-10-669-757A-3	Sequence 3, Appli	81	1350	81	3.7	4015	7	US-11-851-267-15	Sequence 15, Appl
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cl1281	81.5	3.7	1197	7	US-11-801-963A-747	Sequence 747, App	81	cl1354	81	3.7	8145	7	US-11-884-496-30	Sequence 30, Appl
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1284	81.5	3.7	1311	8	US-60-914-361-55	Sequence 55, Appl	81	1357	81	3.7	15346	7	US-11-884-496-711	Sequence 711, App
1285	81.5	3.7	1494	1	PCT-US07-18368A-41	Sequence 41, Appl	80.5	1358	80.5	3.6	753	1	PCT-US07-17776B-812	Sequence 812, App
1286	81.5	3.7	1494	1	PCT-US07-18368A-42	Sequence 42, Appl	80.5	1359	80.5	3.6	754	1	PCT-US07-17776B-5880	Sequence 5880, Ap
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cl1290	81.5	3.7	1870	7	US-11-781-665-2525	Sequence 2525, Ap	80.5	cl1363	80.5	3.6	804	7	US-11-801-963A-170	Sequence 170, App
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1292	81.5	3.7	1892	1	PCT-US07-63132-3	Sequence 3, Appli	80.5	cl1365	80.5	3.6	829	1	PCT-US07-17776B-7517	Sequence 7517, Ap
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1297	81.5	3.7	2257	7	US-11-490-374A-1248	Sequence 1248, Ap	80.5	1370	80.5	3.6	1431	8	US-60-914-361-105	Sequence 105, App
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1299	81.5	3.7	2338	7	US-11-490-374A-1246	Sequence 1246, Ap	80.5	1372	80.5	3.6	1571	7	US-11-374-300-107	Sequence 107, App
1300	81.5	3.7	2338	7	US-11-490-374A-1247	Sequence 1247, Ap	80.5	1373	80.5	3.6	1596	1	PCT-US07-17776B-9539	Sequence 9539, Ap
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cl1302	81.5	3.7	2623	7	US-11-816-601-159	Sequence 159, App	80.5	1375	80.5	3.6	1718	8	US-60-970-876-199	Sequence 199, App
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1310	81.5	3.7	4134	7	US-11-649-155-21	Sequence 21, Appl	80.5	1383	80.5	3.6	2539	7	US-11-884-496-329	Sequence 329, App
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1313	81.5	3.7	5105	7	US-11-830-023-82	Sequence 82, Appl	80.5	1386	80.5	3.6	2731	7	US-11-781-665-3065	Sequence 3065, Ap
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cl1315	81.5	3.7	5831	7	US-11-884-496-162	Sequence 162, App	80.5	cl1388	80.5	3.6	2904	8	US-60-970-876-123	Sequence 123, App
cl1316	81.5	3.7	7849	7	US-11-884-496-163	Sequence 163, App	80.5	cl1389	80.5	3.6	3160	7	US-11-884-496-134	Sequence 134, App
1317	81.5	3.7	18070	6	US-10-552-571-17	Sequence 17, Appl	80.5	cl1390	80.5	3.6	3160	7	US-11-884-496-277	Sequence 277, App
cl1318	81.5	3.7	37253	7	US-11-817-494-1	Sequence 1, Appli	80.5	cl1391	80.5	3.6	3160	7	US-11-884-496-278	Sequence 278, App
1319	81	3.7	549	1	PCT-US07-18368A-275	Sequence 275, App	80.5	1392	80.5	3.6	3203	7	US-11-816-601-134	Sequence 134, App
1320	81	3.7	585	1	PCT-US07-17776B-5572	Sequence 5572, Ap	80.5	1393	80.5	3.6	3203	7	US-11-816-601-287	Sequence 287, App
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1324	81	3.7	708	7	US-11-665-940-61	Sequence 61, Appl	80.5	1397	80.5	3.6	6000	1	PCT-US07-13803-169	Sequence 169, App
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1402	80.5	3.6	14760	7	US-11-490-374A-1332	Sequence 1332, Ap	c1475	80	3.6	14001	7	US-11-851-267-7	Sequence 7, Appli
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1407	80	3.6	776	7	US-11-374-300-714	Sequence 714, App	c1480	80	3.6	36909	8	US-60-970-281-7	Sequence 7, Appli
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1420	80	3.6	1382	7	US-11-374-300-546	Sequence 546, App	c1493	80	3.6	49911	8	US-60-956-153-6	Sequence 6, Appli
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c1423	80	3.6	1494	7	US-11-781-665-790	Sequence 790, App	c1496	80	3.6	49911	8	US-60-970-281-6	Sequence 6, Appli
c1424	80	3.6	1500	7	US-11-490-374A-1749	Sequence 1749, Ap	c1497	80	3.6	52701	8	US-60-970-281-41	Sequence 41, Appl
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c1430	80	3.6	1703	7	US-11-490-374A-1754	Sequence 1754, Ap							
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1437	80	3.6	2504	7	US-11-837-468-3	Sequence 3, Appli							
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1447	80	3.6	3782	8	US-60-970-876-148	Sequence 148, App							
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1450	80	3.6	3830	7	US-11-774-254A-26	Sequence 26, Appl							
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c1453	80	3.6	3886	7	US-11-844-963-77	Sequence 77, Appl							
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1460	80	3.6	4431	7	US-11-354-210-110	Sequence 110, App							
1461	80	3.6	4555	7	US-11-884-496-390	Sequence 390, App							
1462	80	3.6	4779	7	US-11-354-210-106	Sequence 106, App							
c1463	80	3.6	5312	7	US-11-835-336-44	Sequence 44, Appl							
1464	80	3.6	5337	1	PCT-US07-13803-312	Sequence 312, App							
1465	80	3.6	6000	1	PCT-US07-13803-198	Sequence 198, App							
1466	80	3.6	6328	1	PCT-US07-13803-485	Sequence 485, App							
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c1468	80	3.6	8111	7	US-11-835-336-85	Sequence 85, Appl							
c1469	80	3.6	9535	7	US-11-490-374A-1806	Sequence 1806, Ap							
c1470	80	3.6	11185	1	PCT-US07-13803-307	Sequence 307, App							
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77	606	27.4	533	3	BM087304	BM087304	500042 MA	150	552	25.0	573	14	DA063309	DA063309
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79	603	27.3	593	14	DB196788	DB196788	DB196788	152	551	24.9	574	14	DA764515	DA764515
80	599.5	27.1	790	13	DT848455	DT848455	LB00482.C	153	551	24.9	581	14	DA750536	DA750536
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83	597	27.0	592	14	DB031358	DB031358	DB031358	156	547	24.7	364	3	BI029201	BI029201 IL5-MT026
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87	592	26.8	594	4	BP247838	BP247838	BP247838	160	547	24.7	569	14	DB270706	DB270706
88	592	26.8	603	14	DB264701	DB264701	DB264701	161	547	24.7	573	14	DA164351	DA164351
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91	588	26.6	584	14	DB261530	DB261530	DB261530	164	547	24.7	575	14	DA278922	DA278922
92	588	26.6	590	14	DB206324	DB206324	DB206324	165	547	24.7	575	14	DB204597	DB204597
93	588	26.6	591	14	DA529624	DA529624	DA529624	166	543	24.6	573	14	DA016588	DA016588
94	588	26.6	764	13	DT848580	DT848580	LB00482.C	167	542	24.5	561	14	DA017673	DA017673
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96	585	26.5	961	5	BY720875	BY720875	BY720875	169	542	24.5	566	14	DA486096	DA486096
97	584.5	26.4	631	8	CF746243	CF746243	UI-M-GV0-	170	542	24.5	568	14	DA629218	DA629218
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117	567.5	25.7	886	4	BQ922735	BQ922735	AGENCOURT	190	535	24.2	559	14	DA950526	DA950526
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366	343	15.5	559	14	DAL30901	DAL30901 DAL30901	439	199.5	9.0	845	13	DT234157	DT234157 JGI_CAAT8
C 367	343	15.5	630	9	CK963012	CK963012 4077498 B	440	198.5	9.0	804	13	DT226240	DT226240 JGI_CAAT2
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369	341	15.4	946	2	BG242060	BG242060 602334602	442	195.5	8.8	1987	6	AF370372	AF370372 Homo sapi
370	335	15.2	604	12	EC327580	EC327580 GUTF09168	443	195	8.8	1365	13	DR419675	DR419675 GPGC_EST0
371	334	15.1	874	1	AJ456451	AJ456451 AJ456451	444	194.5	8.8	986	4	BU111386	BU111386 603127015
372	330	14.9	456	14	DB204351	DB204351 DB204351	445	193.5	8.8	841	8	CD752203	CD752203 AGENCOURT
C 373	328.5	14.9	1057	1	AL525390	AL525390 AL525390	446	192.5	8.7	451	9	CJ125832	CJ125832 CJ125832
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379	305.5	13.8	506	3	BM439543	BM439543 pgr1c.pk0	C 452	183.5	8.3	916	5	BX363088	BX363088 BX363088
380	305	13.8	657	13	DN374275	DN374275 LIB38529	C 453	181	8.2	630	1	AJ735763	AJ735763 AJ735763
381	303	13.7	549	18	DU218553	DU218553 109855369	454	178	8.1	836	9	CK139504	CK139504 AGENCOURT
C 382	302	13.7	600	7	AW937332	AW937332 PM2-DT004	455	178	8.1	1350	19	DQ054172	DQ054172 Homo sapi
383	302	13.7	784	9	CJ462354	CJ462354 CJ462354	456	176.5	8.0	301	2	BE927563	BE927563 MR0-CT045
384	299	13.5	641	9	CK979245	CK979245 4111113 B	C 457	175	7.9	1033	5	BX343326	BX343326 BX343326
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387	288	13.0	443	8	CB789377	CB789377 AMGNNUC:N	460	173	7.8	573	3	BJ074280	BJ074280 BJ074280
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389	286	12.9	469	14	DB262059	DB262059 DB262059	462	172	7.8	852	5	BX915688	BX915688 BX915688
390	286	12.9	496	14	DA703232	DA703232 DA703232	463	170.5	7.7	664	8	CD675180	CD675180 fs19h12.Y
391	284	12.8	383	8	CB704160	CB704160 AMGNNUC:M	C 464	170	7.7	1058	5	BX464809	BX464809 BX464809
C 392	280.5	12.7	383	1	AJ735766	AJ735766 AJ735766	465	169.5	7.7	881	6	CR600976	CR600976 full-leng
393	278	12.6	439	12	DY199153	DY199153 001017BEM	466	168.5	7.6	859	12	EB006927	EB006927 GtraSEQ15
394	271	12.3	388	3	BI024344	BI024344 CM3-MT029	C 467	168.5	7.6	995	5	BX360410	BX360410 BX360410
395	270	12.2	480	2	BF898786	BF898786 289362 MA	468	167.5	7.6	799	13	DT097656	DT097656 JGI_ANNN3
396	269	12.2	439	14	DB444501	DB444501 DB444501	C 469	167.5	7.6	1032	5	BX375412	BX375412 BX375412
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CR730357 Tetraodon  
BQ246719 Tae15006E  
BQ472442 HB09K01T  
DW201650 EST17920  
DT616365 ACAH-aaa6  
BF473033 WHE0927\_D  
BQ805692 WHE3569\_H  
BX053588 Single re  
CL682472 PRI0134a  
CB677062 OSJNEel13K  
CK698379 ZF101-P00  
BJ235568 BJ235568  
BF580970 602100673  
CG750976 P045-2-H1  
DN671967 CFW65-G09  
CG756648 P051-4-D0  
BU986225 HF11B10r  
DB330538 DB330538  
CD896958 G174.104G  
BW525622 BW525622  
BE402376 CSB007C10  
BQ607819 BRY\_3717  
CO358455 DR\_ATE OR  
DW208543 EST24807  
CB407960 IPG023D02  
DW202160 EST18430  
BJ984581 BJ984581  
BJ984616 BJ984616  
BJ985635 BJ985635  
CO058527 Lr\_PAHCF\_  
BJ985192 BJ985192



C 803	136.5	6.2	717	7	BB990245	BB990245 BB990245	876	135.5	6.1	1217	13	DT970234	DT970234 CLJ127-C1
C 804	136.5	6.2	719	3	BJ984644	BJ984644 BJ984644	877	135.5	6.1	1337	13	DT976995	DT976995 CLJ168-A0
C 805	136.5	6.2	719	3	BJ984759	BJ984759 BJ984759	878	135.5	6.1	2139	2	BF128407	BF128407 601810317
C 806	136.5	6.2	723	3	BJ985446	BJ985446 BJ985446	879	135	6.1	491	3	BM184713	BM184713 ft81e06.Y
C 807	136.5	6.2	726	7	BB990352	BB990352 BB990352	880	135	6.1	515	4	BU975121	BU975121 HB30C14r
C 808	136.5	6.2	727	3	BJ984379	BJ984379 BJ984379	881	135	6.1	521	4	BQ245204	BQ245204 TaE15029C
C 809	136.5	6.2	728	8	CD910612	CD910612 G550.001L	882	135	6.1	525	4	BU975275	BU975275 HB30K07r
C 810	136.5	6.2	744	3	BJ983223	BJ983223 BJ983223	883	135	6.1	525	4	BU975437	BU975437 HB31C02r
C 811	136.5	6.2	756	8	CB565469	CB565469 AGENCOURT	884	135	6.1	530	4	BQ464672	BQ464672 HF02024r
812	136.5	6.2	835	2	BE194402	BE194402 HVSMEH08	885	135	6.1	532	5	CA557042	CA557042 K0221C02-
813	136.5	6.2	855	13	DR879237	DR879237 JGI_CABJ6	886	135	6.1	535	4	BU966695	BU966695 HB02B06r
814	136.5	6.2	873	13	DT435822	DT435822 JGI_CABJ1	887	135	6.1	537	4	BU968991	BU968991 HB10D04r
815	136.5	6.2	923	2	BE196299	BE196299 HVSMEH009	888	135	6.1	549	4	BU968705	BU968705 HB08F09r
C 816	136.5	6.2	975	6	CNS08ERP	BX008561 Single re	889	135	6.1	551	4	BU968512	BU968512 HB07M04r
817	136.5	6.2	993	17	CL960565	CL960565 OsIFCC004	890	135	6.1	556	5	CA558769	CA558769 K0249D04-
818	136.5	6.2	1007	12	DY303037	DY303037 KN0AAQ4YK	891	135	6.1	561	4	BU967514	BU967514 HB04I21r
819	136.5	6.2	1116	16	CC296896	CC296896 CH261-2E1	892	135	6.1	569	8	CD897643	CD897643 GI74.106K
820	136	6.2	518	4	BQ607049	BQ607049 BRY_2931	893	135	6.1	574	12	EB099446	EB099446 EST61878
821	136	6.2	528	4	BU988890	BU988890 HF19A16r	894	135	6.1	588	4	BU969031	BU969031 HB10F06r
822	136	6.2	628	8	CF915716	CF915716 B0984C04-	895	135	6.1	595	5	CA560020	CA560020 K0266F11-
823	136	6.2	635	4	BU989593	BU989593 HF22C16r	896	135	6.1	597	10	CV065784	CV065784 WNEL26f6
824	136	6.2	647	4	BQ805480	BQ805480 WHE3567 D	897	135	6.1	598	4	BU969253	BU969253 HB10P23r
825	136	6.2	673	4	BQ806706	BQ806706 WHE3582-C	898	135	6.1	607	4	BU990058	BU990058 HF23023r
826	136	6.2	674	8	CF428050	CF428050 PH1_12_E0	899	135	6.1	619	3	BJ236211	BJ236211 BJ236211
827	136	6.2	675	14	CX611100	CX611100 ANR1_22_D	900	135	6.1	630	3	BJ235111	BJ235111 BJ235111
828	136	6.2	678	4	BQ807117	BQ807117 WHE3587_A	901	135	6.1	636	3	BJ244387	BJ244387 BJ244387
829	136	6.2	703	3	BJ290249	BJ290249 BJ290249	902	135	6.1	643	8	CF914438	CF914438 B0964A09-
830	136	6.2	704	5	BW478868	BW478868 BW478868	903	135	6.1	648	8	CF915734	CF915734 B0984E06-
831	136	6.2	734	8	CF870512	CF870512 tric023xm	904	135	6.1	649	4	BQ789334	BQ789334 WHE4160 B
C 832	136	6.2	738	13	DR722706	DR722706 AGENCOURT	905	135	6.1	659	12	DW191574	DW191574 EST07844
833	136	6.2	740	14	CX618749	CX618749 GABR1_41	906	135	6.1	665	9	CJ636812	CJ636812 CJ636812
834	136	6.2	746	4	BQ807120	BQ807120 WHE3587_A	907	135	6.1	665	12	EB008943	EB008943 LedoSEQ10
835	136	6.2	751	4	BQ839109	BQ839109 WHE3589_D	908	135	6.1	670	4	BQ752919	BQ752919 WHE4120_F
836	136	6.2	754	9	CN126162	CN126162 RHOH1_15	909	135	6.1	705	4	BQ806802	BQ806802 WHE3583_E
837	136	6.2	764	9	CJ717112	CJ717112 CJ717112	910	135	6.1	710	9	CJ669730	CJ669730 CJ669730
C 838	136	6.2	776	5	BW723400	BW723400 BW723400	C 911	135	6.1	711	18	DX938142	DX938142 CHOR1105-
839	136	6.2	799	17	CL666241	CL666241 PRI0151d	912	135	6.1	715	3	BJ406237	BJ406237 BJ406237
840	136	6.2	807	8	CB900701	CB900701 tric023xm	913	135	6.1	736	9	CJ664671	CJ664671 CJ664671
841	136	6.2	832	12	EB025460	EB025460 Lsc0SEQ54	914	135	6.1	738	9	CJ668022	CJ668022 CJ668022
842	136	6.2	856	6	CNS09ODV	BX067679 Single re	915	135	6.1	743	9	CJ716530	CJ716530 CJ716530
843	136	6.2	865	8	CB666685	CB666685 OSJNEd13K	916	135	6.1	745	9	CJ724800	CJ724800 CJ724800
844	136	6.2	1095	9	CK214375	CK214375 FGAS02629	917	135	6.1	751	9	CJ722701	CJ722701 CJ722701
845	136	6.2	1725	19	CL975488	CL975488 OsIFCC027	918	135	6.1	756	9	CJ667501	CJ667501 CJ667501
846	136	6.2	2149	17	DQ029920	DQ029920 Homo sapi	919	135	6.1	758	9	CJ722080	CJ722080 CJ722080
847	136	6.2	2536	6	AK156933	AK156933 Mus muscu	920	135	6.1	761	9	CJ666815	CJ666815 CJ666815
848	135.5	6.1	541	2	BE402057	BE402057 CSB004A03	921	135	6.1	770	9	CJ661871	CJ661871 CJ661871
849	135.5	6.1	541	4	BQ607515	BQ607515 BRY_3409	922	135	6.1	776	9	CJ668073	CJ668073 CJ668073
850	135.5	6.1	569	1	AJ432963	AJ432963 AJ432963	C 923	135	6.1	783	5	BW715554	BW715554 BW715554
851	135.5	6.1	573	2	BE500125	BE500125 WHE0978_D	C 924	135	6.1	790	18	CZ874023	CZ874023 OC_Ba027
852	135.5	6.1	597	2	BE601524	BE601524 HVSMEH009	925	135	6.1	791	4	BU444648	BU444648 603214351
853	135.5	6.1	617	8	CF175082	CF175082 B0948D12-	926	135	6.1	800	17	CL656337	CL656337 PRI0126b_
C 854	135.5	6.1	622	3	BJ798476	BJ798476 BJ798476	927	135	6.1	833	9	CK193488	CK193488 FGAS00190
C 855	135.5	6.1	627	3	BJ054923	BJ054923 BJ054923	928	135	6.1	878	4	BQ943319	BQ943319 AGENCOURT
C 856	135.5	6.1	645	3	BJ055129	BJ055129 BJ055129	929	135	6.1	929	4	BU841382	BU841382 AGENCOURT
C 857	135.5	6.1	650	8	CF174393	CF174393 B0938E04-	930	135	6.1	2263	6	CR606886	CR606886 full-leng
858	135.5	6.1	661	8	CD921444	CD921444 G608.120K	931	135	6.1	2520	17	CL979986	CL979986 OsIFCC034
859	135.5	6.1	675	8	CF172040	CF172040 B0901E03-	932	134.5	6.1	495	4	BU975783	BU975783 HB32E19r
860	135.5	6.1	677	4	BQ608489	BQ608489 BRY_4394	933	134.5	6.1	524	4	BU985039	BU985039 HF05P10r
861	135.5	6.1	707	12	DY783730	DY783730 SF1H09046	934	134.5	6.1	524	4	BU988031	BU988031 HF16H15r
862	135.5	6.1	724	8	CF523607	CF523607 AGENCOURT	935	134.5	6.1	525	4	BU989876	BU989876 HF22P01r
C 863	135.5	6.1	727	3	BI281272	BI281272 UI-R-DA0-	936	134.5	6.1	559	9	CJ329206	CJ329206 CJ329206
864	135.5	6.1	730	13	DR041524	DR041524 BNE00023	937	134.5	6.1	585	4	BU986566	BU986566 HF12E03r
C 865	135.5	6.1	757	12	DY238186	DY238186 ZM_BFB025	938	134.5	6.1	614	8	CF173687	CF173687 B0927E07-
866	135.5	6.1	759	8	CB671800	CB671800 OSJNE051	939	134.5	6.1	629	8	CD281214	CD281214 G39215.41
867	135.5	6.1	772	2	BE193188	BE193188 HVSMEH008	940	134.5	6.1	639	2	BE414402	BE414402 SCU009.D0
C 868	135.5	6.1	779	10	CV643503	CV643503 EST922256	941	134.5	6.1	641	3	BM625487	BM625487 170006874
869	135.5	6.1	843	3	BI946806	BI946806 HVSME1000	942	134.5	6.1	645	5	CA559798	CA559798 K0263F08-
870	135.5	6.1	858	11	FE184283	FE184283 ZM_BFC016	C 943	134.5	6.1	675	3	BJ098483	BJ098483 BJ098483
871	135.5	6.1	892	18	CZ216254	CZ216254 AIAA-aaf2	944	134.5	6.1	677	3	BJ237074	BJ237074 BJ237074
872	135.5	6.1	901	4	BQ922333	BQ922333 AGENCOURT	C 945	134.5	6.1	681	7	BB990655	BB990655 BB990655
873	135.5	6.1	1003	2	BE196487	BE196487 HVSMEH009	C 946	134.5	6.1	682	3	BJ983340	BJ983340 BJ983340
874	135.5	6.1	1014	6	CNS08HPL	BX012373 Single re	947	134.5	6.1	686	4	BQ245977	BQ245977 TaE15017G
875	135.5	6.1	1170	18	CW934254	CW934254 EDCCN29TR	C 948	134.5	6.1	701	3	BJ983659	BJ983659 BJ983659

C 949	134.5	6.1	717	3	BJ983611	BJ983611 BJ983611
C 950	134.5	6.1	717	7	BB990525	BB990525 BB990525
C 951	134.5	6.1	718	3	BJ983290	BJ983290 BJ983290
C 952	134.5	6.1	718	3	BJ983320	BJ983320 BJ983320
C 953	134.5	6.1	718	3	BJ983357	BJ983357 BJ983357
C 954	134.5	6.1	718	3	BJ984171	BJ984171 BJ984171
C 955	134.5	6.1	718	3	BJ983322	BJ983322 BJ983322
C 956	134.5	6.1	747	7	BB990271	BB990271 BB990271
957	134.5	6.1	828	9	CK811348	CK811348 Rasgsc692
958	134.5	6.1	829	9	CK239262	CK239262 AGENCOURT
959	134.5	6.1	888	12	EB024301	EB024301 LscOSEQ40
960	134.5	6.1	936	2	BE196491	BE196491 HVSMEh009
961	134.5	6.1	936	12	EB003879	EB003879 GtraSEQ12
962	134.5	6.1	939	2	BE196573	BE196573 HVSMEh009
963	134.5	6.1	1112	13	DR122909	DR122909 49329377
964	134.5	6.1	1531	2	BE306182	BE306182 601101310
C 965	134	6.1	393	10	CV354692	CV354692 MR4-CN014
966	134	6.1	480	1	AJ483282	AJ483282 AJ483282
967	134	6.1	500	4	BU967231	BU967231 HB03L08r
968	134	6.1	509	4	BU969161	BU969161 HB10L15r
969	134	6.1	551	8	CB879363	CB879363 HP10L06T
970	134	6.1	552	2	BE606272	BE606272 HPE0905 H
971	134	6.1	555	4	BU969192	BU969192 HB10N04r
C 972	134	6.1	558	2	BF432736	BF432736 nad12e05
973	134	6.1	559	4	BU975214	BU975214 HB30G24r
974	134	6.1	565	1	AJ435660	AJ435660 AJ435660
975	134	6.1	566	4	BU984508	BU984508 HF04C04r
976	134	6.1	573	2	BE194117	BE194117 HVSMEh008
977	134	6.1	584	19	DE225508	DE225508 Trifolium
978	134	6.1	610	13	DN245792	DN245792 ACAB-aaa4
979	134	6.1	618	4	BU987557	BU987557 HF15B06r
980	134	6.1	630	4	BQ239992	BQ239992 TaE05023H
981	134	6.1	639	8	CD902543	CD902543 G356.107F
982	134	6.1	651	8	CF913839	CF913839 B0955B02-
983	134	6.1	660	17	CL696555	CL696555 PRI019b E
984	134	6.1	661	8	CD901091	CD901091 G356.102L
985	134	6.1	661	14	DN136070	DN136070 tam64e11
986	134	6.1	668	1	AL642887	AL642887 AL642887
987	134	6.1	671	8	CF862249	CF862249 ps25003xA
988	134	6.1	690	4	BQ246985	BQ246985 TaE15002G
989	134	6.1	707	4	BQ247122	BQ247122 TaE15001B
990	134	6.1	710	1	AU002237	AU002237 AU002237
991	134	6.1	710	3	BM576218	BM576218 170006871
992	134	6.1	724	12	DV819897	DV819897 LB01730.C
C 993	134	6.1	739	3	BJ983897	BJ983897 BJ983897
994	134	6.1	740	2	BE603128	BE603128 HVSMEh010
C 995	134	6.1	754	7	BB990227	BB990227 BB990227
996	134	6.1	755	4	BQ245996	BQ245996 TaE15017E
997	134	6.1	756	2	BE193514	BE193514 HVSMEh008
C 998	134	6.1	757	13	DT063631	DT063631 AGENCOURT
C 999	134	6.1	764	3	BJ983747	BJ983747 BJ983747
1000	134	6.1	776	17	CL674503	CL674503 PRI0112b
1001	134	6.1	805	2	BE195121	BE195121 HVSMEh008
1002	134	6.1	813	6	CNS08SXX	BX026916 Single re
1003	134	6.1	822	19	DE266607	DE266607 Oryzias l
1004	134	6.1	889	12	EB450211	EB450211 KT7C.106B
1005	134	6.1	891	9	CK154529	CK154529 FGAS03323
1006	134	6.1	908	11	EE048236	EE048236 ZM_BFC012
1007	134	6.1	1183	13	DN733739	DN733739 CNB71-G04
1008	134	6.1	1327	12	DY291280	DY291280 IC0AA77C
1009	133.5	6.0	474	7	AU242628	AU242628 AU242628
1010	133.5	6.0	480	1	AJ482311	AJ482311 AJ482311
1011	133.5	6.0	480	1	AJ482312	AJ482312 AJ482312
1012	133.5	6.0	500	4	BU984352	BU984352 HF03L03r
1013	133.5	6.0	506	4	BU972187	BU972187 HB20003r
1014	133.5	6.0	513	4	BU989293	BU989293 HF21F11r
1015	133.5	6.0	533	1	AA495649	AA495649 c079 Zhou
1016	133.5	6.0	535	7	AV962757	AV962757 AV962757
1017	133.5	6.0	558	4	BU986245	BU986245 HF11C10r
1018	133.5	6.0	571	10	CV894467	CV894467 PA017H9 m
1019	133.5	6.0	610	13	DR438063	DR438063 ACAC-aac1
1020	133.5	6.0	614	4	BQ246658	BQ246658 TaE15007C
1021	133.5	6.0	616	4	BQ240366	BQ240366 TaE05018E

1022	133.5	6.0	632	8	CD898029	CD898029
1023	133.5	6.0	649	8	CD312012	CD312012
1024	133.5	6.0	652	5	BW239427	BW239427
C1025	133.5	6.0	675	3	BJ983463	BJ983463
1026	133.5	6.0	677	8	CF916423	CF916423
1027	133.5	6.0	678	4	BQ245396	BQ245396
1028	133.5	6.0	679	2	BF473065	BF473065
1029	133.5	6.0	681	5	BW308031	BW308031
1030	133.5	6.0	690	8	CD294616	CD294616
1031	133.5	6.0	706	4	BW213510	BW213510
1032	133.5	6.0	710	4	BQ247102	BQ247102
1033	133.5	6.0	714	12	EC392273	EC392273
1034	133.5	6.0	715	2	BE455174	BE455174
1035	133.5	6.0	726	12	DY997425	DY997425
1036	133.5	6.0	734	4	BQ245390	BQ245390
1037	133.5	6.0	751	13	DN744030	DN744030
1038	133.5	6.0	754	2	BE193536	BE193536
1039	133.5	6.0	778	8	CB654692	CB654692
1040	133.5	6.0	780	4	BQ804567	BQ804567
1041	133.5	6.0	799	2	BG367090	BG367090
1042	133.5	6.0	804	8	CF436558	CF436558
1043	133.5	6.0	812	14	CX995840	CX995840
1044	133.5	6.0	822	2	BG366988	BG366988
1045	133.5	6.0	823	8	CD818579	CD818579
1046	133.5	6.0	854	3	BI951055	BI951055
1047	133.5	6.0	884	10	CO545357	CO545357
1048	133.5	6.0	899	4	BQ277541	BQ277541
C1049	133.5	6.0	978	6	CNS092XP	CNS092XP
1050	133.5	6.0	1067	6	BC075667	BC075667
1051	133.5	6.0	2105	6	BC075667	BC075667
1052	133	6.0	360	1	AJ484922	AJ484922
1053	133	6.0	458	4	BU984125	BU984125
1054	133	6.0	480	1	AJ483285	AJ483285
C1055	133	6.0	503	14	CX807924	CX807924
1056	133	6.0	538	5	CA559656	CA559656
1057	133	6.0	539	5	CA556312	CA556312
1058	133	6.0	539	5	CA558048	CA558048
1059	133	6.0	545	1	AJ904299	AJ904299
1060	133	6.0	554	4	BU985818	BU985818
1061	133	6.0	567	5	CA559283	CA559283
1062	133	6.0	567	5	CA560179	CA560179
1063	133	6.0	574	4	BQ805851	BQ805851
1064	133	6.0	578	8	CF696569	CF696569
1065	133	6.0	584	4	BQ244692	BQ244692
1066	133	6.0	591	5	CA561439	CA561439
1067	133	6.0	594	5	CA561924	CA561924
1068	133	6.0	597	5	CA559493	CA559493
1069	133	6.0	600	1	AJ483321	AJ483321
1070	133	6.0	600	5	CA560259	CA560259
1071	133	6.0	601	5	CA557320	CA557320
1072	133	6.0	602	5	CA561917	CA561917
1073	133	6.0	615	5	CA559956	CA559956
1074	133	6.0	621	1	AJ436631	AJ436631
1075	133	6.0	623	5	CA558825	CA558825
1076	133	6.0	624	5	CA560196	CA560196
1077	133	6.0	630	12	DV646385	DV646385
1078	133	6.0	635	8	CF174340	CF174340
1079	133	6.0	636	4	BQ244610	BQ244610
1080	133	6.0	640	2	BE427016	BE427016
1081	133	6.0	640	3	BJ233156	BJ233156
1082	133	6.0	641	2	BG262155	BG262155
1083	133	6.0	643	1	AJ433357	AJ433357
1084	133	6.0	648	4	BQ246938	BQ246938
1085	133	6.0	649	8	CF914947	CF914947
1086	133	6.0	652	8	CF916153	CF916153
1087	133	6.0	653	5	BY725915	BY725915
1088	133	6.0	656	9	CJ637006	CJ637006
1089	133	6.0	677	9	CK808723	CK808723
1090	133	6.0	695	9	CJ713065	CJ713065
1091	133	6.0	704	1	AJ904240	AJ904240
1092	133	6.0	725	4	BQ246336	BQ246336
1093	133	6.0	725	12	EB013422	EB013422
1094	133	6.0	726	8	CD910419	CD910419

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BQ245396	TaE15025B
BF473065	WHE0925_C
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CD294616	StrPu691.
BW213510	BW213510
BQ247102	TaE15001D
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BQ245390	TaE15025B
DN744030	GL-Cf-822
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CB654692	OSJNEC07G
BQ804567	WHE3556 B
BG367090	HVSMEi001
CF436558	EST672903
CX995840	JGI_CAAPI
BG366988	HVSMEi000
CD818579	BN20.0450
BI951055	HVSME1002
CO545357	LYEST1347
BQ277541	AGENCOURT
BX039881	Single re
BC075667	Mus muscu
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BU984125	HF03B02r
AJ483285	AJ483285
CX807924	JGI_CAAJ1
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BU985818	HF08L14r
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CA560179	K0268H01-
BQ805851	WHE3571 G
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BQ244692	TaE15038H
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CA561924	K0294A05-
CA559493	K0259E10-
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CA557320	K0225G01-
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CF914947	B0971F05-
CF916153	B0990H01-

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1096	133	6.0	739	2	BE603255
1097	133	6.0	742	2	BG262242
1098	133	6.0	749	1	AJ894074
1099	133	6.0	761	8	CF438936
c1100	133	6.0	771	5	BW728626
1101	133	6.0	772	8	CF435316
c1102	133	6.0	774	17	CL979366
c1103	133	6.0	775	5	BW730182
1104	133	6.0	813	12	EB014561
1105	133	6.0	818	12	EB016279
1106	133	6.0	822	12	EB426847
1107	133	6.0	829	12	EB015180
1108	133	6.0	830	12	EB015499
1109	133	6.0	831	12	EB018045
1110	133	6.0	849	12	EB013133
c1111	133	6.0	857	12	EC3119940
1112	133	6.0	900	12	EB450888
1113	133	6.0	991	2	BE196284
1114	133	6.0	1105	8	CD505439
1115	133	6.0	1216	13	DN696618
1116	133	6.0	1455	6	AK089214
1117	133	6.0	1601	6	AK172077
1118	133	6.0	1634	2	BG028384
1119	133	6.0	2219	6	AK139822
1120	133	6.0	3240	19	AY405254
1121	132.5	6.0	420	1	AJ481830
1122	132.5	6.0	420	1	AJ481831
1123	132.5	6.0	420	1	AJ485287
1124	132.5	6.0	470	4	BU975350
1125	132.5	6.0	507	4	BU975519
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1127	132.5	6.0	534	3	BI948392
1128	132.5	6.0	535	5	CA717672
1129	132.5	6.0	540	1	AJ481829
1130	132.5	6.0	570	4	BU968447
1131	132.5	6.0	582	4	BU968521
1132	132.5	6.0	589	7	BB936609
1133	132.5	6.0	595	4	BQ472381
1134	132.5	6.0	599	5	BY929517
c1135	132.5	6.0	605	8	CD311352
1136	132.5	6.0	606	4	BQ245034
1137	132.5	6.0	607	3	BM307956
1138	132.5	6.0	611	5	BY916359
1139	132.5	6.0	617	3	BJ233981
c1140	132.5	6.0	623	3	BJ818316
c1141	132.5	6.0	632	3	BJ080503
1142	132.5	6.0	637	12	DY215293
1143	132.5	6.0	644	3	BJ233232
c1144	132.5	6.0	653	3	BJ984281
1145	132.5	6.0	657	9	CK494148
1146	132.5	6.0	669	8	CB307515
c1147	132.5	6.0	686	3	BJ985245
1148	132.5	6.0	690	13	DT467748
c1149	132.5	6.0	698	3	BJ984116
1150	132.5	6.0	699	13	DR118856
1151	132.5	6.0	702	1	AJ433139
c1152	132.5	6.0	703	3	BJ794932
1153	132.5	6.0	706	7	AW448684
c1154	132.5	6.0	719	3	BJ985374
c1155	132.5	6.0	732	3	BJ984396
1156	132.5	6.0	733	2	BE602094
1157	132.5	6.0	735	10	CO157883
1158	132.5	6.0	738	17	CL671012
1159	132.5	6.0	749	9	CK123232
1160	132.5	6.0	752	12	EB017088
1161	132.5	6.0	752	17	CL653959
1162	132.5	6.0	754	2	BE193541
1163	132.5	6.0	758	3	BM169717
c1164	132.5	6.0	760	13	DR163927
c1165	132.5	6.0	806	6	CNS08LQJ
c1166	132.5	6.0	810	13	DR744562
c1167	132.5	6.0	818	10	CO163724

c1168	132.5	6.0	835	17	CL669986
c1169	132.5	6.0	869	9	CK159167
1170	132.5	6.0	870	12	DW242488
1171	132.5	6.0	884	4	BQ938992
1172	132.5	6.0	895	2	BE454277
1173	132.5	6.0	920	17	CL461353
1174	132.5	6.0	964	6	CNS08EMV
c1175	132.5	6.0	971	6	CNS0937V
1176	132.5	6.0	977	6	CNS08E4C
1177	132.5	6.0	1066	18	CW9224086
1178	132.5	6.0	1086	12	DY273578
1179	132.5	6.0	1163	12	DY288996
1180	132.5	6.0	1188	6	CNS0FHAL
1181	132.5	6.0	1649	6	CR615151
1182	132.5	6.0	2585	6	AK164929
1183	132.5	6.0	2602	6	AK131887
1184	132.5	6.0	3075	19	DQ052043
1185	132.5	6.0	4082	6	HSM801801
1186	132	6.0	485	4	BU990034
1187	132	6.0	492	4	BU972719
1188	132	6.0	493	2	BE591055
1189	132	6.0	494	4	BU969388
1190	132	6.0	495	4	BU972055
1191	132	6.0	495	4	BU989074
1192	132	6.0	511	3	BM004465
1193	132	6.0	514	5	CA555934
1194	132	6.0	516	4	BU975347
1195	132	6.0	522	4	BU969002
1196	132	6.0	523	4	BU968362
1197	132	6.0	526	4	BU972981
1198	132	6.0	532	5	CA718482
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1200	132	6.0	538	4	BU973334
1201	132	6.0	539	5	CA561723
1202	132	6.0	539	5	CA561723
1203	132	6.0	540	4	BU975714
1204	132	6.0	544	2	BE402545
1205	132	6.0	544	4	BQ608208
1206	132	6.0	544	5	CA734311
1207	132	6.0	550	5	CA561080
1208	132	6.0	557	10	CV930252
1209	132	6.0	561	5	CA556446
1210	132	6.0	562	4	BU973468
1211	132	6.0	563	5	CA560353
1212	132	6.0	565	4	BU971853
1213	132	6.0	569	4	BU974183
1214	132	6.0	569	5	CA734306
1215	132	6.0	571	5	CA734330
1216	132	6.0	572	4	BU990606
1217	132	6.0	573	4	BU990629
1218	132	6.0	575	4	BU970547
1219	132	6.0	575	5	CA555615
1220	132	6.0	578	4	BQ607175
1221	132	6.0	584	4	BU970446
1222	132	6.0	585	3	BJ235257
1223	132	6.0	586	4	BQ246110
1224	132	6.0	592	8	CF172080
1225	132	6.0	605	5	CA734391
1226	132	6.0	606	4	BQ244875
1227	132	6.0	607	4	BU971786
1228	132	6.0	611	5	CA559368
1229	132	6.0	611	5	CA727303
1230	132	6.0	613	2	BE590559
1231	132	6.0	615	2	BF484916
1232	132	6.0	615	4	BU975104
1233	132	6.0	615	5	CA727069
1234	132	6.0	618	2	BE401906
1235	132	6.0	618	4	BQ607600
1236	132	6.0	618	5	CA727346
1237	132	6.0	618	8	CF914440
1238	132	6.0	620	3	BJ234978
1239	132	6.0	621	4	BU971376
1240	132	6.0	624	8	CF276479

CL669986	PRI0160d_
CK159167	FGAS04056_
DW242488	GH_TSMB_1
BQ938992	AGENCOURT
BE454277	HVSMEh009
CL461353	SAIL_1145
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BX040247	Single re
BX007720	Single re
CW9224086	EDCB241TR
DY273578	IC0AAA34B
DY288996	IC0AAA71A
CR671751	Tetraodon
CR615151	full-leng
AK164929	Mus muscu
AK131887	Mus muscu
DQ052043	Homo sapi
AL136833	Homo sapi
BU990034	HF23M19r
BU972719	HB22I08r
BE591055	WHE0861_G
BU969388	HB11G05r
BU972055	HB20H12r
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BU975347	HB30O04r
BU969002	HB10D18r
BU968362	HB07E15r
BU972981	HB23F23r
CA718482	wdk5c.pk0
BU969115	HB10I16r
BU973334	HB24J05r
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BU975714	HB32B09r
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BQ608208	BRY_4112
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BU973468	HB25A20r
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BU971853	HB19N21r
BU974183	HB27C09r
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CA734330	wde2f.pk0
BU990606	HF25I16r
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BU970547	HB14P15r
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BJ235257	BJ235257
BQ246110	TaE15016A
CF172080	B0902B08-
CA734391	wde2f.pk0
BQ244875	TaE15034B
BU971786	HB19K17r
CA559368	K0257G09-
CA727303	wde1f.pk0
BE590559	WHE0858_H
BF484916	WHE2333_B
BU975104	HB30B18r
CA727069	wde1f.pk0
BE401906	CSB002D08
BQ607600	BRY_3494
CA727346	wde1f.pk0
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BJ234978	BJ234978
BU971376	HB17G24r
CF276479	14ETL--01



1241	132	6.0	627	5	CA734355	CA734355 wde2f.pk0	1314	131.5	5.9	593	4	BU986813	BU986813 HF12P18r
1242	132	6.0	628	8	CF913543	CF913543 B0950C07-	1315	131.5	5.9	594	4	BU988787	BU988787 HF18L11r
1243	132	6.0	631	3	BJ234843	BJ234843 BJ234843	1316	131.5	5.9	594	4	BU990742	BU990742 HF25O21r
1244	132	6.0	631	4	BU970367	BU970367 HB14G09r	1317	131.5	5.9	596	4	BU972894	BU972894 HB23B06r
1245	132	6.0	631	8	CD919465	CD919465 G608.113H	1318	131.5	5.9	596	4	BU990659	BU990659 HF25L03r
1246	132	6.0	633	5	CA734173	CA734173 wde2f.pk0	1319	131.5	5.9	599	4	BU969241	BU969241 HB10P10r
1247	132	6.0	634	2	BG262160	BG262160 WHE0871_F	1320	131.5	5.9	601	4	BU987556	BU987556 HF15B05r
1248	132	6.0	635	2	BE590791	BE590791 WHE0857_B	1321	131.5	5.9	602	4	BU970331	BU970331 HB14F06r
1249	132	6.0	637	4	BQ245757	BQ245757 TaE15020E	1322	131.5	5.9	603	4	BU971328	BU971328 HB17E18r
1250	132	6.0	640	2	BE427078	BE427078 PSR6382_I	1323	131.5	5.9	606	4	BU973159	BU973159 HB23P04r
1251	132	6.0	642	5	CA726954	CA726954 wdel.f.pk0	1324	131.5	5.9	609	4	BU968507	BU968507 HB07L22r
1252	132	6.0	646	9	CN141007	CN141007 OX1_48_F0	1325	131.5	5.9	609	4	BU974986	BU974986 HB29L23r
1253	132	6.0	648	8	CF915856	CF915856 B0986B12-	1326	131.5	5.9	614	5	CA012993	CA012993 HT07B05r
1254	132	6.0	649	4	BU987815	BU987815 HF15N11r	1327	131.5	5.9	620	4	BU968452	BU968452 HB07J04r
1255	132	6.0	655	8	CF914014	CF914014 B0957G05-	1328	131.5	5.9	622	4	BU968817	BU968817 HB08K23r
1256	132	6.0	668	4	BQ789089	BQ789089 WHE4157_D	1329	131.5	5.9	622	4	BU986885	BU986885 HF13D01r
1257	132	6.0	670	4	BQ245752	BQ245752 TaE15020F	1330	131.5	5.9	623	4	BQ606982	BQ606982 BRY_2860
1258	132	6.0	670	4	BQ245935	BQ245935 TaE15018C	1331	131.5	5.9	623	4	BU987810	BU987810 HF15N06r
1259	132	6.0	679	4	BQ246243	BQ246243 TaE15014D	1332	131.5	5.9	626	13	DR631147	DR631147 EST102127
1260	132	6.0	682	4	BQ245343	BQ245343 TaE15025H	1333	131.5	5.9	634	18	CZ338619	CZ338619 ZMMBF0106
cl261	132	6.0	695	3	BJ984589	BJ984589 BJ984589	1334	131.5	5.9	639	-4	BU987615	BU987615 HF15E06r
cl262	132	6.0	703	3	BJ984619	BJ984619 BJ984619	1335	131.5	5.9	639	12	DY251055	DY251055 PMAH-aaa0
1263	132	6.0	722	4	BQ246023	BQ246023 TaE15017B	1336	131.5	5.9	642	4	BU968699	BU968699 HB08E24r
cl264	132	6.0	726	5	BW712644	BW712644 BW712644	1337	131.5	5.9	645	4	BQ606993	BQ606993 BRY_2871
1265	132	6.0	728	4	BQ245556	BQ245556 TaE15023B	1338	131.5	5.9	645	4	BU970238	BU970238 HB14A24r
1266	132	6.0	728	12	DY999472	DY999472 GtraseQ38	1339	131.5	5.9	645	4	BU971636	BU971636 HB19D12r
1267	132	6.0	728	12	EB489391	EB489391 109934122	1340	131.5	5.9	649	3	BI641907	BI641907 SD25571.5
cl268	132	6.0	747	5	BW717680	BW717680 BW717680	1341	131.5	5.9	652	4	BU967464	BU967464 HB04G09r
cl269	132	6.0	754	18	DX954702	DX954702 CHOR1105-	1342	131.5	5.9	659	4	BQ464258	BQ464258 HF01M10T
1270	132	6.0	762	9	CN322012	CN322012 AGENCOURT	1343	131.5	5.9	659	5	CA734124	CA734124 wde2f.pk0
cl271	132	6.0	772	10	CV639858	CV639858 EST918611	1344	131.5	5.9	662	4	BQ472453	BQ472453 HB09J04T
cl272	132	6.0	776	5	BW724093	BW724093 BW724093	1345	131.5	5.9	664	2	BE194933	BE194933 HVSMEh008
cl273	132	6.0	781	5	BW724392	BW724392 BW724392	1346	131.5	5.9	670	3	BJ232465	BJ232465 BJ232465
1274	132	6.0	782	8	CB665147	CB665147 OSJNEd11F	1347	131.5	5.9	675	4	BU988134	BU988134 HF16M05r
1275	132	6.0	796	12	EB602461	EB602461 AGENCOURT	1348	131.5	5.9	683	13	DN9556804	DN9556804 Fh_mx0_23
1276	132	6.0	814	4	BQ605974	BQ605974 BRY_1570	1349	131.5	5.9	688	4	BQ608967	BQ608967 BRY_4884
1277	132	6.0	814	7	AW448827	AW448827 BRY_1570	1350	131.5	5.9	700	4	BQ464239	BQ464239 HF01L15T
1278	132	6.0	823	17	CL653867	CL653867 PRI0119c	1351	131.5	5.9	708	5	BW435192	BW435192 BW435192
1279	132	6.0	842	8	CB668023	CB668023 OSJNEd15K-	1352	131.5	5.9	725	8	CF841495	CF841495 pSHB014xL
1280	132	6.0	855	17	CL129509	CL129509 'LSB1-96M1	1353	131.5	5.9	729	9	CK808946	CK808946 Rasgsc192
1281	132	6.0	857	11	EC884606	EC884606 ZM_BFC002	1354	131.5	5.9	731	5	BW435376	BW435376 BW435376
1282	132	6.0	870	12	EB463520	EB463520 AGENCOURT	1355	131.5	5.9	739	4	BQ247079	BQ247079 TaE15001F
1283	132	6.0	891	11	EE182981	EE182981 ZM_BFC016	1356	131.5	5.9	748	4	BQ807161	BQ807161 WHE3587_E
1284	132	6.0	893	11	EC899901	EC899901 ZM_BFC004	cl357	131.5	5.9	751	5	BW712172	BW712172 BW712172
1285	132	6.0	895	12	EB004877	EB004877 GtraseQ69	1358	131.5	5.9	755	14	DN124497	DN124497 1125405_M
cl286	132	6.0	899	5	BX373599	BX373599 BX373599	1359	131.5	5.9	767	12	EB628381	EB628381 AGENCOURT
1287	132	6.0	955	2	BE195650	BE195650 HVSMEh009	1360	131.5	5.9	768	8	CF450211	CF450211 EST686556
cl288	132	6.0	987	18	DU777961	DU777961 ASXB1940.	cl361	131.5	5.9	774	14	CX995841	CX995841 JGI_CAAP1
1289	132	6.0	1336	19	AY416946	AY416946 Homo sapi	1362	131.5	5.9	775	18	DX947674	DX947674 CHOR1105-
1290	132	6.0	4599	19	DQ053423	DQ053423 Homo sapi	1363	131.5	5.9	784	12	EB622068	EB622068 AGENCOURT
1291	131.5	5.9	388	5	BY133746	BY133746 BY133746	1364	131.5	5.9	802	12	EB021319	EB021319 LscOSEQ13
1292	131.5	5.9	469	4	BU985259	BU985259 HF06J15r	cl365	131.5	5.9	843	16	BZ643413	BZ643413 OGAOW57TM
1293	131.5	5.9	484	4	BU974972	BU974972 HB29L07r	1366	131.5	5.9	855	4	BU912494	BU912494 AGENCOURT
1294	131.5	5.9	500	4	BU975415	BU975415 HB31B02r	1367	131.5	5.9	865	12	EB483329	EB483329 AGENCOURT
1295	131.5	5.9	500	4	BU987295	BU987295 HF14F20r	1368	131.5	5.9	871	8	CB199736	CB199736 AGENCOURT
1296	131.5	5.9	507	4	BU988714	BU988714 HF18H16r	1369	131.5	5.9	875	8	CD378055	CD378055 PTMM03224
1297	131.5	5.9	519	4	BU975838	BU975838 HB32H09r	1370	131.5	5.9	892	2	BE454215	BE454215 HVSMEh009
1298	131.5	5.9	522	4	BU985356	BU985356 HF06O04r	1371	131.5	5.9	900	9	CN330418	CN330418 AGENCOURT
1299	131.5	5.9	536	4	BU972829	BU972829 HB22N12r	1372	131.5	5.9	908	4	BQ952669	BQ952669 AGENCOURT
1300	131.5	5.9	540	13	DT615857	DT615857 ACAH-aab1	1373	131.5	5.9	911	8	CD381062	CD381062 PTMM06231
1301	131.5	5.9	550	4	BU973533	BU973533 HB25D23r	1374	131.5	5.9	916	13	DR846419	DR846419 JGI_CABE1
1302	131.5	5.9	551	9	CJ635447	CJ635447 CJ635447	cl375	131.5	5.9	920	13	DT773879	DT773879 125254279
1303	131.5	5.9	556	4	BU986590	BU986590 HF12F05r	1376	131.5	5.9	941	8	CD789014	CD789014 EST660375
1304	131.5	5.9	567	4	BU970400	BU970400 HB14I11r	1377	131.5	5.9	954	6	CNS08N1W	BN019908 Single re
1305	131.5	5.9	567	4	BU971896	BU971896 HB19P23r	1378	131.5	5.9	969	6	AY383694	AY383694 Rattus no
cl306	131.5	5.9	576	17	CL651500	CL651500 PRI0112b-	1379	131.5	5.9	986	6	CNS08GHQ	BN010794 Single re
1307	131.5	5.9	577	4	BU988097	BU988097 HF16K13r	1380	131.5	5.9	1128	19	AG139608	AG139608 Pan trogl
1308	131.5	5.9	581	4	BU971635	BU971635 HB19D11r	1381	131.5	5.9	1279	12	DY263081	DY263081 IC0AAA10D
1309	131.5	5.9	582	4	BU988569	BU988569 HF18A11r	cl382	131	5.9	477	5	CA743784	CA743784 wrils.pk0
1310	131.5	5.9	584	4	BU988716	BU988716 HF18H18r	1383	131	5.9	486	4	BU971530	BU971530 HB17O13r
1311	131.5	5.9	588	9	CJ632047	CJ632047 CJ632047	1384	131	5.9	509	8	CD899086	CD899086 G174.111A
1312	131.5	5.9	590	4	BU966995	BU966995 HB02P24r	1385	131	5.9	512	8	CB931796	CB931796 ri63c08.Y
1313	131.5	5.9	590	4	BU990186	BU990186 HF24F09r	1386	131	5.9	526	8	CD908608	CD908608 G468.110G



1387	131	5.9	570	4	BU970459	BU970459 HB14L08r
1388	131	5.9	583	4	BU968659	BU968659 HB08D04r
1389	131	5.9	605	4	BQ244707	BQ244707 TaE15038F
1390	131	5.9	611	4	BQ472392	BQ472392 HB09M02T
1391	131	5.9	617	5	CA558994	CA558994 K0252G03-
1392	131	5.9	640	2	BE427257	BE427257 PSRG6175 I
1393	131	5.9	642	2	BE194902	BE194902 HVSMEh008
1394	131	5.9	652	8	CB619065	CB619065 OSIEa03G
1395	131	5.9	654	2	BG467984	BG467984 Na_L4_02C
1396	131	5.9	663	4	BQ605715	BQ605715 BR_1243
1397	131	5.9	687	5	BW427333	BW427333 BW427333
1398	131	5.9	688	5	BW427326	BW427326 BW427326
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1400	131	5.9	707	9	CJ633221	CJ633221 CJ633221
1401	131	5.9	709	12	DW204365	DW204365 EST20629
1402	131	5.9	718	8	CF387722	CF387722 RTDR1_19
1403	131	5.9	726	13	DR434535	DR434535 ACAE-aaa4
1404	131	5.9	743	12	EB616995	EB616995 AGENCOURT
c1405	131	5.9	745	5	BW713288	BW713288 BW713288
	131	5.9	762	8	CB677339	CB677339 OSJNEe14C
1406	131	5.9	770	13	DR723203	DR723203 AGENCOURT
1407	131	5.9	771	12	EB076755	EB076755 TverSEQ78
1408	131	5.9	774	12	EB616819	EB616819 AGENCOURT
1409	131	5.9	778	4	BQ807225	BQ807225 WHE3588 C
1410	131	5.9	779	4	BQ838790	BQ838790 WHE3592_G
1411	131	5.9	789	18	DX951709	DX951709 CHORI105-
c1412	131	5.9	793	5	BW719413	BW719413 BW719413
c1413	131	5.9	794	5	BW718665	BW718665 BW718665
c1414	131	5.9	827	4	BQ838774	BQ838774 WHE3592_E
1415	131	5.9	838	16	BZ987860	BZ987860 PUGGF95TB
1416	131	5.9	845	9	CK663255	CK663255 A374 Apos
1418	131	5.9	868	12	EB627899	EB627899 AGENCOURT
1419	131	5.9	883	2	BE870352	BE870352 601447518
1420	131	5.9	976	2	BE196246	BE196246 HVSMEh009
1421	131	5.9	1018	2	BG821611	BG821611 602727614
1422	131	5.9	1028	12	DW635463	DW635463 CLJ364-I1
1423	131	5.9	1034	6	CNS090VH	BX037209 Single re
1424	131	5.9	1078	19	CNS06QG9	AL410623 T3 end of
1425	131	5.9	1129	9	CK206308	CK206308 FGAS01789
c1426	131	5.9	1265	13	DN662920	DN662920 CFW100-H0
1427	131	5.9	1532	6	AK089188	AK089188 Mus muscu
1428	131	5.9	6320	6	AF161390	AF161390 Homo sapi
1429	130.5	5.9	416	4	BU988249	BU988249 HF17B17r
1430	130.5	5.9	470	8	CB883713	CB883713 HB19D07r
1431	130.5	5.9	488	4	BQ244869	BQ244869 TaE15034C
1432	130.5	5.9	492	4	BU974826	BU974826 HB29D19r
1433	130.5	5.9	504	4	BU985135	BU985135 HF06D21r
1434	130.5	5.9	511	2	BE602853	BE602853 HVSMEh010
1435	130.5	5.9	518	2	BE423417	BE423417 WHE0065 H
1436	130.5	5.9	543	2	BE402547	BE402547 CSB009B01
1437	130.5	5.9	543	4	BQ608053	BQ608053 BRY_3954
1438	130.5	5.9	545	5	CA734305	CA734305 wde2f.pk0
1439	130.5	5.9	548	17	CL674970	CL674970 PRI0113c_
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1442	130.5	5.9	575	4	BU987892	BU987892 HF16B01r
1443	130.5	5.9	624	8	CD890355	CD890355 G118.114H
1444	130.5	5.9	625	4	BQ239521	BQ239521 TaE05029H
1445	130.5	5.9	626	5	CA727076	CA727076 wde1f.pk0
1446	130.5	5.9	627	5	CA726894	CA726894 wde1f.pk0
1447	130.5	5.9	638	8	CB883716	CB883716 HB22G04r
1448	130.5	5.9	640	2	BE193957	BE193957 HVSMEh008
1449	130.5	5.9	668	4	BQ245771	BQ245771 TaE15020B
1450	130.5	5.9	670	4	BQ239891	BQ239891 TaE05025E
1451	130.5	5.9	675	4	BQ246774	BQ246774 TaE15005F
c1452	130.5	5.9	679	5	BW694564	BW694564 BW694564
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1454	130.5	5.9	715	2	BE601931	BE601931 HVSMEh010
1455	130.5	5.9	715	2	BE602228	BE602228 HVSMEh009
1456	130.5	5.9	715	3	BM640342	BM640342 170006876
c1457	130.5	5.9	716	3	BJ985194	BJ985194 BJ985194
1458	130.5	5.9	769	13	DT058624	DT058624 AGENCOURT
1459	130.5	5.9	794	4	BU523226	BU523226 AGENCOURT

1460	130.5	5.9	826	12	DW228724	DW228724 GH_ONEFM_
1461	130.5	5.9	834	2	BE194417	BE194417 HVSMEh008
1462	130.5	5.9	864	12	EE029126	EE029126 LscSEQ98
1463	130.5	5.9	895	12	DW243137	DW243137 GH_TSnorm
1464	130.5	5.9	901	12	EB022095	EB022095 LscSEQ14
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1468	130.5	5.9	924	4	BQ956745	BQ956745 AGENCOURT
1469	130.5	5.9	988	2	BF585024	BF585024 602098925
1470	130.5	5.9	1029	2	BF584192	BF584192 602096332
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c1473	130.5	5.9	1416	13	DN662502	DN662502 CFW09-D04
1474	130.5	5.9	1536	19	DQ035260	DQ035260 Pan trogl
1475	130	5.9	420	1	AJ485890	AJ485890 AJ485890
1476	130	5.9	420	4	BU038466	BU038466 DH11901 H
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1478	130	5.9	458	4	BU974698	BU974698 HB28N01r
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1484	130	5.9	509	4	BU972320	BU972320 HB21F02r
1485	130	5.9	515	4	BU987066	BU987066 HF13L08r
1486	130	5.9	517	5	CA557386	CA557386 K0226G06-
1487	130	5.9	521	4	BU975959	BU975959 HB32N07r
1488	130	5.9	527	4	BU975122	BU975122 HB30C15r
1489	130	5.9	528	5	CA556251	CA556251 K0209C08-
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1492	130	5.9	530	5	CA556136	CA556136 K0207F09-
1493	130	5.9	531	5	CA557753	CA557753 K0232D05-
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1496	130	5.9	533	5	CA556576	CA556576 K0213H11-
1497	130	5.9	533	5	CA559665	CA559665 K0261G07-
1498	130	5.9	534	5	CA557474	CA557474 K0228A05-
1499	130	5.9	534	8	CF174139	CF174139 B0934E08-
1500	130	5.9	536	4	BU972749	BU972749 HB22J17r

ALIGNMENTS

RESULT 1	AY401136	1296 bp	DNA	linear	GSS 12-DEC-2003
LOCUS	AY401136				
DEFINITION	Homo sapiens HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY401136				
VERSION	AY401136.1				GI:39757125
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1296)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1296)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .1296

gene /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" <1.->1296 /locus\_tag="HCM0790"

ORIGIN

Alignment Scores:

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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	19	Gaps:	0

US-09-944-929-83 (1-431) x AY401136 (1-1296)

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QY 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100

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Db 1201 CTCGTCCTCTGGGTAGAAATCCTCTCGGAATCACTCCGAGGAAACGTTACTCAAGACTG 1260

QY 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431

Db 1261 GATTATTTGATCAATGGGATCTATGTGGACATC 1293

RESULT 2

AY401137 1296 bp DNA linear GSS 12-DEC-2003

LOCUS Pan troglodytes HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

DEFINITION

AY401137 GI:39757126

VERSION

AY401137.1

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Pan.

REFERENCE

1 (bases 1 to 1296)

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL

Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

2 (bases 1 to 1296)

AUTHORS

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE

Direct Submission

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT

This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers

source 1. .1296 /organism="Pan troglodytes"





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ORIGIN																																																					
Alignment Scores:		3.5e-175		Length:		4613																																															
Pred. No.:		2111.00		Matches:		411																																															
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Best Local Similarity:		95.5%		Indels:		0																																															
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DB:																																																					
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Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp	40																																																		
Db	340	CTAAGGCTGTCTGCTAGTCAGGATTGCCTCAACAAGAGCTAGAAGATGTTGTCAATTGAC	399																																																		
Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60																																																		
Db	400	ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCATATATACTTCAACTCAA	459																																																		
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Db	460	GAAGACTGCATTAATTCCTGCTGTTCAACAAAACATATCAGGGGACAAAGCATGTAAC	519																																																		
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Db	520	TTGATGATCTTCGACACTCGAAAAACAGCTAGACACCCCAACTGCTACCTATTTTCTGT	579																																																		
Qy	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120																																																		
Db	580	CCCGATGAGGAAGCCTGTCCATTGAGACCAGCAAAAGGACTTATGAGTTACAGGATAATT	639																																																		
Qy	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140																																																		
Db	640	AGAGATTTTCCATCTTTGACCAGAAATTTGTCAAGCCCAAGAGTTACCCCGAGGAGATTCT	699																																																		
Qy	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160																																																		
Db	700	CTCTTACATGGCCAATTTTACCAGCAGTCACCTCCCTAGCCCATCATCACAGATTAT	759																																																		
Qy	161	SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp	180																																																		
Db	760	TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT	819																																																		
Qy	181	HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu	200																																																		
Db	820	CACCTGGAGAAACTATTTAAGATGGACGAAGCAAGTGCCCGAGCTCCTTGCTTATAAGGAA	879																																																		
Qy	201	LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro	220																																																		
Db	880	AAAGGCCATTCTCAGAGTTACAGTTTTCCTCTGTATCAAGAAACGGCTCATCTGCTGCCT	939																																																		
Qy	221	GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla	240																																																		

Db	940	GAAAAATGTGAGTGCAATTCCTAGCTACGGTGGCAGTTGCTTCTCCACATACCACTCAGCT	999
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Db	1000	ACTCCAAAGCCCAACCACTTTTACCCAGCAATGCTTCAGTGACACCTTCTGGGACTTCC	105
Qy	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280
Db	1060	CAGCCACAGCTGGCCACCAACAGCTCCACCTGTAAACCACTGTCACTTCTCAGCCTCCACA	111
Qy	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
Db	1120	ACCTCATTTCTACAGTTTTTACACGGGCTATGGCTACACTCCAAGCAATGGCTACAACA	117
Qy	301	AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320
Db	1180	GCAGTTCTGACTACCACTTTTACGGCACCTACGGACTCGAAAGGCAGCCTAGGAACGATA	123
Qy	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
Db	1240	CCATTACAGAGACCTCCAACCTAACTTTGAACACAGGGAATGTATATAACCTTACTGCA	129
Qy	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg	360
Db	1300	CTTCTATGTCAAATGAGGAGTCTTCCACTATGAATAAAACTGCTCCCTGGGAAGTAGG	135
Qy	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1360	GAGCCAGTCCAGGCAGTTCCTCCAGGGCAGGGTTCCAGAAATCAGTATGGCCTTCCA	141
Qy	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1420	TTTGAAAAAGTGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTGTTCTGTGATAGGC	147
Qy	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu	420
Db	1480	CTCATCTCTCTGGGTAGAAATCCTCTCGGAATCACTCCGCAGGAACGTTACTCAAGACTG	153
Qy	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
Db	1540	GATTATTGATCAATGGGATCTATGTGGACATC	1572
RESULT 4			
CR621081	1965 bp mRNA linear HTC 21-JUL-2000		
LOCUS	full-length cDNA clone CSODI054YH07 of Placenta Cot 25-normalized		
DEFINITION	of Homo sapiens (human).		
ACCESSION	CR621081		
VERSION	CR621081.1 GI:50501888		
KEYWORDS	HTC; CNSLT cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;		
	Carrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 1965)		
AUTHORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished		
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue		
REFERENCE	2 (bases 1 to 1965)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr		
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prim end enriched, double-strand cDNA was digested with Not I and clone into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.		

Db	940	GAATAATGTGAGTGCAATTCCTAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCAGCT	999
Qy	241	ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer	260
Db	1000	ACTCCAAAGCCCAACACCCCTTTTACCAGCAATGCTTCAGTGACACCTTCTGGGACTTCC	1059
Qy	261	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr	280
Db	1060	CAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACCTGTCACCTTCTCAGCCTCCACA	1119
Qy	281	ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr	300
Db	1120	ACCCTCATTTCTACAGTTTTTTACACGGGCTATGGCTACACTCCAAGCAATGGCTACAACA	1179
Qy	301	AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle	320
Db	1180	GCAGTTCTGACTACCACTTTTCAGGCACCTACGGACTCGAAAGGCAGCCTAGGAACGATA	1239
Qy	321	ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla	340
Db	1240	CCATTTACAGAGACCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCCTACTGCA	1299
Qy	341	LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg	360
Db	1300	CTTTCTATGTCAAATGAGGAGTCTTCCACTATGAATAAACTGCTCCCTGGGAAGGTAGG	1359
Qy	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1360	GAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGGGTTCCAGAAATCAGTATGGCCTTCCA	1419
Qy	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1420	TTTGAAAAGTGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTCTTCTCTGCTGATAGGC	1479
Qy	401	LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu	420
Db	1480	CTCATCTCTCTGGGTAGAAATCCTCTCGGAATCACTCCGCAGGAAACGTTTACTCAAGACTG	1539
Qy	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
Db	1540	GATTATTGATCAATGGGATCTATGTGGACATC	1572
RESULT 4			
CR621081			
LOCUS		1965 bp mRNA linear HTC 21-JUL-2004	
DEFINITION			
full-length cDNA clone CS0DI054YH07 of Placenta Cot 25-normalized			
of Homo sapiens (human).			
ACCESSION		CR621081	
VERSION		CR621081.1 GI:50501888	
KEYWORDS		HTC; CNSLT CDNA.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;			
Catarrhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 1965)	
AUTHORS		Li,W.B., Gruber,C., Jessee,J. and Polayes,D.	
TITLE		Full-length cDNA libraries and normalization	
JOURNAL		Unpublished	
REMARK		Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue	
REFERENCE		2 (bases 1 to 1965)	
AUTHORS		Genoscope.	
TITLE		Direct Submission	
JOURNAL		Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr	
COMMENT		- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primed end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	

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Best Local Similarity:	100.0%	Mismatches: 0
Query Match:	82.8%	Indels: 0
DB:	6	Gaps: 0
US-09-944-929-83 (1-431) x CR621081 (1-1965)		
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Db	147	GGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTAGACAAACCAAC 206
QY	95	CysTyrLeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeu 114
Db	207	TGCTACCTATTTTCTGTCCCAACGAGGAGCCTGTCCATTGAAACCAGCAAAAGGACTT 266
QY	115	MetSerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSerGlnGlu 134
Db	267	ATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGCCAAGAG 326
QY	135	LeuProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAla 154
Db	327	TTACCCCGAGGAAGATTCTCTTTACATGGCCAAATTTTCAAGCAGTCACTCCCTAGCC 386
QY	155	HisHisHisThrAspTyrSerLysProThrAspIleSerTyrArgAspThrLeuSerGln 174
Db	387	CATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAG 446
QY	175	LysPheGlySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGln 194
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QY	195	LeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGlu 214
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QY	215	IleAlaHisLeuLeuProGluAsnValSerAlaLeuProAlaThrValAlaValAlaSer 234
Db	567	ATAGTTCATCTGCTGCTGAAATGTGAGTGGCTCCAGCTACGGTGGCAGTTGCTTCT 626
QY	235	ProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerVal 254
Db	627	CCACATACCACCTCGGCTACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTG 686
QY	255	ThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThrThrVal 274
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QY	275	ThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeu 294
Db	747	ACTTCTCAGCCTCCACGACCCTCATTCTACAGTTTTTACAGGGCTGGGGCTACACTC 806
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Db	807	CAAGCAATGGCTACAAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAA 866
QY	315	GlySerLeuGluThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsn 334
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Db	927	GTGTATAACCTACTGCACCTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACT 986
QY	355	AlaSerTrpGluGlyArgGluAlaSerProGlySerSerGlnGlySerValProGlu 374
Db	987	GCTTCTGGGAAGGTAGGGAGGCCAGTCCAGCAGTTCTCTCCAGGGCAGTGTTCAGAA 1046
QY	375	AsnGlnTyrGlyLeuPropheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyVal 394
Db	1047	AATCAGTACGGCCTTCCATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTGGTGTC 1106
QY	395	LeuPheLeuValIleGlyLeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArg 414
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LOCUS		
DEFINITION		
clone CS0DI054YH07 3-PRIME, mRNA sequence.		
ACCESSION		
VERSION		
KEYWORDS		
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REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
Contact: Genoscope		
Genoscope - Centre National de Sequencage		
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6656.r		
For more information about this cluster, see		
http://www.genoscope.cns.fr/cdna?s=CS0BAI023A03_CS02129_1&c=6656.r		
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
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Pred. No.:	8.5e-112	Length: 884
Score:	1383.00	Matches: 283
Percent Similarity:	97.3%	Conservative: 1
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Query Match:	62.6%	Indels: 3
DB:	5	Gaps: 0
US-09-944-929-83 (1-431) x BX350141 (1-884)		

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QY 165 AspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLys 184
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QY 245 AlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnProGlnLeu 264
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5', mRNA sequence.
ACCESSION BQ424639
VERSION BQ424639.1 GI:21119954
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 853)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13509 row: d column: 14
High quality sequence stop: 735.
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Average insert size 2 kb. Library constructed by Life
Technologies."
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ORIGIN

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Db 437 CAAGAAATAGCTCATCTGCTGCCTGAAATGTAGTGGCTCCAGCTACGGTGGCAGTT 496
QY 233 AlaSerProHisThrThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAla 252
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Qy	273	ThrValThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAla	292
Db	617	ACTGTCACTTCTCAGCTCCACGACCTCATTTCTACAGTTTTCACACGGCTGCGGCT	676
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Qy	313	SerLysGlySerLeuGluThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThr	332
Db	737	TCGAAAGGCAGCTTAGAAACCATACCGTTTACAGAAATCTCCCACTTAACCTTTGAACACA	796
Qy	333	-GlyAsnValTyrAsn-ProThrAlaLeuSerMetSerAsnVal	346
Db	797	GGGGAATGTATACCCCTACTGCACCTTCTATGTCAAATGTG	840
RESULT 7			
AL525434			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
On Feb 13, 2001 this sequence version replaced gi:31063298.			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen. This sequence belongs to sequence cluster			
6656.r			
For more information about this cluster, see			
http://www.genoscope.cns.fr/cdna?s=CS0DC011AD04QP1&c=6656.r.			
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primer. Five prime end enriched, double-strand cDNA was			
digested with Not I and cloned into the Not I and EcoR V			
sites of the pCMVSPORT 6 vector. Library was normalized."			
ORIGIN			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			

DB:	1	Gaps:	1
US-09-944-929-83 (1-431) x AL525434 (1-1050)			
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Qy	21	LeuArgLeuSerAlaSerGlnAsnCysLeuLysSerLeuGluAspValValIleAsp	40
Db	308	CTAAGGCTGTCTGTAGTCAGAAATGCCTCAAAAAGAGTCTAGAAGATGTTGTCTATTGAC	367
Qy	41	IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	60
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Qy	61	GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	80
Db	428	GAAGACTGCATTAATTCTTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTYAC	487
Qy	81	LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys	100
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Qy	101	ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle	120
Db	548	CCCAACGAGGAAGCCTGTTCATTGAAACCCAGCAAAAGGACTTATGAGTTACAGGATAATT	607
Qy	121	ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer	140
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Qy	141	LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr	160
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Qy	220	oGluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAl	240
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Qy	240	aThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSe	260
Db	966	YWATGCMAARCCSGCAMCCTTYYTACCMM---CAATGCTTAGTGAMACCTYYTGGACTYCM	1022
Qy	260	rGln	261
Db	1023	RCAA	1026
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ACCESSION			
AY401138			
VERSION			
AY401138.1 GI:39757127			
KEYWORDS			
GSS.			
SOURCE			
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ORGANISM			
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.			

REFERENCE 1 (bases 1 to 1245)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1245)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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DB: 19 Gaps: 6  
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DEFINITION AK171842  
ACCESSION AK171842.1 GI:74178910  
VERSION AK171842.1  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
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REFERENCE 1  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 10349636  
REFERENCE 2

AUTHORS  TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159 3	TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12456851 6
AUTHORS  TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861 4	TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12456851 6
AUTHORS  TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y. RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 11217851 5	TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12456851 6
AUTHORS  TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kwasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Naltas,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y. FANTOM Consortium; RIKEN Genome Exploration Research Group Phase I & II Team	TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12456851 6
AUTHORS  TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Georgii-Hemming,P., Gingeras,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Gustincich,S., Harbers,M., Hayashida,Y., Ikeo,K., Iwama,A., Ishikawa,T., Hill,D., Hummichek,L., Iacono,M., Ikeo,K., Iwama,A., Kitamura,H., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavese,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Sempile,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiuira,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessey,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y. FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group) The transcriptional landscape of the mammalian genome Science 309 (5740), 1559-1563 (2005) 16141072 7	TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12456851 6
AUTHORS  TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C. RIKEN Genome Exploration Research Group; Genome Science Group (Genome Network Project Core Group); FANTOM Consortium Antisense transcription in the mammalian transcriptome Science 309 (5740), 1564-1566 (2005) 16141073 8 (bases 1 to 2284)	TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12456851 6
AUTHORS  TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp)	TITLE  JOURNAL PUBMED REFERENCE  AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420 (6915), 563-573 (2002) 12456851 6



URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>

COMMENT

FEATURES

source

1. .2284  
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CDS

Alignment Scores:

Pred. No.: 8.17e-93 Length: 2284  
Score: 1176.50 Matches: 258  
Percent Similarity: 68.9% Conservative: 39  
Best Local Similarity: 59.9% Mismatches: 117  
Query Match: 53.2% Indels: 17  
DB: 6 Gaps: 6

US-09-944-929-83 (1-431) x AK171842 (1-2284)

Qy 1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20  
Db 288 ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTGCTGGTTCATTTCTTCCTGACA 344  
Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40  
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Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
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Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140

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Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
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Qy 421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431  
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RESULT 10

AK033526

LOCUS

DEFINITION

AK033526 2235 bp mRNA linear HTC 02-SEP-2005  
Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030601P12 product:weakly similar to NT2RMI001115  
PROTEIN (Homo sapiens), full insert sequence.

ACCESSION

AK033526

VERSION

AK033526.1 GI:26329204

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus



Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
KatoH., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,  
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,  
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.

Direct Submission

TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.jp,  
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.

FEATURES

source

1. .2235  
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CDS

Alignment Scores:

Pred. No.: 9.14e-92 Length: 2235  
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Best Local Similarity: 59.9% Mismatches: 119  
Query Match: 52.7% Indels: 17  
DB: 6 Gaps: 6

US-09-944-929-83 (1-431) x AK033526 (1-2235)

Qy 1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20  
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Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
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Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerGluArgLysArgTyrSerArgLeu 420  
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Db 1492 GACTACTTGTATCAACGGGATCTATGTTGACATC 1524

RESULT 11  
AK018635



LOCUS AK018635 2265 bp mRNA linear HTC 02-SEP-2005  
DEFINITION Mus musculus adult male cecum cdNA, RIKEN full-length enriched library, clone:9130017N16 product:weakly similar to NT2RM1001115 PROTEIN [Homo sapiens], full insert sequence.  
ACCESSION AK018635  
VERSION AK018635.1 GI:12858442  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
PUBMED 11076861  
REFERENCE 4  
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bernaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.  
RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium  
FUNCTIONAL annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409 (6821), 685-690 (2001)  
PUBMED 11217851  
REFERENCE 5  
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

CONSRSTM  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420 (6915), 563-573 (2002)  
PUBMED 12466851  
REFERENCE 6  
AUTHORS Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Humnieceki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakouchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavese,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Sempile,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiuira,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.  
FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group)  
The transcriptional landscape of the mammalian genome  
JOURNAL Science 309 (5740), 1559-1563 (2005)  
PUBMED 16141072  
REFERENCE 7  
AUTHORS Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

CONSRMT RIKEN Genome Exploration Research Group; Genome Science Group  
(Genome Network Project Core Group); FANTOM Consortium  
TITLE Antisense transcription in the mammalian transcriptome  
JOURNAL Science 309 (5740), 1564-1566 (2005)  
PUBMED 16141073  
REFERENCE 8 (bases 1 to 2265)  
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,  
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,  
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,  
Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,  
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,  
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,  
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,  
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,  
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,  
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,  
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
Direct Submission  
TITLE Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
JOURNAL Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,  
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.jp/  
URL:http://fantom.gsc.riken.jp/.  
FEATURES  
source  
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/codon\_start=1  
/protein\_id="BAB31319.1"  
CDS  
Alignment Scores:  
Pred. No.: 9.34e-92 Length: 2265  
Score: 1164.50 Matches: 258  
Percent Similarity: 68.4% Conservative: 37  
Best Local Similarity: 59.9% Mismatches: 119  
Query Match: 52.7% Indels: 17  
DB: 6 Gaps: 6  
US-09-944-929-83 (1-431) x AK018635 (1-2265)  
Qy 1 MetPheGlyGlyGluGlySerLeuThrTyrThrLeuValIleCysPheLeuThr 20  
Db 262 ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTGCTGCTCATTTCTCTCTGACA 318  
Qy 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValIleAsp 40  
Db 319 CCAAGGTGCTGCTGGTCAGAACTGCCTCACCAGAGTCTAGAAGACGTTGTCATTGAC 378

Qy 41 ileGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60  
Db 379 AFCCAATCGTCGCTTTCAAAGGCATTCGAGGCAATGAGCCCATACACTTGGCAACTCAG 438  
Qy 61 GluAspCysIleAsnSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80  
Db 439 GAAGACTGTATCGGTGCCTGCTGTTCAACAAAGACATAGCAGGGGACAGGCATGTAAT 498  
Qy 81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  
Db 499 TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACTGTTTCTGT 558  
Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120  
Db 559 CCCAGCAGGATGCCTGTCGCTGAAGCCAGCCAAAGGCGCTTGTGACCTACAGGCTCATC 618  
Qy 121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140  
Db 619 AGAGATTTTCGCTGACCAGCGCTAATTCATCCTCCACAGTTAACACAGGAGAGGTTT 678  
Qy 141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyr 160  
Db 679 CTCTTACTTGACCATTCGTCACCCAGGAGCCACCCCTGGGTTTCGTACCCACGAGGTTAC 738  
Qy 161 SerLysProThrAspIleSerTyrArgAspThrLeuSerGlnLysPheGlySerSerAsp 180  
Db 739 CCAAAGCCACCGGCTGTCTTGGAGTGACAGATCTTCTCTGAAGTCCACAGCCCCCTGT 798  
Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  
Db 799 CACTTGCGCAAAACACATCAAGGCTGATGAACAAAGCATGCAGCTC-----CCTGAAGAA 852  
Qy 201 LysGlyHisSerGlnSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220  
Db 853 AAAAGCCATTCAGAGTTTACAGCTTCCCTCAGAACTAAAAATGGCTCATCTGCTCCCT 912  
Qy 221 GluAsnValSerAlaLeuProAlaThrValAlaAlaValAlaSerProHisThrThrSerAla 240  
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Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260  
Db 973 ACCCTGAAGCCTGAGCTTCTGTGTG---ACCAGCATTTTCAGTGACAGCTTAAGACTTTGAAG 1029  
Qy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280  
Db 1030 CAGAAGGAG--GCCACCACAGCATCACCTGTCTCACCACCGTGACCTCGAAGTCCCCAGGA 1086  
Qy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300  
Db 1087 GTCCCCAGGGTCTACAAGTTTTTACA-----CCCCGTGGTTTACACATCAG 1128  
Qy 301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320  
Db 1129 GCAGCTTTGACTAACACCTTTTCAGGCACATACAGACTCCAAAGGCATCTTAGAAACAATG 1188  
Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340  
Db 1189 CCCTTTCAAGGAGGCTCTACGCTGACT-----TCAGACCCGAGGCAC 1230  
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Qy 361 GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  
Db 1291 AGGGTCAGTGTAGGCAGCGCATCGCTGAACAAGGGTCCAAAAGCCAGCATGGCCTTCA 1350  
Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  
Db 1351 TTTGAGAAAGTGGCTTCTCATTTGGGACCCCTCTTGTGGTGTGTTTGTCTGTTAATAGGT 1410  
Qy 401 LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgLysArgTyrSerArgLeu 420

Db	1411	CTCGTCTCTTGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAACGGTATTCAAGACTT	1470	
QY	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431	
Db	1471	GACTACTTGATCAACGGGATCTATGTTGACATC	1503	
RESULT 12				
AK046837				
LOCUS				
DEFINITION	AK046837 2265 bp mRNA linear HTC 02-SEP-2005			
	Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN			
	full-length enriched library, clone:B830022E21 product:weakly			
	similar to NT2RM1001115 PROTEIN [Homo sapiens], full insert			
	sequence.			
ACCESSION	AK046837			
VERSION	AK046837.1 GI:26338441			
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			
	Sciurognathi; Muroidea; Muridae; Murinae; Mus.			
REFERENCE	1			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,			
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
	Normalization and subtraction of cap-trapper-selected cDNAs to			
	prepare full-length cDNA libraries for rapid discovery of new genes			
	Genome Res. 10 (10), 1617-1630 (2000)			
JOURNAL	11042159			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,			
	Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,			
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,			
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,			
	Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,			
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,			
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
	RIKEN integrated sequence analysis (RISA) system--384-format			
	sequencing pipeline with 384 multicapillary sequencer			
	Genome Res. 10 (11), 1757-1771 (2000)			
JOURNAL	11076861			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,			
	Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,			
	Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,			
	Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,			
	Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,			
	Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,			
	Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,			
	Quackenbush, J., Schriml, L.M., Staabli, F., Suzuki, R., Tomita, M.,			
	Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,			
	Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,			
	Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,			
	Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,			
	Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,			
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	Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,			
	Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,			
	Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S.			
	and Hayashizaki, Y.			
CONSRMT	RIKEN Genome Exploration Research Group Phase II Team and the			
	FANTOM Consortium			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409 (6821), 685-690 (2001)			
PUBMED	11217851			
REFERENCE	5			
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,			





QY	361	GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro	380
Db	1289	AGGTGAGTGTAGGCAGCGCATCGCTGAACAAGGGTCCAAAAGCCAGCATGGCCTTTCA	1348
QY	381	PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly	400
Db	1349	TTTGAGAAAGTGGCTTCTCATTTGGGACCCCTCCTTTGTTGGTGTGTTTGTCTTCTGGTAATAGGT	1408
QY	401	LeuValLeuLeuGlyVArgIleLeuSerGluSerLeuArgArgGlySArgTyrSerArgLeu	420
Db	1409	CTCGTCTCTTTGGGTAGGATGCTGTTGAAGCCCTCCGTAGGAACGGTATTCAAGACTT	1468
QY	421	AspTyrLeuIleAsnGlyIleTyrValAspIle	431
Db	1469	GACTACTTGATCAACGGGATCTATGTTGACATC	1501
RESULT	13		
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LOCUS	AK018660	2286 bp mRNA linear	HTC 02-SEP-2005
DEFINITION	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130403P13 product:weakly similar to NT2RMI001115		
ACCESSION	AK018660		
VERSION	AK018660.1	GI:12858477	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.		
	1		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S.		

CONSRTM	and Hayashizaki, Y.		
	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
PUBMED	11217851		
REFERENCE	5		
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.		
CONSRTM	FANTOM Consortium; RIKEN Genome Exploration Research Group Phase I & II Team		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420 (6915), 563-573 (2002)		
PUBMED	12466851		
REFERENCE	6		
AUTHORS	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E., Ambesi-Impiombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Humnietcki, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempile, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiuira, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M.,		

Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.  
FANTOM Consortium; RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group)  
The transcriptional landscape of the mammalian genome  
Science 309 (5740), 1559-1563 (2005)  
16141072

CONSRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

RIKEN Genome Exploration Research Group; Genome Science Group (Genome Network Project Core Group); FANTOM Consortium  
Antisense transcription in the mammalian transcriptome  
Science 309 (5740), 1564-1566 (2005)  
16141073

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AUTHORS

8 (bases 1 to 2286)  
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/  
URL:http://fantom.gsc.riken.jp/.

FEATURES  
source

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CDS

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Score:		68.4%	Conservative:	37
Percent Similarity:		59.9%	Mismatches:	119
Best Local Similarity:		52.7%	Indels:	17
Query Match:		6	Gaps:	6
DB:				
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Db	284	ATGCTCTTCAGGGGAACC---AGCTTGGCTTACTCGTTGCTGATTCCTTCCTGACA	340	
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